European Cooperative Programme for Crop Genetic Resources Networks
ECP/GR

Cereal Genetic Resources in Europe

IPGRI

Report of a Cereals Network
First Meeting, 3-5 July 2003, Yerevan, Armenia

Report of a Working Group on Wheat
Second Meeting, 22-24 September 2005, La Rochelle, France

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FUTURE HARVEST

IPGRI is a Future Harvest Centre supported by the Consultative Group on International Agricultural Research (CGIAR)

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The International Plant Genetic Resources Institute (IPGRI) is an independent international scientific organization that seeks to improve the well-being of present and future generations of people by enhancing conservation and the deployment of agricultural biodiversity on farms and in forests. It is one of 15 Future Harvest Centres supported by the Consultative Group on International Agricultural Research (CGIAR), an association of public and private members who support efforts to mobilize cutting-edge science to reduce hunger and poverty, improve human nutrition and health, and protect the environment. IPGRI has its headquarters in Maccarese, near Rome, Italy, with offices in more than 20 other countries worldwide. The Institute operates through four programmes: Diversity for Livelihoods, Understanding and Managing Biodiversity, Global Partnerships, and Improving Livelihoods in Commodity-based Systems.

The international status of IPGRI is conferred under an Establishment Agreement which, by January 2005, had been signed by the Governments of Algeria, Australia, Belgium, Benin, Bolivia, Brazil, Burkina Faso, Cameroon, Chile, China, Congo, Costa Rica, Côte d'Ivoire, Cyprus, Czech Republic, Denmark, Ecuador, Egypt, Greece, Guinea, Hungary, India, Indonesia, Iran, Israel, Italy, Jordan, Kenya, Malaysia, Mauritania, Morocco, Norway, Pakistan, Panama, Peru, Poland, Portugal, Romania, Russia, Senegal, Slovakia, Sudan, Switzerland, Syria, Tunisia, Turkey, Uganda and Ukraine.

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The European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR) is a collaborative programme among most European countries aimed at facilitating the long-term conservation and the increased utilization of plant genetic resources in Europe. The Programme, which is entirely financed by the member countries and is coordinated by IPGRI, is overseen by a Steering Committee composed of National Coordinators nominated by the participating countries and a number of relevant international bodies. The Programme operates through nine networks in which activities are carried out through a number of permanent working groups or through *ad hoc* actions. The ECP/GR networks deal with either groups of crops (cereals; forages; fruit; oil and protein crops; sugar, starch and fibre crops; vegetables, medicinal and aromatic plants) or general themes related to plant genetic resources (documentation and information; *in situ* and on-farm conservation; inter-regional cooperation). Members of the working groups and other scientists from participating countries carry out an agreed workplan with their own resources as inputs in kind to the Programme.

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REPORT OF A CEREALS NETWORK

First Meeting, 3-5 July 2003, Yerevan, Armenia

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PART I. SUMMARY OF THE MEETING

Introduction

Opening and welcome

The first meeting of the ECP/GR Cereals Network was opened by Lorenzo Maggioni, the ECP/GR Coordinator, who welcomed the representatives from 32 countries. Among these, it was a pleasure to also welcome observers from Georgia, Latvia, Morocco, the Russian Federation and Ukraine, as well as a representative from FAO. Jan Konopka, documentation specialist from ICARDA (International Center for Agricultural Research in the Dry Areas), was also invited to the meeting and expressed interest in participating, but was unable to attend.

It was noted that it was the first time an ECP/GR meeting was held in Armenia and this would be a great opportunity to visit the protected sites where several wild relatives of cereal crops were growing.

Thanks were extended to the local organizers from the Armenian Ministry of Agriculture for the tremendous effort made to ensure a smooth and effective meeting.

Welcome by the Minister of Agriculture

David Lokyan, Minister of Agriculture, addressed the guests of this meeting by welcoming everybody to this ancient land.

As it is known, Armenia is part of Western Asia, a centre of origin for a great number of crops and has developed agriculture since ancient times, despite harsh soil and climatic conditions. Therefore, it was a remarkable event that the Cereals Network Meeting was being held in Armenia, a country distinguished by rich plant biodiversity and where activities on genetic resources conservation and sustainable use were of vital importance.

Plant genetic resources have a global importance and should not be considered as the property of a specific country. Consequently, it is reasonable and appropriate that conservation and sustainable use be implemented with a joint effort.

The Minister underlined the significance of the activities undertaken by the International Plant Genetic Resources Institute (IPGRI) in the field of genetic resources conservation, in favour of food security and poverty reduction.

This meeting, which was gathering 46 specialists representing 32 countries, will certainly facilitate exchange of experience and closer collaboration between Armenia and other countries.

Once again, D. Lokyan greeted all the participants and wished them a productive meeting.

Collaboration with IPGRI in Armenia - main aims and achievements

Levon Rukhkyan, Deputy Minister of Agriculture and National Coordinator for plant genetic resources in Armenia, expressed his great pleasure to welcome all the participants to the hospitable land of Armenia and wished the meeting to be intensive and fruitful.

It is well known that Armenia is the country of origin for a great number of cultivated plants, which are of enormous importance not only on a regional but also on a world scale. For over 6000 years, the extremely rich plant resources of this country were used for food and fodder, medicine and timber. The Armenian Plateau is one of the regions where the agriculture originated since the dawn of civilization and still today a considerable number of crop wild relatives grow in this area.

The flora of Armenia comprises around 3500 species of vascular plants, i.e. more than half of the 6000 that can be found in the entire Transcaucasian region. Over 520 wild relatives of crops currently grow in the country, representing 16% of the Armenian flora. The outstanding treasure of Armenia, of which the country is rightfully proud, is the wild relatives of cereals, represented by 22 species and 218 infraspecific taxa. Armenia is considered one of the most important centres of diversity for the genus *Triticum*, still preserving the prototypes and donors of cultivated wheat. Thirteen species of wheat, including three of wild wheat and 358 botanical varieties are growing within its relatively small territory. The genus *Hordeum* is represented by eight species of wild barley and is another precious asset. Therefore, hosting the meeting on cereals in Armenia is a notable and symbolic event.

It is believed that the conservation of the rich genetic diversity and its sustainable use is a task of paramount importance. In Armenia, emphasis was placed on germplasm conservation and on development of the legislation and strategy for sustainable use of and access to genetic resources. The role of international agencies in supporting Armenia in this effort, both financially and technically, is considered of vital importance, particularly in the period of transition economy.

In 2000 Armenia, together with Bolivia, Madagascar, Sri Lanka and Uzbekistan prepared a regional PDF B UNEP/GEF project, under the coordination of IPGRI, on *in situ* conservation of crop wild relatives by enhancing information management and field application. The ultimate goal of the project is to gather broad information on wild relatives from both national and international information sources, and to establish a national information system linked to international systems.

In 2000, Armenia also became a member of the European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR), which is aimed at facilitating the long-term conservation and increased utilization of plant genetic resources in Europe. The implementation of the ECP/GR programmes in Armenia is coordinated by the Ministry of Agriculture. Armenia is at the same time a member of the Regional Network on plant genetic resources in the Central Asia and Caucasus region.

An intensive collaboration between the Ministry of Agriculture and the Centers of the Consultative Group on International Agricultural Research (CGIAR), such as IPGRI, ICARDA, CIMMYT (International Maize and Wheat Improvement Center) and CIP (International Potato Center) provided help to increase public awareness of the importance of plant genetic resources, to create databases of *ex situ* collections and to acquire computer facilities.

Close collaboration with IPGRI started in the mid-1990s and the efforts were focused in several directions simultaneously.

Assisting Armenia to develop its own capacity to conserve, manage and use its own plant genetic resources is an important component of IPGRI's support. Training courses for a number of scientists from the Armenian Agricultural Academy, the Scientific Centre for Vegetables and Industrial Crops and the Institute of Botany were carried out and included topics such as strategy and methods for plant conservation and documentation.

Another very significant step for Armenia was the possibility of participating in the EPGRIS project for the Establishment of a Plant Genetic Resources Infra-Structure, with IPGRI's support (see details on EPGRIS below, pp. 34-35). This sped up the creation of the *ex situ* collection inventory and therefore fully integrated Armenia with the rest of Europe in this process.

The scientific centres under the authority of the Ministry of Agriculture are now regularly provided with information on workshops and meetings, IPGRI descriptors and other publications. The opportunity to receive recent scientific publications can be hardly overestimated, since this allows Armenian scientists to keep abreast of recent scientific developments.

In conclusion, the achievements following the collaboration between Armenia and IPGRI are evident and illustrate the efficiency of joint activities in the field of plant genetic resources conservation and sustainable use, not only for the benefit of the present, but also for the future generations. L. Rukhkyan wished this trend could be continued, considering as an ultimate goal to be able to contribute to the prosperity of our beautiful planet.

Main activities on plant genetic resources conservation in the Republic of Armenia

Alvina Avagyan (Agricultural Support Republican Center, Yerevan) provided data illustrating the high level of plant diversity in Armenia, including about 3500 species (the largest species density of any country in the world) and 106 endemic species (about 3% of the total flora). Almost half of Armenia's plant species currently need some measure of conservation, while 386 species (12% percent of the country's flora) are included in the Red Book of Armenia. The following aspects of plant genetic resources (PGR) activities were then presented:

- National legislation was enforced and conventions related to PGR conservation were ratified (Convention on Biological Diversity and Framework Convention on Climate Change ratified in 1993, Convention to Combat Desertification in 1997)
- National strategies were prepared: Biodiversity Strategy and Action Plan (1999); Strategy on developing specially protected areas and national action plan; Strategy on access to genetic resources and benefit sharing; and Strategy on taxonomic investigations and development of biodiversity monitoring
- Sites for *in situ* conservation (natural reserves, parks etc.) amount to a total surface area of 311 000 ha, i.e. about 10% of the country's territory
- *Ex situ* conservation sites include botanical gardens, dendroparks, seed collections and a special *ex situ* collection of fruits and grapes.

International collaboration includes many projects carried out with CGIAR centres and other international agencies. For example, Armenia is a member of ECP/GR and takes part in the EPGRIS project with IPGRI support. An IPGRI (UNEP/GEF-funded) project has been prepared and is being launched on "*In situ* conservation of crop wild relatives through enhanced information management and field application". Field explorations and germplasm exchange are carried out in collaboration with the Plant Genetic Resources Unit of ICARDA; collaboration with CIMMYT consists in "restoring food security and economic growth in Central Asia and Caucasus" and it involves evaluation of breeding lines and hybrids and seed exchange; a herbarium database has been created with USDA-MAP (United States Department of Agriculture-Marketing Assistance Project in Armenia); UNDP/GEF is supporting Assessment of Capacity Building.

Information on ECP/GR and current international PGR events

Introduction

L. Maggioni, ECP/GR Coordinator, explained that, according to the decisions of the ECP/GR Steering Committee, a Network meeting was intended to review progress made, to increase integration of activities and make plans for the future at the Network level. All attending members of the Working Groups on *Avena*, barley and wheat were invited to participate, together with the managers of the databases on maize, *Secale*, triticale, and the specialist on minor cereals from the Minor Crops Network.

Progress of the Cereals Network during ECP/GR Phase VI

He went on with a summary of the decisions taken by the Cereals Network Coordinating Group in its meeting in Radzików, Poland, in July 2000. On this occasion, activities and mode of operation of the Working Groups were planned and recommendations were made to focus on documentation (i.e. the addition of characterization, evaluation and pedigree data to the central databases; use of geographical information systems (GIS) for data analysis; integration of European data with other regions' databases), emergency actions (safety-duplication), *in situ* conservation (identify strategies) and *ex situ* conservation (develop quality standards and share responsibilities).

Highlights of the recent progress of the various Working Groups were reported, indicating that those on *Avena* and Barley were able to further develop their databases as a result of the evaluation work carried out by EU-funded projects. The Barley Working Group also focused on pedigree data, established a network and a database of genetic stocks and advanced the status of the International Barley Core Collection (BCC). The Wheat Working Group met for the first time in 2001 and revised the status of national collections, established a central database and proposed a system of responsibility sharing for conservation, similar to that of the Barley Working Group.

All the cereals central databases are accessible from the ECP/GR Cereals Network Web pages; they are either searchable on-line or downloadable off-line, except for the triticale database which is still under construction.

Recommendations of the Steering Committee

A brief account was given of the outcomes of the Mid-term meeting of the ECP/GR Steering Committee held in St. Petersburg, Russian Federation, 14-17 October 2001.

On this occasion, the Steering Committee recommended all the groups to give more attention to facilitate increased utilization of PGR in Europe and to enhance awareness of the importance of PGR conservation and use.

In order to develop a strategy for the next Phase (VII), a task force composed of a few Steering Committee members was established to propose the future priorities and mode of operation of ECP/GR, to be discussed and approved during the Ninth Steering Committee meeting in October 2003. The list of five priorities for the future, as drafted by this task force was presented:

1. Documentation
2. Application and use of high technology (molecular markers, genomics)
3. Task-sharing
4. Characterization and evaluation
5. *In situ* and on-farm conservation.

Discussion

The FAO representative, Elcio Guimarâes, suggested that the Cereals Network members could include in the list of activities proposed as priority for Phase VII to "promote the increased use of PGRFA". This would be in line with the recommendation made by the Steering Committee during its eighth meeting.

Considering the possibility that the International Treaty on PGRFA enters into effect early next year (2004), governments would be encouraged to allocate resources to help implement sustainable use of plant genetic resources for food and agriculture (PGRFA), since this is one of the priority activities described in the Global Plan of Action (GPA). Thus, the ECP/GR Cereals Network would be in a stronger position to request support from the member countries.

Loek van Soest asked for details of an initiative discussed by the Vegetables Network for collaboration between the private sector and genebanks. Lorenzo Maggioni confirmed that the ECP/GR Secretariat had offered to help initiating a system of collaboration. Genebanks would make available material in urgent need of regeneration to breeding companies who would include these samples in their breeding trials, use them for crossing if appropriate, and multiply the material for return to the genebanks. Mike Leggett expressed some doubts that breeding companies would get involved without a clear profit, but L. Maggioni indicated that, in the case of vegetables, a number of companies had already expressed their interest, in principle, to participate in this type of initiative and this was indeed the reason why the Secretariat decided to offer its help.[1]

Current international PGR events

- **International Treaty**

It was mentioned that on 3 November 2001 the renegotiation of the FAO International Undertaking (IU) was completed. The revised text, adopted through a vote, is called the "International Treaty on Plant Genetic Resources for Food and Agriculture" (http://www.fao.org/AG/cgrfa/itpgr.htm). This new legally binding international agreement will enter into force 90 days after having been ratified by at least 40 states.[2] The Treaty establishes a Multilateral System ensuring facilitated access to a list of crop genetic resources for food and agriculture. Most cereals are included in this list (*Avena*, *Eleusine*, *Hordeum*, *Oryza*, *Pennisetum*, *Secale*, *Sorghum*, *Triticosecale*, *Triticum “et al.”*, including *Agropyron* and *Elymus*, and *Zea*), while *Aegilops* and wild relatives of maize are excluded. Access and benefit sharing for all crops excluded from the Multilateral System would be regulated through the Convention on Biological Diversity (CBD). The appropriate reference in this case is given by the Bonn guidelines on access to genetic resources and the fair and equitable sharing of the benefits arising from their utilization (http://www.biodiv.org/programmes/socio-eco/benefit/bonn.asp).

- **Global Crop Diversity Trust** [3]

This initiative of FAO and CGIAR aims to raise US$ 100 million by the end of 2003 to establish a trust fund that would be used to maintain in perpetuity the world’s most important collections of PGRFA. The Trust will be an independent organization with an association agreement with FAO. Eligibility principles to access the funds will include: 1) priority for existing collections of crops that are of high value for food security and for which there is a high degree of interdependence; 2) availability of material in the collection to be guaranteed under terms of access and benefit sharing of the Treaty; 3) the commitment of the holder of a collection to its long-term conservation has government recognition; and 4) the holder of a collection is committed to working in partnership to develop and maintain an efficient and effective global conservation system. The Trust could encourage holders of collections of crops in common, to come forward for funding support in consortia whereby they organize their respective holdings to ensure coverage of the unique diversity, and the collaboration in the conservation operation to fit the Trust’s eligibility principles and specific criteria. A “rational” system would:

- Conserve existing crop diversity;
- Have minimal unintentional replication of material/accessions;
- Have safety back-up arrangements for the materials;

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1 For more information see http://www.ecpgr.cgiar.org/Networks/Vegetables/Collaboration_GB_PS.htm

2 The International Treaty entered into force on 29 June 2004 (see http://www.fao.org/Legal/TREATIES/033s-e.htm)

3 For more information see http://www.croptrust.org

– Allow access/ensure availability;
– Be cost-effective in terms of conservation and management of the collections;
– Meet national and international needs.

- **The European Workshop on National Plant Genetic Resources Programmes**

This workshop, held in Alnarp, Sweden, on 24-26 April 2003, with nearly 100 participants, concluded with a statement calling for European governments to ensure funding for sustainable conservation and use of European genetic resources. Among the highlights of the meeting, the need for an integrated European System for conservation of PGRFA was emphasized and ECP/GR was indicated as a possible leader in the process to develop a vision, gaining support and identify sources of funding, such as from the European Commission.

Funding opportunities from the European Commission

- **The 6th Framework Programme for Research (2002-2006)**

This programme, funded by the EC Directorate for Research (http://fp6.cordis.lu/fp6/home.cfm), has identified two priority thematic areas with some relevance for plant genetic resources research, i.e. "Food safety and quality" (safer and environmentally friendly production methods and technologies and healthier foodstuff) and "Sustainable development, global change and ecosystems" (better understanding of marine and terrestrial biodiversity and ecosystem functioning). However, the terms of reference for upcoming calls for proposals do not provide an obvious opportunity for proposals related to genetic resources research.

- **New EC Regulation for PGRFA**

A brief account was given on the expected launching of the new Council Regulation for a Community programme on the conservation, characterization, collection and utilization of genetic resources in agriculture and repealing Regulation (EC) 1467/94. The first call for proposals is expected for the end of 2003 or early 2004 with a budget of 7-10 million € for 3 years (2003-2006), which is expected to be dedicated to animal (approximately 50%), crops (40%) and forest (10%) genetic resources projects. Only the European Community countries would be eligible to receive financial contributions. Third countries could participate without grant of funds. The 10 countries that will be joining the EU in 2004 (Cyprus, Czech Republic, Estonia, Hungary, Latvia, Lithuania, Malta, Poland, Slovakia and Slovenia) would also be eligible. According to the draft text of the new regulation, the objective is to help ensure and improve conservation, characterization, documentation, evaluation, collection and utilization of plant, microbial and animal genetic resources which are or could be of use in agriculture in the Community and measures would be pursued in conjunction, where appropriate, with FAO, ECP/GR, EUFORGEN (European Forest Genetic Resources Programme), etc. Eligible actions should concern genetic resources occurring within the territory of the Community, with priority given to species that are already, or might in future be economically significant in agriculture, horticulture or forestry and with a view to increasing the use of a broad spectrum of genetic resources. Preference would be given to the use of genetic resources for:

- Diversification of production;
- Improved product quality;
- Sustainable management and use;
- Better care for the environment.

Theoretical studies, testing of hypotheses, improvement of tools or techniques, and all other research activities would not be eligible for funding. In the current draft form, actions aiming at *ex situ* and *in situ* conservation should seek added value (spreading knowledge, increasing use, improving methodologies). Participation of non-governmental organizations (NGOs) would be encouraged, particularly in the field of *in situ*/on-farm conservation.[4]

A stepwise approach would be requested for targeted actions that would be funded up to 50% of their cost:

- Step 1. Establishment of the partner's network and formulation of objectives
- Step 2. Creation of a database
- Step 3. Primary characterization of the genetic resources
- Step 4. Secondary characterization of the genetic resources
- Step 5. Rationalization and conservation of the genetic resources and eventual establishment of a core collection
- Step 6. Acquisition or collection of genetic resources
- Step 7. Dissemination of results
- Step 8. Continued network coordination
- Step 9. On-farm management of genetic resources

According to information provided by EC officers, modification of this sequence would be possible, but should be justified.

Organization of the meeting

On behalf of the Cereals Network Coordinating Group (CNCG), Merja Veteläinen presented the organization of the meeting as discussed at the preparatory meeting of the CNCG held on 2 July.

On the first day, parallel sessions on *Avena*, barley and wheat would be held in order to:

- review their activities and identify the main achievements to prepare a workplan for the coming years and discuss the detail of their activities;
- identify priorities for the future, focusing on the recommendations of the Steering Committee for Phase VII of ECP/GR. The Working Groups were asked to comment on these recommendations, taking into consideration their own specialism and crop range.

On the second day the whole Network would meet and work at an integrated level on the issues identified (documentation/databases, characterization, evaluation, regeneration, safety-duplication, conservation and management of wild relatives, pre-breeding, and others if needed). It was proposed to discuss one by one the activities of the different Working Groups in order to identify common tasks and proposals for future activities at Network level.

4 The text of the new Regulation 870/2004 was published on the EU Official Journal of 24 April 2004. The document is available from http://europa.eu.int/comm/agriculture/res/gen/index.htm

Reports of the Working Group Sessions

Working Group on Avena

J. Mike Leggett

Agenda

1. Welcoming address
2. Introduction of the participants
3. Approval of/amendments to the agenda
4. Chairperson's report
5. Progress since the 5th *Avena* Working Group meeting (May 1998, Vilnius, Lithuania)
6. Research activities and other ongoing activities: Results from work 1998-2003, relevant to oats genetic resources conservation
7. Survey of oat work throughout 'greater' Europe
8. Safety-duplication
9. Incorporation of passport, evaluation and characterization data to the European *Avena* Database (EADB)
10. Unique material
11. Regeneration needs
12. Gaps and potential needs for collecting identified
13. Appropriate *in situ* strategies
14. Drafting of the report
15. Conclusion
    Presentation of the report/adoption of recommendations
    Election of Chairperson
    Closing remarks

Welcoming address

The Chairman welcomed everyone and explained what his connection with the Group was.

Introduction of the participants

The participants briefly introduced themselves and explained their connection with plant genetic resources.

Approval/amendments of the agenda

The amended draft agenda as presented above was accepted

Chairperson's report

The Chair expressed his unease at running the three working groups simultaneously as the *Avena* Working Group (AWG) was always going to be second priority for those who were also involved with either wheat or barley. Thus very few full members of the AWG were able to attend.

- **Phase VI ECP/GR**

At the ECP/GR Steering Committee's Seventh meeting in Braunschweig, Germany in July 1998, the continuation of ECP/GR into Phase VI was approved, covering the years 1999-2003. The operational structure of Phase V was reaffirmed, with seven crop networks and three thematic networks and with the addition of Network Coordinating Groups, composed of Chairs, Vice-Chairs and database managers, within each crop network. The number of Working Groups in the course of Phase VI was raised to fifteen: *Allium, Avena,* Barley, *Beta, Brassica*, Forages, Grain legumes, *Malus/Pyrus,* Medicinal and Aromatic plants, Potato, *Prunus,* Solanaceae, Umbellifer crops, *Vitis* and Wheat.

- **Technological advances**

At the last Working Group meeting we spoke of molecular technologies and I am aware of several projects which involve these new technologies which are providing a wealth of data for use in genetic resources and breeding programmes. As ever, these programmes are minute in comparison with those involving wheat and barley, but the spin-off from these projects should enable oat workers to utilize at least some of the data which these projects produce.

Clearly these technologies will aid the conservation and utilization of our genetic resources.

- **Information platforms**

The information platforms available to plant genetic resources users continue to be improved and are a valuable source of information and a first point of contact for the user community:

- European *Avena* Database (EADB)
  http://www.fal.de/bgrc/eadb/avena.htm
- EU Project GENRES CT99-106: Evaluation and enhancement of *Avena* collections for extensification of the genetic basis of *Avena* for quality and resistance breeding
  http://www.fal.de/bgrc/eu99106/
- ECP/GR
  http://www.ipgri.cgiar.org/networks/ecpgr/about_ecpgr.htm
- European Plant Genetic Resources Information Infra-Structure (EPGRIS)
  http://www.ecpgr.cgiar.org/epgris/Index.htm

- **6th International Oat Conference, New Zealand 2000**

The conference did not have a specific section with regard to *Avena* genetic resources though of course many of the reports included data which at some point had utilized genetic resources other than cultivars or breeders' lines.

- **Funding opportunities**

Funding for genetic resources programmes is still very scarce despite various governments expressing their concerns about the loss of biodiversity internationally. An example of this was expressed by the Italian representative who said: *"The limiting factor is that in Italy at the moment there is no money for oat genetic resources and this condition reduces activities and possibility of meeting participation"*.

However, under regulation 1467/94 "Conservation, Characterisation, Collection and Utilisation of Genetic Resources in agriculture" Dr Leggett had persuaded Andreas Katsiotis from the Agricultural University of Athens, Greece, to take on the role of coordinator when the third call was finally published.

The application was successful and the project GENRES CT99-106: "Evaluation and enhancement of *Avena* landrace collections for extensification of the genetic basis of *Avena* for quality and resistance breeding" is now in its final year. The Group heard some of the results from this project during the meeting (see paper on *"Update of the* Avena *core collections – Landraces"* by C. Germeier, pp. 79-82).

- **Collecting activities/wild germplasm collections**

The important tetraploid species *A. maroccana* (formally known as *A. magna*) and *A. murphyi* have featured in collections (see paper on *"Distribution and ecology of the wild tetraploid oat species* Avena magna *and* A. murphyi *in Morocco"*, by N. Saidi and G. Ladizinsky, pp. 70-73).

At the last AWG meeting we heard from Professor Ladizinsky of the new tetraploid species *A. insularis*, and the Group recommended that there be more collecting of this species which is the closest tetraploid progenitor of the hexaploid cultivated oat.

The Chairman announced that he would be retiring as Chairperson of the *Avena* Working Group as soon as a replacement Chair is appointed.

Progress since the Fifth *Avena* Working Group meeting

1. Additional passport data added to EADB
2. Taxonomic system agreed and implemented
3. IPGRI multicrop passport descriptors adopted
4. EU 1467/94 Genetic Resources: a project was submitted and accepted and is now in year three
5. Morocco is a centre of diversity for the genus. The Group recommended that every effort be made to encourage the participation of Morocco as observers at future ECP/GR *Avena* Working Group meetings. We are pleased that Nezha Saidi has been able to join the Group
6. Genetic resources information from the Vavilov Institute (VIR, St. Petersburg) is being incorporated into the EADB
7. The AWG recommended that we explore the possibility of including the data from the US and Canadian genebank collection into EADB. This is in progress
8. The Group recommended that the Spanish member look into the possibility of including *A. murphyi* in areas of *in situ* conservation. The Spanish authorities are aware of the situation and it has been devolved to the appropriate agency. Similarly, with *A. insularis,* Luigi Cattivelli has been appointed and is hoping to draw the attention of the authorities to the issue
9. The Chair had undertaken the survey (see agenda item 7)

Research activities and other ongoing activities: Results from work 1998-2003, relevant to oats genetic resources conservation

Full texts of the presentations and additional papers received after the meeting are included in Part II (see pp. 63-101).

Survey of oat work throughout "greater" Europe

The Chairman reported that he had been continually updating the survey as more contacts were made. The list now comprises of over 40 researchers.

> ***Recommendation***
> *It was agreed that subject to checking the data protection requirements of those individuals who had replied, the information could be posted on the EADB Web site.*

Safety-duplication and unique material

There was concern over "unique material" where there is no safety-duplicate. Some wild material is unreplicated and within EADB only 662 of 32 000 accessions are recorded as having safety-duplicates (though the actual number may be in excess of this, but has not been recorded). This situation is clearly far from ideal.

> ***Recommendation***
> *It was agreed that wild material collected in Morocco during 1985 would be repatriated now that there was an* Avena *scientist who could catalogue and maintain the collection. This would fulfil the original agreement with INRA Morocco, which up till now has not been possible as previously there was no specialist in wild* Avena.

Discussions of the various oat collections included a report that there had been a rationalization of the collections in both France and Germany. All the French cereal collections are now held at INRA Clermont-Ferrand, and the whole German oat collection is now kept at the Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), after the merger of the two German genebanks.

INRA was keen to repatriate foreign accessions to the country of origin where this is possible. All accessions would be documented as fully as possible, but if an accession number was the only identifier, this would not be excluded from the database.

Incorporation of passport, evaluation and characterization data to EADB

It was agreed that all available data be submitted to EADB. The GENRES project is contributing a substantial volume of data each year on the landraces.

- **Database**

The *Avena* database is well established and we are incorporating data from the USA and Canada to make the database more complete. However, this is complex because of the different formats involved.

The Group also expressed concerns over the different methodologies used by the different databases to detect duplicates. EADB has developed a system that has been run on the entire data set. This is available as a tool to other database curators who have the multicrop accessions table and a completed duplicate search (see paper by C. Germeier and L. Frese "*Computer-assisted search for duplicates in a medium-size Cereal Central Crop Database - the case of* Avena *(EADB)*", pp. 53-62).

> ***Recommendation***
> *The Group recommends that when data from USA and Canada are included, there is clear reference to the original source of the data.*

> ***Recommendation***
> *That every effort should be made to incorporate additional data from other holders, e.g. Australia.*

> ***Recommendation***
> *That the* Avena *database would make a model system - as it is already well developed and the* Avena *collection is of medium size in comparison to the main cereal collections - for devising such a system of "warehousing" which would benefit the other cereal databases within the Cereal*

Network, and that all efforts should be made to find funding for the project[5] *(possibly under Phase VII).*

Regeneration needs and safety-duplicates

There was particular concern with regard to regeneration needs and the issue of safety-duplicates:

Regeneration of some of the existing collections is still a problem and again, who is going to pay for it? This was raised at the last AWG meeting but there is still no source of funding. We see both of these as political decisions.

Gaps and potential needs for collecting identified

It was clear that there is still a need to collect *A. murphyi* and *A. maroccana*, the former both in Spain and Morocco, the latter in Morocco only. It was also thought that further collections of *A. insularis* and *A. macrostachya* would be desirable, though the latter species is probably not directly under threat of genetic erosion because of its habitat.

Recommendation

The country representatives (Spain and Morocco) will look into the possibility of further collections of A. murphyi *and* A. maroccana, *and further collections of* A. insularis *and* A. macrostachya *are desirable. The possibility of obtaining funding for further collections should be explored within ECP/GR.*

- ***In situ*** **conservation**

The Group has identified particular species that require *in situ* conservation because of their universal scarcity. However, we have concerns as to how this is achieved, and what would be the difference in the level of diversity after say 10 years compared to the diversity which is already present in *ex situ* collections from the same site? Has anyone tested this?

With regard to landraces (loosely defined), should the Cereals Network put more effort into conserving *in situ* or *ex situ* in areas such as Armenia where there may still be genuine landraces of our major crop species?

Recommendation

Continued efforts to ensure that important sites of the former three species are conserved in situ.

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[5] A two-year model project on sharing of responsibilities as a possible model for "A European Genebank Integration System" (AEGIS) was approved for funding under the ECP/GR budget during the Ninth Steering Committee meeting (Turkey, October 2003). *Avena* is one of the four model crops that will be used in a feasibility study aiming at establishing a European integrated system for long-term conservation, high quality of and easy access to genetic material, avoidance of duplication of conservation efforts and capacities making better use of existing but dispersed and capabilities (http://www.ecpgr.cgiar.org/AEGIS/AEGIS.htm).

Appropriate *in situ* strategies

The Spanish delegate reported that *in situ* conservation of the biggest *A. murphyi* population has not yet been implemented because the field is private property.

> ***Recommendation***
> *The representative from Morocco will explore the possibilities of having certain areas designated as* in situ *conservation sites. Similarly the Spanish delegate will check on the current situation with regard to the areas important for* A. murphyi.

Miscellaneous discussions

- **Pre-breeding**

It was felt that pre-breeding strategies were needed but that these should involve collaborative efforts. "Task-sharing" would be one way to initiate such projects within the breeding community, but we feel that countries outside of the EU must be included

> ***Recommendation***
> *Any new projects which are of interest to several Group members could be routed through the AWG.*

Conclusions

The meeting ran out of time before the issue of appointing a new Chairperson could be discussed. However, it is hoped to hold an AWG meeting in parallel with the VIIth International Oat Conference in Helsinki in July 2004 where a new Chair can be appointed.[6]

Working Group on Barley

Roger P. Ellis, Merja Veteläinen and Helmut Knüpffer

Roger Ellis, the Chairman of the ECP/GR Working Group on Barley, welcomed the participants to its meeting in Yerevan, Republic of Armenia, taking place in the framework of the first meeting of the ECP/GR Cereals Network. The draft agenda had been circulated in advance among the members of the Group and the ECP/GR Coordinator.

The Chairman presented the following agenda:
1. Welcome
2. Introduction of the participants
3. Election of rapporteur
4. Approval/amendments of the agenda
5. Chairman's Report
6. European Barley Database
7. Safety-duplication

[6] At the *ad hoc* AWG meeting in Helsinki (23 July 2004), Dr Andreas Katsiotis, Plant Breeding and Biometry, Agricultural University of Athens was elected as acting Chairman. The appointment will be ratified at the next AWG meeting in 2007. The minutes of the *ad hoc* meeting are included as Appendix II.

8. Sharing of responsibilities
9. Germplasm collecting activities
10. International Barley Core Collection (BCC)
11. Pre-breeding
12. Conservation and management of wild relatives
13. On-farm conservation
14. Public awareness
15. Individual country reports
16. Research activities
17. Election of new Chair and Vice-Chair
18. Closing remarks

Merja Veteläinen, Vice-Chair of the Group, was elected as rapporteur. The agenda was accepted by the Working Group members.

Chairman's report – Perspectives for a modern use of barley germplasm

(see paper pp. 103-108)

The Chairman's report set the overall scenario for the meeting by referring to achievements in relation to the Barley Core Collection, the European Barley Database and the excellent accomplishments within the EU GENRES project (CT-98-104). The challenge for the future was to preserve germplasm in the most efficient manner possible. It is necessary for example to review the Core Collection in the light of new evidence from genetic assays as methods of DNA-based markers become more efficient. Current practice in breeding programmes should provide an effective guide for genebank managers as new methods are subject to rigorous proof before their adoption. An important role for genebanks is the preservation of the genetic diversity represented by landraces with the role of databases being to make information of allelic variability available to breeders. We are still some way from this ideal situation but rapid progress is being made.

The European Barley Database (EBDB)

- **Introduction**

Helmut Knüpffer presented the status of the European Barley Database (EBDB). The first version of the EBDB was set up during 1982-1987 and included ca. 55 000 accessions[7]. In 1987, the "European Barley List" [8] was published. The second version of the EBDB with 90 000 accessions was developed in 1997, with the assistance of L. López.[9] At present, as a result of activities by D. Enneking within the EU GENRES project on barley (see below), the EBDB includes data from 155 000 accessions from 23 European countries and from three

[7] Knüpffer, H. 1988. The European Barley Database of the ECP/GR: An introduction. Kulturpflanze 36:135-162.

[8] Knüpffer, H., compiler. 1987. European Barley List. Vol. 1: Introduction. 82pp. Vol. 2, Part 1: Cultivars, lines and special resources - Part 2: Collected material, unnamed accessions - Part 3: Wild species, species hybrids. 829pp. Zentralinstitut für Genetik und Kulturpflanzenforschung Gatersleben/International Board for Plant Genetic Resources, Rome.

[9] Knüpffer, H. and L. López. 1999: Status report on the European Barley Database. Pp. 18-24 *in* Report of a Working Group on Barley. Fifth Meeting, 10-12 July 1997, Alterode/Gatersleben, Germany (L. Maggioni, H. Knüpffer, R. von Bothmer, M. Ambrose, K. Hammer and E. Lipman, compilers). International Plant Genetic Resources Institute, Rome, Italy.

extra-European genebanks (see below).[10] In addition, 1293 accessions from the International Barley Core Collection (BCC, see p. 22) are documented in the EBDB.

- **Progress**

The EBDB is searchable on-line at http://barley.ipk-gatersleben.de/ebdb.php3. Besides passport data, the EBDB includes also evaluation results from the GENRES project on barley genetic resources, which, according to an agreement among the project partners, were accessible only to the partners for some time.[11] The "Dynamic Data Analyser" (DDA) developed by Morten Huldén (former documentation officer of the Nordic Gene Bank) is utilized for visualizing evaluation data. The DDA was adapted to the GENRES evaluation data in consultation with Dag Terje Endresen (Nordic Gene Bank).

The quality of the data has been improved in the following respects:

- completion of geo-references: addition of geographical coordinates, using Web gazetteers[12] and GIS software;[13]
- standardization of accession names utilizing three published cultivar inventories[14], which were also computerized as reference information to the EBDB;
- harmonization of scientific names, using taxonomic treatments of the genus *Hordeum*[15] and of the cultivated barley;[16]

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10 Enneking, D. and H. Knüpffer. 2001. The European Barley Database. Pp. 50-62 *in* Report of a Working Group on Barley. Sixth Meeting, 3 December 2000, Salsomaggiore, Italy (H. Knüpffer, R. von Bothmer, M. Ambrose, R. Ellis, A.M. Stanca, D. Enneking, L. Maggioni and E. Lipman, compilers). International Plant Genetic Resources Institute, Rome, Italy.
Enneking, D. 2001-2002. The ECP/GR European Barley Database (http://barley.ipk-gatersleben.de/ebdb/)

11 The GENRES evaluation data were made freely accessible in August 2003.

12 Online Gazetteers such as the Alexandria Digital Library Gazetteer Server (http://fat-albert.alexandria.ucsb.edu:8827/gazetteer/), the US National Imaging and Mapping Agency's GEOnet Names Server (http://164.214.2.59/gns/html/) and the global gazetteer (http://www.calle.com/world/) have been very useful.

13 "The freely available geographic mapping and analysis software DIVA-GIS developed at CIP (http://www.cipotato.org/diva/) has a batch function to retrieve geo-references based on location name, km distance and direction. Running the raw data for collecting sites (location data) from the EBDB through this system provided only a small percentage of useful assignments. Clearly, extensive editing of the location data is required for utilization of this useful feature. The adoption of the DIVA-GIS location format could be considered for the next version of the IPGRI *Multi-Crop Passport Descriptors*, since it would facilitate the generation of geo-referenced data for hitherto unassigned locations" [from the final report of the GENRES barley project].

14 Arias, G., A. Reiner, A. Penger and A. Mangstl. 1983. Directory of Barley cultivars and lines. Eugen Ulmer, Stuttgart.
Baum, B.R., L.G. Bailey and B.K. Thompson. 1985. Barley register. Cat. No. A53-1783/1985. Canada Governm. Publ. Centre.
Baumer, M. and R. Cais. 2000. Abstammung der Gerstensorten. Freising: Bayerische Landesanstalt für Bodenkultur und Pflanzenbau (http://www.stmelf.bayern.de/lbp/forsch/pz/gerstenstamm.pdf).

15 Bothmer, R. von, N. Jacobsen, C. Baden, R.B. Jørgensen and I. Linde-Laursen. 1995. An ecogeographical study of the genus *Hordeum*. 2nd edition. Systematic and Ecogeographic Studies on Crop Genepools 7. IPGRI, Rome. 129pp.

16 Lukyanova, M.V., A.Ya. Trofimovskaya, G.N. Gudkova, I.A. Terentyeva and N.P. Yarosh. 1990. Flora of cultivated plants. Vol. 2, Part 2, Barley. Agropromizdat, Leningrad. (in Russian).
Mansfeld, R. 1950. Das morphologische System der Saatgerste (*Hordeum vulgare* L. s.l.). Züchter 20:8-24.

- standardization of donor codes: changed from "ECP/GR acronyms" consisting of three letters for country plus up to seven letters for institution abbreviation, into "FAO codes" consisting of three letters for country, plus three digits;
- completion of listing of synonymous accession names;
- completion of passport and geographical data;
- introduction of ICARDA-compatible location codes;
- mutual completion of data sets from different contributors of the same accessions;
- linking of germplasm sets from past expeditions through collection numbers;
- development and application of the "Most Original Number" (MON) concept. The MON is the first traceable number (accession number or collection number) of an accession in its life history in genebanks.

Inter-regional connections with the Australian Winter Cereals Collection (AWCC) in Tamworth, ICARDA and the Barley Germplasm Centre in Kurashiki, Japan, led to the inclusion of ca. 38 000 additional accessions. Furthermore, links from individual EBDB accessions to data from GRIN have been established.

- **Documentation workplan**

After the end of the GENRES project (September 2003), the database appeared to be established in a computing environment (Linux, Php, PostGres) that is not widely used at the host institute, IPK. In addition, the documentation of the EBDB structure and functionality was incomplete. Therefore, a re-engineering of the database (i.e. completion of its technical documentation, description of the relationships between the tables, coding systems used, etc.) and its transition to another database management system, Oracle, the platform under which most IPK databases will be maintained in future, became necessary. To accomplish these tasks, an informatics student was hired.[17] Web search interfaces with extended functionality and better user-friendliness need to be developed. The Group was requested to assist in the formulation of user requirements for the EBDB.

During the GENRES project, the EBDB was not completely updated. Therefore, a new update would be desirable, either from the individual genebanks, or by downloading barley data from EURISCO after its completion. However, it is necessary to ensure that the results of the analysis and improvement of the present database (e.g. defined groups of duplicates, standardization of names, added coordinates and external links) will not be lost by just overwriting the old data.[18] Future approaches for updating Central Crop Databases should leave the full responsibility for the data with the data providers.

The accessibility and the user-friendliness of the search interface have to be improved. Further desirable functions include a "shopping basket" approach, which enables the user to select a set of accessions from different genebanks and send a single seed request that is forwarded to the holders of the respective accessions.

It is also desirable to include more characterization and evaluation data as well as links to such data in the EBDB. In 20% of the accessions, scientific names of botanical varieties are recorded, which in turn refer to a combination of morphological characterization descriptors.

Pedigree information, year of release and other cultivar-related information has been gathered from the three published cultivar inventories mentioned above as reference information about cultivars represented by accessions in the database. This information was also used to standardize the spelling of cultivar names. Some of the pedigree information from these sources still needs to be registered and included in the database.

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17 Riedel, A. 2003. Re-engineering of the BCC/EBDB database. Faculty of Informatics, Univ. Magdeburg. 67pp. Unpublished. (in German).

18 On the identification of duplicates, see also paper by C. Germeier and L. Frese, pp. 53-62.

Information on molecular markers will not be added to the EBDB in the near future. H. Knüpffer reported on ongoing projects at IPK utilizing various molecular marker systems to characterize barley germplasm accessions. A bioinformatics project started in 2002 aims at combining marker and genomics data with genebank accession data.[19] However, most current marker systems produce results that are not easily comparable with data generated by other research groups, even if using the same techniques and marker sets. Therefore, accumulation of such data in databases should be started only when suitable marker systems will have been developed and will be used.[20]

The database needs to be searched for duplicates in order to facilitate the implementation of a mechanism of sharing responsibilities. However, the Barley Working Group felt that the principles of sharing responsibilities should be harmonized among the various crop working groups represented in the Cereals Network (see under "Sharing of responsibilities").

The Barley Working Group suggested additional improvements to the EBDB. Linking accessions to geo-referenced data such as soil types and climatic data would allow searching for accessions collected in a particularly stressful environment, so that, for example, accessions likely to be drought-resistant could be found.[21] Plotting accessions on a map and thereby utilizing geographic information might assist users in selecting accessions, but it may also be useful for identifying geographical gaps in collections. Considerable amounts of evaluation data are available at various PGR information sites, and these should be linked to (but not necessarily duplicated in) the EBDB.[22]

Database on Barley Genes and Genetic Stocks (BGS)

Merja Veteläinen (Nordic Gene Bank) presented information about the Database on Barley Genes and Genetic Stocks (BGS) developed by Morten Huldén in consultation with Udda Lundqvist (Svalöv, Sweden). The database was developed using ACeDB, the database software used also for GrainGenes (see paper pp. 128-129). It will be included in GrainGenes and provides the possibility of including more data on genetic stocks collections. H. Knüpffer mentioned the IPK collection of mutants and other genetic stocks, which is not documented electronically. M. Veteläinen suggested that cooperation with M. Huldén should resolve this problem. It was also recommended that links be established between the Web sites of the ACeDB Barley Genetic Stock Database and the EBDB.

Safety-duplication

The Barley Working Group suggested that the issues of safety-duplication be discussed for the whole Cereals Network in the plenary meeting.

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19 Plant Data Warehouse (PDW) Group, as part of the Bioinformatics Centre Gatersleben-Halle (BIC-GH) funded by the German Ministry of Research and Education (BMBF) (http://www.bic-gh.de/)

20 "*Although a considerable amount of marker data has been generated by now using any of the three marker systems …, individual datasets pertain only to a restricted number of accessions and, regarding DNA markers, are usually based on a unique marker set. Hence, it is at present not possible to pool data in order to further complete the picture of the structure and diversity of the genepool*" (Graner, A., Å. Bjørnstad, T. Konishi and F. Ordon. 2003. Molecular diversity of the barley genome. Pp. 118-138 *in* Diversity in Barley (*Hordeum vulgare*) (R. von Bothmer, Th.J.L. van Hintum, H. Knüpffer and K. Sato, eds). Elsevier Science B.V., Amsterdam, The Netherlands).

21 A prototype of such a system, the "Focused Identification of Germplasm Strategy" (FIGS) was presented by M. Mackay (Australia) and J. Konopka (ICARDA) during the Workshop on Barley Genetic Resources at the 9th IBGS.

22 Note: The UK CROPNET summarizes public information from UK research programmes. From the main page (http://ukcrop.net/db.html), it is possible to select a barley database that contains information on genetic maps and markers.

Sharing of responsibilities for conservation

The Barley Working Group had set up a workplan for sharing of responsibilities for conservation in its previous meeting in Salsomaggiore in 2000. This workplan was presented by M. Veteläinen. The procedures described in that report implied a heavy workload both for the database manager and the curators, therefore no progress was made so far. H. Knüpffer suggested that a suitable Web-based interface to the EBDB should enable curators to interactively select accessions for which they accept responsibility. Since this task is considered common to all Cereals Working Groups, it was decided to submit the matter to the Network plenary meeting, in order to search for joint solutions.[23]

Germplasm collecting activities

Tzion Fahima (Haifa, Israel) gave a presentation on collections in the Fertile Crescent and Jordan (see paper pp. 116-117).

International Barley Core Collection (BCC)

- **Introduction**

In his introduction, Roger Ellis reported that marker-assisted studies revealed that the current European subset of the BCC does not include some of the interesting ancestral lines of present-day European barley cultivars (see paper pp. 103-108). H. Knüpffer then explained the status of the BCC. This collection was established based on an initial ECP/GR Barley Working Group initiative since 1989.[24] The objective has been to select a limited, standardized set of accessions that would represent as wide genetic diversity as possible at the global level.[25] The BCC is composed of different subsets, and the responsibility of initial selection of the BCC accessions, their multiplication and distribution has been divided between a number of cooperating scientists and institutions worldwide.

- **Progress made**

Large parts of the BCC have been established, and most of the subsets are available for research and evaluation. A documentation system is under development; currently the BCC documentation is incorporated in the EBDB (see above). The state of the BCC is described in detail in a chapter of the book *Diversity in Barley*.[26]

- **Plans for the future**

In order to complete the BCC, an Ethiopian/Eritrean subset and a subset of genetic stocks need to be created. The Ethiopian/Eritrean BCC subset is presently being developed in the framework of a project involving scientists from Ethiopia and Norway. Furthermore, it is intended to further develop the BCC documentation system, including a "shopping-basket" approach, a Web-based distributed seed stock management, and the provision of integrating

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23 At the ECP/GR Steering Committee Meeting (Turkey, October 2003), following a German proposal to start a project for the development of a European Genebank Integration System, the AEGIS project was approved for funding (http://www.ecpgr.cgiar.org/AEGIS/AEGIS.htm).

24 Anonymous. 1989. Barley Core Collection (preliminary report). Pp. 59-61 *in* Report of a Working Group on Barley (Third Meeting). European Cooperative Programme for the Conservation and Exchange of Crop Genetic Resources/International Board for Plant Genetic Resources.

25 Knüpffer, H., and Th.J.L. van Hintum. 1995. The Barley Core Collection – an international effort. Pp. 171-178 *in* Core Collections of Plant Genetic Resources (T. Hodgkin, A.H.D. Brown, Th.J.L. van Hintum and E.A.V. Morales, eds). Wiley & Sons, Chichester.

26 Knüpffer, H. and Th.J.L. van Hintum. 2003. Summarised diversity – the Barley Core Collection. Pp. 251-259 *in* Diversity in Barley (*Hordeum vulgare*) (R. von Bothmer, Th.J.L. van Hintum, H. Knüpffer and K. Sato, eds). Elsevier Science B.V., Amsterdam, The Netherlands.

characterization/evaluation data from any study or evaluation carried out by researchers worldwide. It was also suggested that the use of molecular markers would ensure wide genetic diversity of the BCC.

Pre-breeding

The Barley Working Group discussed the need for pre-breeding and genetic base broadening. An ECP/GR workshop on these issues held in conjunction with the Barley Working Group meeting in 2000[27] did not result in concrete actions or projects, but it was clear that many breeders wish to take advantage of pre-breeding. Two possible approaches were distinguished. Abraham Korol (Haifa, Israel) had proposed to sow mixtures of genotypes or composite cross populations in various environments to allow for adaptation by natural selection (base-broadening). Breeders were more interested in incorporating desired alleles from unadapted landraces or wild material into a background that would be easy to cross with advanced cultivars to transfer these characteristics, thus bridging the gap between germplasm collections and breeding material. It was realized that there is a need for long-term projects that ensure the incorporation of genetic diversity in barley breeding programmes, and that long-term funding mechanisms different from the usual short-term project funding would be needed.

- **Plans for the future**

The Barley Working Group recommended carrying out a survey among barley workers to sound out interest in pre-breeding. Possibly, an ECP/GR task force could be set up based on the results of this survey leading to regional cooperation. Elcio P. Guimarâes, the FAO representative in the Cereals Network meeting, who participated in the Barley Working Group meeting, offered to be a focal point and support. Marja Jalli agreed to take the lead in the pre-breeding issue; she will, together with Elcio Guimarâes, prepare this topic for the workshop on barley genetic resources at the International Barley Genetics Symposium (IBGS), Brno, 20 June 2004.[28]

Conservation and management of wild relatives

- **Ongoing activities**

The Barley Working Group resolved that the state of *in situ* conservation of wild relatives is to be reported by the ECP/GR task force for *in situ* conservation. Needs for *in situ* conservation of wild *Hordeum* species should also be coordinated with the EU project PGR Forum.

H. Knüpffer summarized a worldwide survey of the state and representation of wild and cultivated barleys in genebank collections by T. van Hintum and co-workers.[29] Information on seed storage behaviour is available only for few of the wild *Hordeum* species, including *H. vulgare* subsp. *spontaneum* (primary genepool), *H. bulbosum* (secondary genepool), and *H. jubatum*, *H. marinum*, *H. murinum* and *H. secalinum* (tertiary genepool). Seed regeneration in genebanks is more difficult for subsp. *spontaneum*, since mechanical sowing is impossible. In wild taxa, seed shattering makes harvesting difficult. *H. bulbosum* and *H. brevisubulatum* are almost obligate outbreeders, thus requiring measures for isolation.

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27 Ambrose, M. and H. Knüpffer. 2000-2001. Pre-breeding initiative. Record of a discussion held in Salsomaggiore, Italy, 6 December 2000. Unpublished report.

28 See Appendix I, Minutes of the *ad hoc* Barley meeting in Brno, pp. 212-216.

29 Hintum, Th.J.L. van and F. Menting. 2003. Diversity in *ex situ* genebank collections of barley. Pp. 240-250 *in* Diversity in Barley (*Hordeum vulgare*) (R. von Bothmer, Th.J.L. van Hintum, H. Knüpffer and K. Sato, eds). Elsevier Science B.V., Amsterdam, The Netherlands.

Among ca. 371 000 barley accessions in genebanks, according to this study, 10% belong to *H. vulgare* subsp. *spontaneum*, 0.4% to *H. bulbosum*, and 1.7% to the other wild *Hordeum* species belonging to the tertiary genepool. Accessions of subsp. *spontaneum* are predominantly found in genebanks in the Near East (e.g. ICARDA, Israel), but also in Europe and North America. In Europe, 44% of the world *spontaneum* accessions are kept by the John Innes Centre (UK), followed by the German Gene Bank (IPK Gatersleben, including the former BAZ Gene Bank in Braunschweig, total 1.6%), and the Swedish University of Agricultural Sciences in Alnarp (0.8%). An additional 24.5% of the world holding is kept in two Israeli collections. The vast majority of the accessions at the John Innes Centre results from joint British-Israeli collecting in 1978 at only 213 different sites in Israel, and it is very likely that this material is duplicated in Israel.[30] European genebanks maintain 411 of the 1370 *H. bulbosum* accessions kept in genebanks worldwide. Forty-eight percent of the *ex situ* collections of the tertiary genepool can be found in Europe (among these, 39% in Alnarp). *H. murinum* and *H. marinum* have the highest numbers of accessions worldwide (1505 and 566, respectively), whereas both *H. guatemalense* and *H. erectifolium* are represented by a single accession only, both in Alnarp. With the present inventories alone, it is difficult to estimate gaps in *ex situ* collections of wild barleys.

To design conservation plans for wild relatives, information on their distribution in Europe is necessary. As a contribution to an assessment on wild *Hordeum* species growing in European countries, H. Knüpffer compiled data on several cereal genera from the database of the Euro+Med project, an EU-funded project coordinated by the University of Reading, UK, aiming at bringing together data from the *Flora Europaea* and the Mediterranean Plant Checklist. The data on the European wild flora was kindly provided by the University of Reading for the preparation of a list of European crop wild relatives for the EU project "PGR Forum", which aims at an assessment of crop wild relatives occurring in Europe. Since the Euro+Med database also included some unverified "raw data" from regional floras, the scientific names and the distributions of the wild relatives of cereals need to be further checked. From the ECP/GR mandate region, the Transcaucasian republics, the Asian part of Turkey, and Israel are not covered by *Flora Europaea*.[31]

M. Veteläinen mentioned that a similar work, but focussing on the flora of cultivated plants, is being carried out in Sweden.[32]

- **Plans for the future**

The previous meeting of the Barley Working Group (Salsomaggiore, December 2000) had discussed a recommendation[33] from the Cereals Network Coordinating Committee (Radzików, July 2000) to establish a project on *in situ* conservation of wild relatives of cereals

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30 Within the EU GENRES project on barley, some interesting *H. spontaneum* material evaluated in Sweden (Svalöv-Weibull) and Germany (Aschersleben) was traced to the JIC (former PBI) collection. Through geo-referencing, based on data from a previous study (Prochnow, 1998) some promising hot spots for leaf rust resistance could be located in the Galilee and Judaea regions of Israel (after EU GENRES CT98-104 final report).

31 Data on these countries have to be requested from the extended database on European + Mediterranean flora from the University of Reading.

32 The "Swedish Cultivated Plants Database" is being developed and financed by the Swedish National Programme for Plant Genetic Resources. The project leader is Björn Alden (University of Gothenburg) and the database manager is Morten Huldén (former information officer at the NGB).

33 "*Strategies for* in situ *conservation of the most endangered wild relatives should be identified.*" (p. 4 *in* Maggioni, L. and O. Spellman, compilers. 2001. Report of a Network Coordinating Group on Cereals. *Ad hoc* meeting, 7-8 July 2000, Radzików, Poland. International Plant Genetic Resources Institute, Rome, Italy).

in Europe (pp. 12-13 in that Report[34]). It was suggested that information on the distribution of candidate species be obtained from *Flora Europaea* and a published account,[35] and that IPGRI take the lead in this initiative. It was proposed to organize a meeting about *in situ* conservation of wild cereals either during the Triticeae meeting (Córdoba, Sept. 2001) or the EUCARPIA Cereals section meeting (Salsomaggiore, October 2002). However, this satellite meeting was not organized. According to the ECP/GR Secretariat, this type of action should find its way through the initiative of the task force on "wild species conservation in genetic reserves".

On-farm conservation

The Barley Working Group expressed a wish that the Cereals Network would encourage the ECP/GR on-farm conservation task force to pay more attention to cereals.

Public awareness

It was stressed that public awareness and support is important to the genetic resources community.

Individual country reports

The status of barley collections and related activities in their respective countries were presented by Zapryanka Popova (Bulgaria), Danela Murariu (Romania) and Michaela Benková (Slovakia). Additional country reports were submitted during and after the meeting from Czech Republic, France and Lithuania (see papers in Part II, pp. 109-127).

Novo Pržulj (Serbia and Montenegro) also presented the barley collections in his country and provided additional information on a project funded by SIDA (Swedish International Development Agency) for cooperation on genetic resources in the Balkans.

Research activities

Tzion Fahima reported to the Barley Working Group on genetic mapping and expression analysis on *Hordeum vulgare* subsp. *spontaneum* ecotypes and *Hordeum vulgare* subsp. *vulgare*.

Overview on barley GENRES project

H. Knüpffer (project coordinator) gave an overview on the results of the EU-funded barley GENRES project[36], which was carried out from April 1999 to September 2002. The project included 28 partners from EU member states and seven from non-EU countries, whose

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34 Knüpffer, H., R. von Bothmer, M. Ambrose, R. Ellis, A.M. Stanca, D. Enneking, L. Maggioni and E. Lipman, compilers. 2001. Report of a Working Group on Barley, Sixth meeting, 3 December 2000, Salsomaggiore, Italy. International Plant Genetic Resources Institute, Rome, Italy.

35 Heywood, V.H. and D. Zohary, editors. 1995. A catalogue of the wild relatives of cultivated plants native to Europe. Flora Mediterranea 5:375-415.

36 Enneking, D. 1999-2002. Evaluation and conservation of barley genetic resources to improve their accessibility to breeders in Europe. Project homepage: http://barley.ipk-gatersleben.de.

Enneking, D. and H. Knüpffer. 2001. Fishing in the gene pool: Evaluation of barley genetic resources in Europe. P. 79 *in* EUCARPIA Section Genetic Resources "Broad Variation and Precise Characterization – Limitations for the Future". Abstracts. Poznań, Poland. IGR/IHAR/IPGRI.

Enneking, D., E. Schliephake and H. Knüpffer. 2001. Documentation and evaluation of barley genetic resources in Europe. P. 26 *in* 4th International Triticeae Symposium, in Córdoba, Spain. Junta de Andalucia. Consejera de Agricultura y Pesca, Córdoba.

Enneking, D., E. Schliephake and H. Knüpffer. 2003. Enhancing the practical value of barley genetic resources in Europe through evaluation and documentation. Pp. 15-17 *in* From biodiversity to genomics: breeding strategies for small grain cereals in the third millennium. Proceedings EUCARPIA Cereal Section Meeting, 21-25 November 2002, Salsomaggiore, Italy (C. Marè, P. Faccioli and A.M. Stanca, eds).

evaluation activities during the last project year and participation in project meetings were financially supported by ECP/GR. Dirk Enneking was the project and database manager at IPK. During the project, substantial progress in the development of the EBDB was achieved (see above). The main tasks of the project consisted in the evaluation of a large number of barley accessions, especially of the BCC, for their reaction to a number of biotic and abiotic stress factors with standardized methods. Promising material for breeding purposes was identified, especially for leaf-stripe and barley yellow mosaic virus (BYMV) resistance.[37] In the end of the project, the participating breeders expressed their interest in a follow-up project, which would also include pre-breeding. The project homepage (http://barley.ipk-gatersleben.de) includes a list of the partners, the project description, the searchable European Barley Database, searchable evaluation results, descriptions of the standardized evaluation methods used, various downloadable documents and links to available evaluation data.[38]

Upcoming meetings

The Barley Working Group suggested holding an *ad hoc* meeting and an open workshop on barley genetic resources in connection with the International Barley Genetics Symposium (IBGS) in Brno, Czech Republic, in June 2004.[39]

Publications

A paper on the European Barley Database is to be presented at the IBGS.[40] The preparation of publications about the results of the GENRES project on various disease and stress resistances is also desirable. A few of these have already been published or at least prepared, and some results have been reported at conferences.

Priorities of the Barley Working Group for ECP/GR Phase VII

(This section was updated after the meeting and finalized during the IBGS in Brno, June 2004)[41]

At its ninth meeting in October 2003, the ECP/GR Steering Committee defined priority areas for Phase VII (see above, p. 8). With respect to these priorities, the Working Group recommended the following:

1. **Characterization and evaluation (including use of modern technologies)**
    - Barley Core Collection (BCC) to be extended by an Ethiopian/Eritrean subset and a subset on genetic stocks; BCC documentation to be further developed; study the BCC using molecular markers.
    - Set up an ECP/GR task force of barley breeders and scientists with an interest in pre-breeding and develop regional cooperation in this issue, also in collaboration with FAO. This group will prepare a background paper together with FAO as a basis for possible funding of pre-breeding activities.
    - Continue the ring test on barley net blotch which started as an activity of the Barley WG in the Barley WG meeting in Salsomaggiore in 2000. The main objective of the ring test is to test the behaviour of net blotch resistant breeding material under different environments (under the coordination of Marja Jalli, Finland).

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37 GENRES CT98-104 Final project report (unpublished).

38 Enneking, D. and H. Knüpffer. 2002. Gen Res Barley project successfully completed. IPGRI Newsletter for Europe 25:9.

39 See Appendix I, pp. 212-216.

40 H. Knüpffer presented an invited lecture on "Gene Banks and Access to Barley Genetic Resources Information".

41 See Appendix I, pp. 212-216.

2. **Task sharing**
   - Identification of duplicates and designation of "primary collection holders", as a concerted action in harmony with other groups of the Cereals network; methodology and database-supported procedures to be developed in a pilot study of the Documentation and Information Network (AEGIS project approved by the ECP/GR Steering Committee in October 2003 and started mid-2004).
   - Set up a system for safety-duplication (cooperation with the ECP/GR Documentation and Information Network) – to be developed for all cereals within the Cereals Network.

3. ***In situ* and on-farm conservation**
   - The Barley Working Group stressed the importance of facilitating the conservation of wild relatives and encourages an on-farm task force. Prepare a list of wild *Hordeum* spp. occurring in the ECP/GR mandate region, identify species and areas in need of protection, in cooperation with the EU project PGR Forum and the ECP/GR *In situ* Task Force.

4. **Documentation and Information**
   - Further develop the European Barley Database at IPK, transfer it to Oracle, develop new and user-friendly search interfaces. The Barley Working Group is very keen to ensure that the development of EBDB is guaranteed in the future.
   - Develop updating mechanisms based on retrieving barley data from EURISCO instead of, or in addition to, requesting new updates from data providers (contributing genebanks).[42] The relationship between EURISCO and central crop databases needs to be clarified.
   - Seek cooperation and integration between the EBDB and other international databases and information networks on barley genetic resources (such as SINGER, Global Barley Genetic Resources Inventory, GRIN) and the Database on Barley Genes and Genetic Stocks (BGS).

Election of the Chair/Vice-Chair

Both the present Chair Roger Ellis and the Vice-Chair Merja Veteläinen indicated that they had to resign from these positions. The Barley Working Group then elected Helmut Knüpffer from Germany as the new Chair, and Marja Jalli from Finland as the new Vice-Chair. The new Chair thanked Roger Ellis and Merja Veteläinen for their dedication to the Barley Working Group and the successful meeting.

Recommendations

1. *The relationships and cooperation between the cereal Central Crop Databases (CCDBs) and EURISCO should be discussed at the Cereal Network level among CCDB managers. The discussion should include crop-specific aspects and the handling of data fields that are not recorded in EURISCO.*
2. *The principles of sharing of responsibilities and tasks between the genebanks should also be a topic for the Cereals Network.*
3. *Links should be established between the Database on Barley Genes and Genetic Stocks (BGS) and the EBDB.*
4. *The issue of safety-duplication should be discussed at the Network level.*
5. *The ECP/GR* In situ *Task Force should pay attention also to wild cereals, and links should be established between the Cereals Network and the EU project PGR Forum.*

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[42] It is expected that this updating mechanism will be developed within a new EU GEN RES project.

Concluding remarks

The new Chair thanked the participants for their active involvement in the work of the Barley Working Group during the meeting, and closed the meeting.

Working Group on Wheat[43]

Wolfgang Kainz, Gert Kleijer and Jean Koenig

Status of the European Wheat Database (EWDB)

Anna Michalová presented the progress made in the EWDB on behalf of Iva Faberová and Annick Le Blanc (for details, see paper by I. Faberová on *The European Wheat Database (EWDB) – status in June 2003*, pp. 131-137). The database is now available on the Internet, searchable on-line and downloadable (http://genbank.vurv.cz/ewdb). It currently contains 132 000 records or 56% of all European wheat accessions, which means that about 40% are still not included.

Since 2001 the following workplan has been fulfilled:

- Harmonization of the presented data according to the revised version of the FAO/IPGRI *Multi-crop Passport Descriptors* format (MCPDv2, Dec. 2001) and converting data;
- Delivery of missing data;
- Supply of characterization data for the six descriptors as agreed at the last meeting of the Wheat Working Group (Prague, November 2001): awnedness, grain colour, glume colour, glume hairiness, spike density and plant height.

Most characterization data are missing; so far only those of the Research Institute of Crop Production (RICP), Prague, are included.

The future tasks include:

- Filling the gaps in the list of passport data by downloading from the EURISCO catalogue, which should be available on-line by September 200344; and
- Filling the gaps in the list of characterization data.

The EWDB has been invited to participate in the Global Inventory of Wheat Genetic Resources developed by CIMMYT in 1993.

A primary objective of this project is to establish collaboration among partners and to link passport data with SINGER.

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43 Both co-Chairs, Iva Faberová and Annick le Blanc being unable to attend, the session was chaired by Gert Kleijer.

44 As of September 2003, EURISCO is on-line at http://eurisco.ecpgr.org/

National reports

The session on presentation of the country reports was introduced by a letter sent by Annick Le Blanc, co-Chair of the Working Group, who unfortunately could not attend this meeting. She made the proposal to use the results of data analysis for rationalization of collections and to exchange safety-duplicates as black boxes with another country.

She also proposed to hold the next meeting in La Rochelle, France. The Group approved this offer, provided it is accepted by the Steering Committee.

In the following country reports (see pp. 138-192), the members gave an overview of the impressive outcomes of their work, but it became clear that there are still various problems to be solved:

- Technical problems such as lack of missing equipment (seed dryers, insufficient cold stores, etc.);
- Other problems are the lack of computerization of passport data and nearly all participants reported gaps in the availability of characterization and evaluation data;
- Y. Anikster reported a different problem in Israel, that is the presence of endangered locations of wild-growing *Aegilops* that have to be collected and preserved *ex situ* very quickly (see paper pp. 146-147);
- P. Perrino mentioned reduction of funds in Italy for research in general and therefore genetic resources. The approval of regional laws (such as in Toscana and many others) regulating conservation and access of PGR was quoted as a positive development. Besides, a national law is needed.

Future targets mentioned by the participants include computerization of missing passport data and characterization and evaluation data and to make their collections data searchable on line.

The evaluation of the collections is one of the main targets for the documenting of all characters including stress tolerances and to use molecular markers to map traits for disease resistances, storage protein alleles or dwarfing genes.

Recommendations at Working Group level

- **Characterization and evaluation**

In the discussion, it became clear that it is important that genebanks record morphological trait characteristics of genotypes during regeneration, possibly in collaborative projects.

The evaluation work should be done in collaborative projects with breeders as users of the genetic resources as well as with farmers associations, as stressed by P. Perrino.

Recommendation

It was agreed that characterization and evaluation data increase the value of every collection and database, but due to the large amount of accessions conserved, every genebank should focus on its unique accessions, as identified by the DB manager.

Workplan

After consulting I. Faberová about the possibility of integrating data into the database, existing characterization and evaluation data should be sent to the DB manager.

- **Sharing of responsibilities**

It was noted that I. Faberová had distributed a list of the unique accessions held by each genebank, after analyzing the EWDB. The wild relatives are not included in this list.

Recommendation

The Group agreed that every genebank should take responsibility for its own unique accessions and should also formally make a commitment to conservation, as a first step to increase task sharing.

As a second step, duplicates could be tracked and handled in a rational way, i.e. responsibility could be assigned for the conservation of Most Original Samples.

- **Safety-duplication**

The importance of increasing the level of safety-duplication was stressed. It was also mentioned that the level of safety-duplication in a few cases (Centre for Genetic Resources, the Netherlands (CGN); Bari Genebank) is already high. Y. Anikster questioned whether long-term conservation at –20°C would be adequate for long-term conservation, since wild species would not keep their viability for longer than 20 years and cultivated plants for about 50 years. He suggested that ways should be sought to implement longer-term conservation using liquid nitrogen. The Group considered that there could be no immediate possibility of finding an agency that would finance such a system, but the idea could be re-considered in future meetings.

Recommendation

Every genebank is considered responsible for providing safety-duplication for its own collection. At the same time, it was recommended to establish a quality system to carefully monitor viability, in accordance with ISO 9000.

Newsletter

The Group agreed on the establishment of a *Cereal Newsletter* as proposed by Annick Le Blanc, but this should not conflict with the *IPGRI Newsletter for Europe*.

The *Cereal Newsletter* could be published as an electronic bulletin on the ECP/GR Cereal Web page and would include short information on PGR activities carried out by the Network members.[45]

- **Core collections**

The Group thought that core collections would not be a priority for the Network in the next phase, since the database needs first to be more complete with characterization and evaluation data.

- **Documentation**

The progress made in the EWDB has already been mentioned above. The Group recommended filling the gaps in missing passport data. P. Perrino suggested concentrating on factors preventing a database from being completed and then suggesting strategies to overcome the problems or to find solutions and reach the objective of completing the database.

- **Pre-breeding**

It was considered that pre-breeding had been carried out with some success in the past (e.g. using wild emmer and *Aegilops ventricosa* to transfer resistance). However, this type of work takes a long time, up to 25 years, and it is very difficult to obtain funds for these long-term projects, as well as to guarantee staff continuity.

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[45] The first issue of the *Cereals News Bulletin* was published on-line in December 2004 and the second issue in December 2005 (http://www.ecpgr.cgiar.org/Networks/Cereals/cerealsnews.asp).

It was concluded that, in some cases, pre-breeding work could be very worthwhile, but genebanks could hardly hope to get sufficient funds and commitment for such very long-term research. P. Perrino said that since there is no clear request from the users, genebanks are rather reluctant to do pre-breeding.

- ***In situ* / on-farm conservation**

It was considered that *in situ* conservation of wheat wild relatives is only relevant for a few countries, such as Armenia and Israel.[46] On the other hand, there is increasing interest in on-farm conservation. Examples were quoted from Austria, France, Germany and Switzerland, mostly by private associations, with support by the governments.

It was felt that on-farm conservation of wheat can be an activity where genebanks have a role to play and that this would help the conservation of diversity. P. Perrino cited the example of hulled wheat in Italy.

- **Public awareness**

The Working Group reflected on the importance of public awareness, but thought that it would not be easy to address this item at the Network level and felt that the Steering Committee could perhaps establish a specific task force to improve efforts in this direction.

Priorities of the Wheat Working Group for Phase VII

- Fill the gaps in the EWDB;
- Strengthen work on characterization and evaluation;
- Improve the level of safety-duplication;
- Strengthen quality standards for conservation.

The Working Group concluded that it would be important to hold another meeting in three years' time to ensure a more stable basis for future work with this very important crop.

It was also recommended that A. Le Blanc and I. Faberová continue their role as co-Chairs of the Group.

Loek von Soest stressed the good prospects for a project proposal including wheat genetic resources in GENRES. Wheat is the crop with the largest acreage in Europe and many European collections do exist. Previous GENRES proposals were unfortunately not successful because they particularly focused on setting up a European Database, which was not completely in line with the stepwise approach requested by the EC Regulation 1467/94.

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[46] As pointed out by H. Knüpffer after the meeting, the distribution of wheat wild relatives over several more European countries is documented for example in:
Perrino, P., G. Laghetti, L.F. D'Antuono, M. Al Ajlouni, M. Kanbertay, A.T. Szabò and K. Hammer. 1996. Ecogeographical distribution of hulled wheat species. Pp. 101-119 *in* Hulled wheats. Promoting the conservation and use of underutilized and neglected crops. 4. Proceedings of the First International Workshop on Hulled Wheats, 21-22 July 1995, Castelvecchio Pascoli, Tuscany, Italy (S. Padulosi, K. Hammer and J. Heller, eds). International Plant Genetic Resources Institute, Rome, Italy.

Plenary sessions

Reports on activities on other cereals

Secale activities and Database

Wiesław Podyma presented the European *Secale* Database (ESDB).[47] It contains passport data of 9901 accessions. Twenty-one European institutions contributed to the ESDB. The biggest *Secale* collections are maintained in Poland, Russia and Germany. Thirty-three per cent of accessions maintained in *Secale* collections throughout Europe can be provisionally identified as duplicates.

The ESDB is available on the Internet (www.ihar.edu.pl/gene_bank/secale/secale.html). A network of breeders could be assembled for evaluation of rye materials, and at this stage, assistance from ECP/GR would be important.[48]

Triticale activities and Database

Gert Kleijer presented the recently established European Triticale Database. The database is not available via the Internet. Nine European institutions (including both former BAZ and IPK for Germany) contribute to the database, which currently contains passport data of 5203 accessions. The usefulness of a database depends strongly on the quality of the data recorded. Only 50% of accessions have determined growth habit. Ploidy level, an important character for triticale, has only been determined for 50% of the accessions. Much of this collection comprises breeders' lines. Genetic stability of the maintained materials also poses a problem for regeneration. The number of duplicates has not been determined because of considerable gaps in passport data (see paper pp. 194-195).

In future, the database will be available via the Internet. The PBAI (Plant Breeding and Acclimatization Institute, Radzików, Poland) offered to put triticale on-line on their server. For the moment the development of the database will be continued as before; subsequently the DB Manager would probably need help at the stage of sharing responsibilities.

H. Knüpffer suggested exploring the possibilities of applying flow cytometry to distinguish between ploidy levels in triticale accessions. M. Leggett stressed that this may not work in the case of triticale, since it is composed of different genomes.

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47 See also:
Podyma, W. 1998. Rye genetic resources in European genebanks. Pp. 87-92 *in* Challenges in rye germplasm conservation. Proceedings of an International Conference on Crop Germplasm Conservation with Special Emphasis on Rye, and an ECP/GR Workshop, 2-6 July 1996 Warsaw/Konstancin-Jeziorna, Poland (T. Gass, W. Podyma, J. Puchalski and S.A. Eberhart, compilers). International Plant Genetic Resources Institute, Rome, Italy.
Podyma, W. 2003. Rye genetic resources in Europe. Plant Breeding and Seed Science 48(2/2):37-44.

48 A small meeting on rye was included in the budget of the Cereals Network for Phase VII.

H. Knüpffer informed the participants that Russian colleagues in St. Petersburg and Daghestan[49] have been working on a descriptor list for triticale. They also developed elements of an infraspecific classification of triticale. Z. Stehno informed the participants about the existence of a Czech triticale descriptor list with parallel versions in English and Russian.[50] If the participants of the ECP/GR *ad hoc* initiative on triticale consider it essential to update the international descriptor list on triticale[51], these activities should be taken into account as starting point, once translated.

The European Maize Database

Dražen Jelovac presented the European Maize Central Database, which is available on the Internet and can be downloaded. It is intended to develop a project on a searchable database. The information on landraces evaluated in the RESGEN project on European landraces is included in the database. Inclusion of information on resources maintained by breeding companies is being considered.

Initiatives on minor cereals

Anna Michalová, focal point for the Minor Crops Group, presented the current state of the database. The database contains information on minor crops that are not covered by other databases (e.g. buckwheat), but also on some minor cereals that are covered by other central crop databases, such as the "multicaule" forage rye or naked barleys. The reason for the inclusion of the latter in a separate database is their suitability for utilization in organic farming. A. Michalová explained that such a thematic database is more useful for users. Many important collections have not been included so far, e.g. VIR's millet and buckwheat accessions, and the French collection of buckwheat (see paper pp. 196-200).

The discussion was focused on duplication of information with the other cereal databases. H. Knüpffer said that since other CCDBs are covering the whole genera *Hordeum*, *Secale* or *Triticum*, respectively, there is no need to duplicate this work for the minor crops. Loek van Soest found some advantages in this duplication, since it is easier to find specific items in the minor crops database.

In addition, difficulties are expected to extract data on naked barley and "multicaule" rye (which are in the interest of the Minor Crops Network) from EURISCO due to problems in handling taxonomic information in many genebanks, and subsequently in EURISCO.

Anna Michalová said that the Network will focus on documentation of buckwheat and millet as target plants.

Recommendations

1. *The ECP/GR Steering Committee is requested to give its agreement for an* ad hoc *meeting of the* ad hoc *groups' database managers with other experts to define strategy for the databases.*[52]
2. *Development of the databases should be continued. Efforts to fill gaps, inclusion of data from new partners, and inclusion of characterization and evaluation data should be continued.*

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49 Their addresses have been communicated to G. Kleijer.

50 Rychtárik, J., V.I. Mogileva, F. Beneš, J. Sehnalová and I. Bareš. 1991. Descriptor List Genus x*Triticale*. Müntzing, Prague. 33pp.

51 IBPGR. 1985. Descriptors for Rye and Triticale. International Board for Plant Genetic Resources, Rome, Italy. 13pp.

52 The Cereals Network Coordinating Group eventually proposed for Phase VII that a triticale *ad hoc* meeting would be held in 2005 or 2006, possibly but not necessarily in conjunction with a rye *ad hoc* meeting, to be held jointly with the EUCARPIA Rye Meeting, Gross Lüsewitz, Germany, 2006.

Thematic issues

Documentation/databases

- **Progress of the EPGRIS project and the EURISCO catalogue**

L. Maggioni presented the progress of the EU-funded project EPGRIS (http://www.ecpgr.cgiar.org/epgris/index.htm) for the Establishment of a Plant Genetic Resources Infra-Structure. The objective is to establish a European Internet Search Catalogue (EURISCO) with passport information of plant genetic resources maintained *ex situ* in Europe. Before the end of 2003, the first version of EURISCO is expected to be launched on-line and to contain a combination of data available from the existing national inventories and from the existing Central Crop Databases (CCDBs).[53] EURISCO is expected to gradually develop and become the most complete and reliable source of passport data in Europe. The catalogue will host an important minimum set of passport data, frequently and automatically updated from the national inventories. These data will be based on the revised version of the FAO/IPGRI *Multi-crop Passport Descriptor List* (MCPDv2) finalized in December 2001 (http://www.ipgri.cgiar.org/publications/pubfile.asp?ID_PUB=124). National focal points, already designated in all European countries, will be responsible for data sources, data quality and accuracy, data availability and provision of data in the EURISCO–MCPD format. The central node receiving the data at IPGRI will be responsible for checking data compatibility with the catalogue, providing feedback to national partners, importing data into EURISCO and developing and maintaining the front end.

The launching of the first version of EURISCO is expected to take place at the occasion of the final meeting of the EPGRIS project, which is planned for September 2003 in Prague, Czech Republic, jointly with a meeting of the ECP/GR Documentation and Information Network. On this occasion, all European National Inventory focal persons and Central Crop Database managers will have the chance to discuss the future relationship between EURISCO and the CCDBs. A document distributed in April 2002 to the ECCDB managers by the EPGRIS project contained a suggested way forward in this relationship, i.e.:

1. CCDBs to harmonize their structure with EURISCO (the Centre for Genetic Resources, The Netherlands has already converted available CCDBs into the EURISCO format and has sent subsets of national data combined from the different CCDBs to the respective national focal points for inclusion into the national inventory and eventually into EURISCO).
2. CCDBs to continue gathering data until EURISCO becomes the preferred source of passport data.
3. Once EURISCO becomes operational, consider retrieving data from EURISCO.

Three possible scenarios are also expected to exist at any point in time, depending on the specific crop, i.e. that:

1. EURISCO contains less data than CCDB,
2. EURISCO contains more data than CCDB, and
3. EURISCO contains different data than CCDB.

[53] At the final EPGRIS conference (Prague, 11-13 September 2003) it was said that EURISCO contains only the data from National Inventories. Work on the possible inclusion of data from CCDBs did not lead to their direct inclusion in EURISCO, but helped to facilitate their possible inclusion in the respective National Inventories, and through them, into EURISCO.

A transition phase is considered likely to last 2-3 years before a good harmonization between EURISCO and the CCDBs is completed. The role of the CCDBs and their managers will also be on the agenda of the Prague meeting. It is foreseen that this role will increasingly focus on helping improve data quality, tracing duplicates, gaps, Most Original Samples, gathering characterization/evaluation data, analyzing information (GIS, etc.), providing the users with data in various formats, helping defining core collections, safety-duplication and collecting needs, etc.[54]

- **Computer-assisted search for duplicates in a medium-size Cereal Central Crop Database – the case of *Avena* (EADB)**

(see paper by C. Germeier and L. Frese, pp. 53-62)

On-farm conservation

- **On-farm conservation of hulled wheat in Italy**

(see paper by P. Perrino, pp. 154-161)

Discussion and recommendations at Network level

Sharing of responsibilities and safety-duplication

C. Germeier gave a demonstration of the tools and properties of the European *Avena* database, which were implemented in order to identify duplicates conserved in several genebanks. He also stressed the importance of a clear distinction between original information provided by collectors, breeders or other donors of specific accessions to genebanks and secondary information derived from literature and other data sources on cultivars, etc. The CCDBs should provide both types of data, while the secondary data should be primarily held on a duplicate group level by the central crop database.

He further explained an application specially designed to record the level of responsibility for conservation that each curator agreed to take for each accession. The application could be distributed as a runtime module on the Windows operating system to genebank curators for entering their decisions for their accessions. Results can be exported to an Excel worksheet, which should be sent back to the database manager for inclusion of the decisions into the CCDB.

I. Loskutov demonstrated serious inconsistencies that he found in CCDBs and pointed out the importance of the use of taxonomic characters to identify duplicates.

There were differences in opinion about the importance of expanding effort to identify duplicates, as opposed to simply conserving them, as there was little additional cost.

The importance of identifying duplicates depends on the priorities for conservation across the region (i.e. it would not be necessary for several genebanks to multiply the same accession for distribution to users and regeneration could also be rationalized). The identification of duplicates would broaden the information available for the accessions in a duplicate group, would help users who wish to work with diverse accessions and also help to define core collections.

On the other hand, a correct identification of the samples in storage could be sufficient and possibly more useful than searching for duplicates.

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54 As of September 2003, EURISCO is on-line at http://eurisco.ecpgr.org. Presentations and papers prepared for the EPGRIS Final Meeting (11-13 Sept. 2003, Prague, Czech Republic) are available on-line at http://www.ecpgr.cgiar.org/Networks/Info_doc/FinalMeetingReports.htm.

Recommendation

1. *DB managers agree to analyze their databases to define lists of unique accessions conserved in different genebanks and send these lists to the Working Group members.*
2. *Working Group members and genebank curators, in consultation with appropriate authorities and after further interaction with the DB manager, are encouraged to take the responsibility for conservation, according to the terms agreed in the previous meeting of the CNCG.*

Additionally, H. Knüpffer suggested that small groups with representation from the different Working Groups should be established to prepare documents for the attention of the Network in order to find solutions to common problems such as sharing of responsibilities and safety-duplication.

Evaluation data

It was considered important to find a general solution, such as following the examples of CGN and the USDA. It was also believed that the issue of inclusion of characterization and evaluation data should be addressed by the Documentation and Information Network since it is a general issue relevant to all crops.

Recommendation

A proposal was made that a specific meeting of the Documentation and Information Network to discuss the issue of characterization and evaluation data should be held in the near future. This meeting could either initially involve only a small group of experts to draft a proposal for action, or it could be a full meeting of all the CCDB managers. This proposal is being sent to the attention of the Documentation and Information Network for further elaboration.

In situ conservation

H. Knüpffer presented a list of wild relatives of cultivated cereals occurring in European countries (see above, session of the Barley Working Group, p. 24). This list was derived from data received from the Euro+Med project (University of Reading, UK). The taxonomy needs some editing, and members of the Network volunteered to work on it and communicate results to *Flora Europaea* via H. Knüpffer.

W. Podyma expressed concern for the risk of loss of some wild relative species that are very rare and therefore at high risk of loss, such as the recently discovered *Avena insularis* in Sicily.

In the discussion, it was suggested that similar lists of crop wild relatives in each country be developed for other crops, such as those covered by the Vegetables Network.

On-farm conservation

W. Podyma suggested that countries that are implementing the EC regulation 1257/1999 on rural development might provide the possibility of financial support for farmers who grow local varieties. The biggest progress has been achieved in Finland where special legislation and agro-environmental programmes were established. He also said that it is expected that a modification of the seed law in the EU will allow growing and trade of local varieties of importance for genetic diversity conservation and use. The importance of cooperation with NGOs in this area should also be stressed. Non-governmental organizations very often are involved in projects with farmers on maintaining old and local varieties. P. Perrino stressed the importance of on-farm conservation remaining self-sustainable, as a marketable product. This kind of activity needs long-term effort and training of farmers.

Recommendation
It is suggested to the Steering Committee to look for the possibility of cooperation in the area of PGR with agro-environmental programmes and the European Ecological Network NATURA 2000 in particular countries.

Utilization
E.P. Guimarâes from FAO expressed a wish to discuss utilization of genetic resources with the whole Group (see also reports from the Working Groups' sessions on Wheat and Barley). R. Jonsson explained that there are differences between crops and how difficult it is to incorporate genetic variation from wild into cultivated species. E.P. Guimarâes explained that FAO country focal points had been requested to provide information on the utilization of genetic resources. M. Leggett responded that he was unaware of such a request, but could provide examples of the use of genetic resources in cultivar production and research from each of the three *Avena* genepools:

- **Primary genepool**
  - 'Starter' Spring oat, has a high-protein *A. sterilis* accession in its pedigree;
  - Similarly, 'Ozark', with improved winter hardiness, was derived from an *A. sterilis* cross;
  - Spring oat 'Jay', includes crown rust resistance from *A. sterilis;*
  - A number of Brazilian varieties contain *A. sterilis* lines.

- **Secondary genepool**
  - Crown rust resistance genes from *A. maroccana* were an integral part of the synthetic hexaploid 'Amagalon';
  - 'CDC Bell' and a sister line, 'CDC Baler', forage oats were derived from an original cross involving *A. maroccana*.

- **Tertiary genepool**
  - A source of mildew resistance from the C-genome species *A. eriantha* transferred to the hexaploid cultivated oat has and is being used in the production of cultivars;
  - The cultivars 'Hinoat', 'Gemini' and 'Foothill' produced by Agriculture and Agri-Food Canada were all derived from an initial cross between *A. sativa* and the diploid *A. strigosa;*
  - *A. strigosa* x *A. sativa* crosses have also been used as sources of crown rust resistance in a complicated breeding programme at the University of Wisconsin and a second source of *A. strigosa.*

See also papers on *Wild* Avena *genetic resources for breeding and research* (pp. 98-99); *Using molecular mapping to access and understand valuable traits in wild relatives of oats* (p. 100); and *Phylogeny of ACCase in* Avena (p. 101).

Recommendation
The Network Group members were encouraged to contact their FAO country focal points so that they can provide additional information to FAO in this respect.

Public awareness

It was considered very difficult to find appropriate ways of increasing public awareness at a crop network level.

C. Germeier stressed the fact that there is a very tight connection between on-farm conservation and public awareness. It is important that the general public becomes familiar with genetic resources by seeing them used in the fields and having the chance of consuming them.

P. Perrino stated that NGOs such as organic farming associations and the special quality food initiatives could play a big role in raising public awareness. It is a strategy that has worked in Italy as a consequence of integrated actions started by the Bari genebank.

L. van Soest reported that the CGN Web site improved public awareness of the genebank.

FAO and IPGRI might work more closely together to create awareness. E. Guimarâes reminded the Network that it is not enough to involve only specialists or political authorities, but also the public, who are important in sustaining political support and funding of genetic resources work.

News bulletin

The Network Group decided to create an electronic news bulletin, to be included on the Web page of the Cereals Network for exchange of short information. The aim is to inform and stimulate Network members and to raise public awareness. The ECP/GR Secretariat will inform the Network members twice a year, 20 days before updating, in order to receive contributions on time.

Priorities at the Network Level for ECP/GR Phase VII

(This section was updated after the ECP/GR Steering Committee meeting in Izmir, October 2003)

At its ninth meeting in October 2003, the ECP/GR Steering Committee defined the following priority areas for Phase VII:

1. **Characterization and evaluation** for conservation (e.g. genetic integrity, genetic drift, diversity analysis), and **sustainable utilization** of genetic resources (including for traits of agronomic importance) using *inter alia* modern technologies such as **molecular markers, genomics and bioinformatics**;
2. **Task sharing** through collaboration, rationalization and specialization of activities and collections (formation of core collections, identification of most original samples) to maximize efficient use of human and financial resources;
3. ***In situ* and on-farm conservation**, including an analysis of material subject to *in situ* and on-farm conservation, and development of conservation and management techniques in relation to the existing opportunities of *ex situ* conservation;
4. **Documentation** – establishment, completion, improvement and maintenance of national PGR inventories, central crop databases, including validation of data, integration of characterization and evaluation data, improved and integrated data management, completion of infrastructure for automatic updating and completion and maintenance of the national inventories and the EURISCO catalogue.

The Network recommended the following priorities at the Network level:

1. **Characterization and evaluation**: no additional priorities over those discussed and presented by the Working Groups (see above).
2. **Task sharing**: a common view from all working groups is needed to harmonize procedures (to be documented by members of the Working Groups)

3. ***In situ* and on-farm conservation**: no additional priorities over those discussed and presented by the Working Groups (see above).
4. **Documentation:** most priorities have already been described in the Working Groups' reports. Additional priorities would be passed on to the Documentation and Information Network.
5. **Application and use of high technology (molecular markers, genomics)**: deployment of molecular markers is a high priority in appropriate genetic resources studies
6. The Network stressed as a high priority the increased, sustainable and continuous utilization of PGR as envisaged by the International Treaty on Plant Genetic Resources for Food and Agriculture.

Conclusion

Appraisal of the Cereals Network meeting

The formula of a full Network meeting was generally appreciated, since it offered the opportunity to exchange experiences throughout the Network. However, it was also felt that the time had not been sufficient for the Working Groups to discuss in separate sessions. The fact that some participants belong to several WGs that met in parallel led to under-representation, especially of the A*v*ena and Barley WGs. Similarly, the possibility of setting up small groups discussing themes of general interest was considered important for a future meeting. Overall, the Group believed that meetings of the entire Cereals Network would be useful and should be repeated, but perhaps it would be necessary to add at least one day of work. Therefore, the next Cereal Network meeting should reserve three separate days for the individual WGs and two days for the plenary session, allowing also for parallel thematic group discussions (suggestion from the Network Coordinating Group).

The Group recommended to the Steering Committee that the activities of the Cereals Network be continued into Phase VII.

The meeting was concluded with special thanks to the local hosts for the excellent organization provided in Yerevan, including a very interesting excursion to visit the wild cereal relative sites in the Erebuni State Reserve.

PART II. PRESENTATIONS AND PAPERS

Avena

Progress made in the European Avena Database (EADB)

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Up to now the ECP/GR central crop databases (CCDBs) have primarily been lists of multicrop passport data. This function will be taken over by EURISCO. However, important tasks will remain for the central crop databases. They can be developed into crop-specific genetic resources expert systems, primarily by advancing their functionality in relating and aggregating data. That is, they will find groups of duplicate accessions, compile and harmonize passport data for these duplicate groups, undertake geographic mapping of data, cover different taxonomic opinions and allow calculations on pedigree data (see Germeier and Frese, this volume, pp. 53-62). As a further task, the presentation of evaluation and characterization data will remain. If these are to be scientifically interpretable, they should be provided as the original data as taken by the observer (preferably counted or measured in SI units). Additional descriptive data on the experimental setting, treatments, observation and measurement technology, date of observation and the developmental stage of the crop observed should be available. For a quick overview, an additional easy-to-read score (normally 1-9), abstracting the information from different rating schemes and measurement units should be available. However, breeders searching evaluation data for practical purposes, are often interested not only in mean values, but also in the heterogeneity and diversity observed within the populations.

Fulfilling the tasks listed above requires a much more elaborate database architecture than is currently available for most of the central crop databases. A new object relational design of the database with several distinct modules (cf. Figs. 1, 2, 4, 5 *in* Germeier and Frese 2004) has been developed for both of the central crop databases held at the BAZ Gene Bank (European *Avena* Database, EADB, and International Database for *Beta*, IDBB). Functionality has first been implemented within a Microsoft Office environment using Visual Basic for Application (MS Access VBA). This provides the most easy-to-use development environment currently available and a simple connection to other MS Office products. These features make it most useful especially for prototype development. In a further step it would be feasible to redesign at least parts of the applications as Web applications, which could be used on-line on the Internet. A new pilot version for querying the new database implemented with PHP will be available within the framework of the project GENRES CT99-106.

Developments have been targeted at the following objectives:

1. Computer-assisted duplicate searching within the in-stock data and during database updates

More details on database design, database application, concepts and results related to duplicate checking are given in Germeier and Frese (this volume, pp. 53-62).

2. Providing a framework for storing corrected, harmonized and normalized data together with original data provided by holding genebanks for their accessions within duplicate groups

See Germeier and Frese (this volume, pp. 53-62) and Germeier and Frese (1994).

3. Providing a framework for the sharing of responsibilities

Terms and concepts for the sharing of responsibilities have been presented already at the *ad hoc* meeting of the Network Coordinating Group on Cereals (Germeier and Frese 2001) and in Germeier *et al.* (2003). An application has been developed enabling curators to view the duplicate groups involving their accessions and to make assessments regarding their duplicate status and the responsibility which their institutions intend to take over for accessions within the respective duplicate groups (see Germeier and Frese, this volume, pp. 53-62).

4. Data cleansing in passport data

A compilation of the original FAO/IPGRI *Multi-crop Passport Descriptors* (MCPD) table as an ACCESSION table has been embedded into a system of relational tables (see Germeier and Frese 1994). Normalization, harmonization, correction of probable wrong and inconsistent data is done within these additional tables, while the original data within the ACCESSION table remain untouched. Fig. 1 shows support of searching for accession names and the representation of harmonized and original passport data within the new database by the MS Access database application.

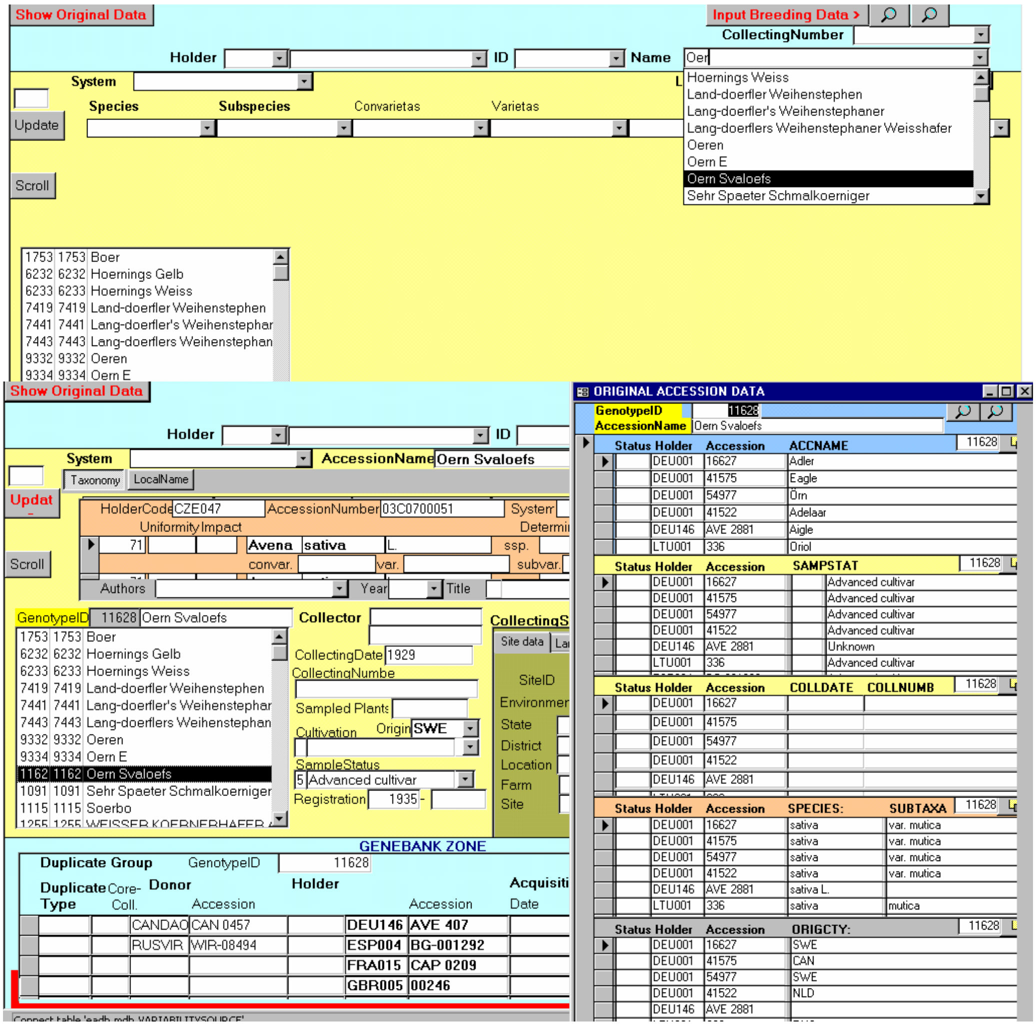

Fig. 1. Representation in the MS Access EADB application of harmonized and original passport data for a duplicate group represented by Svalöf's cultivar 'Oern'. Accession data are listed in the GENEBANK ZONE. Inconsistent original data are displayed accession-wise on the right window (ORIGINAL ACCESSION DATA).

5. Extracting and normalizing site data

Collecting and evaluation sites have been extracted into a distinct site table and geographic information has been atomized.[55] In addition to country, geographical coordinates and site, as demanded by the MCPDs, state (province) – district (region) – location (city, town, village) – and farm have been included. 'Site' as the smallest entity treats the name of a field or such qualifying information as "5 km SW". The MCPD COLLSITE will be available as a concatenation of these additional descriptors.

The more thorough geographical atomization will facilitate the following tasks:

1. Hierarchic querying of geographic data, which will facilitate search at sub-country level.
2. Computer-assisted completion of missing geographic coordinates with gazetteers.

Fig. 2 shows the representation of collected material in the MS Access database application.

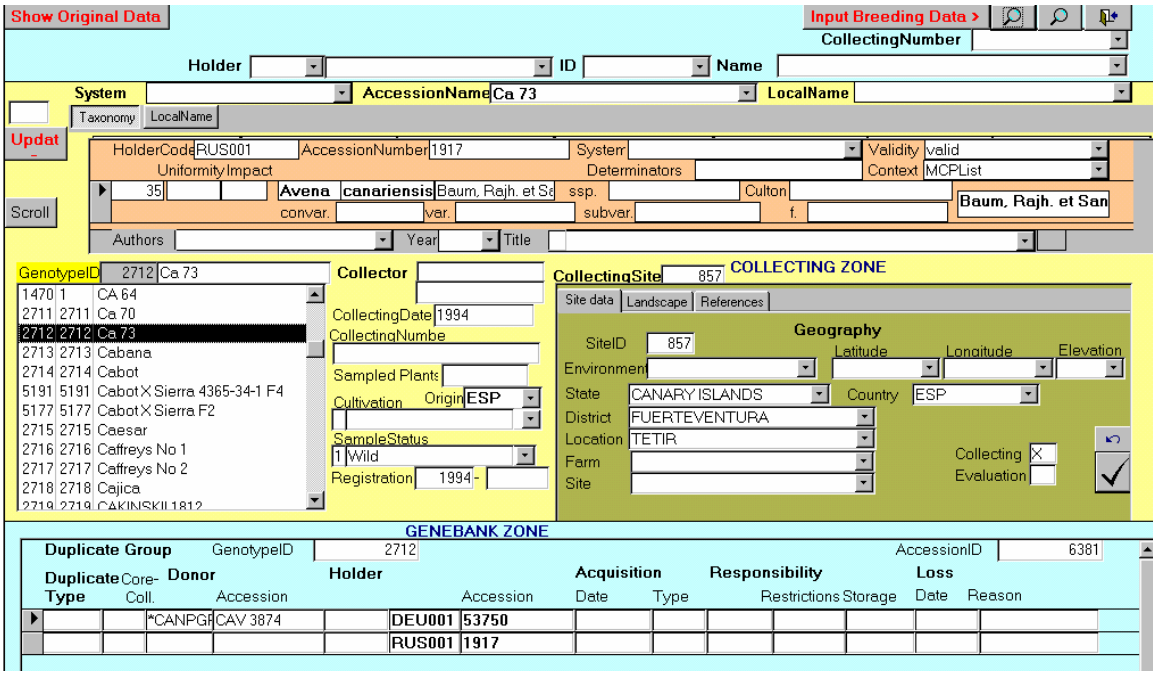

Fig. 2. Representation of collected material and collecting information including geographic information for a collecting site in the MS Access application for the EADB.

6. Implementation of a relational data model for pedigree data

Pedigree data are represented as a text field in the MCPDs. This requires a full text search for querying ancestors or descendants, which is not very effective. Selecting e.g. cultivars having a certain ancestor in their pedigree or querying disease resistance of ancestors of a certain cultivar would not be well supported.

While we were searching for cultivar history information regarding landrace and traditional cultivar accessions during the preparation of the GENRES project, a relational design for breeding and pedigree data was developed. Fig. 3 shows a representation of cultivar history data in the MS Access application. Translation from the MCPD text representation to the relational design and vice versa still has to be implemented.

[55] Atomization means placing only one instance of a single concept in a single field in the database.

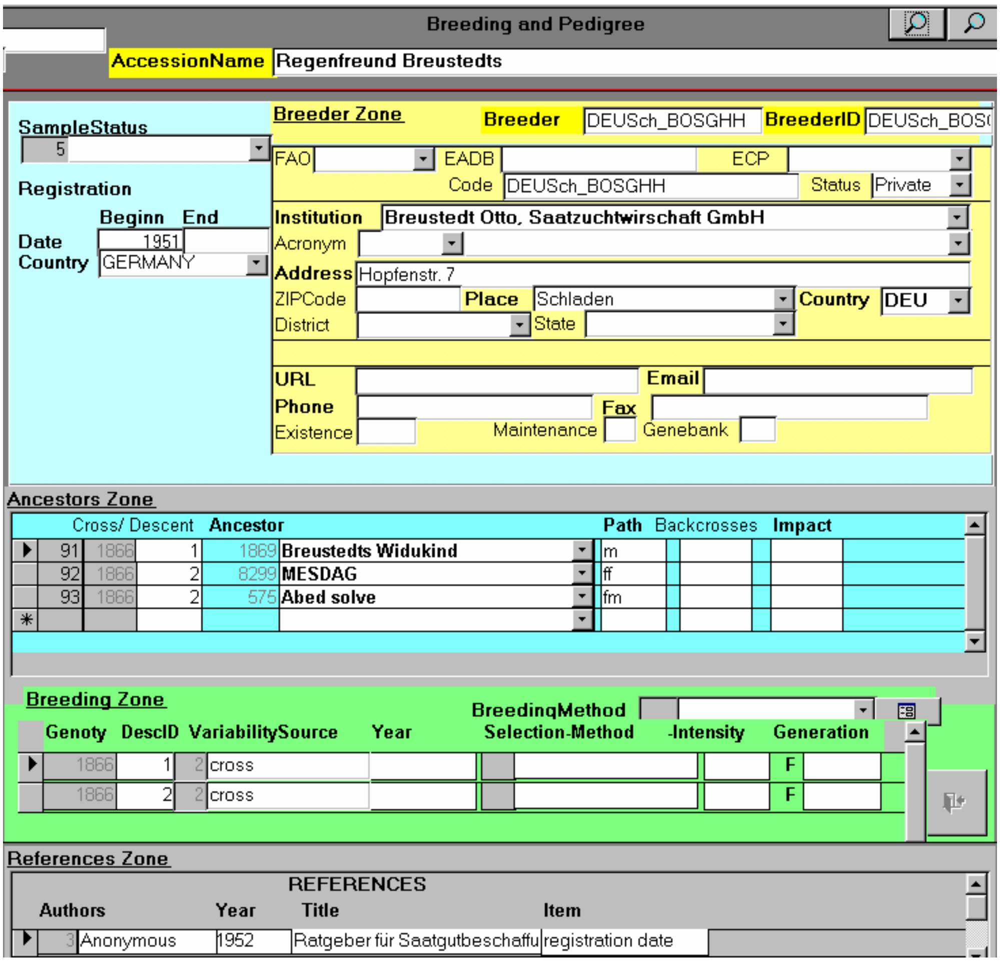

Fig. 3. Representation of breeding information in the MS Access application for the EADB.

7. Taxonomy

Botanical names provided by the various holders of the accessions have been extracted into a TAXONNAME table for harmonizing spelling, levels and authority. In a collaborative effort, together with Igor Loskutov (VIR) and supported by ECP/GR, it is planned to establish a parallel taxonomic system including Rodionova's taxonomic system alongside the Ladizinsky system. In further steps, the GRIN system (Wiersema) and the Canadian system (Baum) should also be integrated.

8. Including additional data

As in other working groups, there is a wish in the *Avena* Working Group to expand the database to an international level, including non-European data. Regarding oats, the most interesting is the Canadian collection with about 30 000 *Avena* accessions. More than 8000 are wild specimens, which effectively means that this has the status of a world base collection for wild *Avena*. Breeders would also be interested in Australian material. The Canadian genebank has adopted the USDA Genetic Resources Information Network (GRIN) implemented with the Oracle RDBMS for its documentation. The USDA itself records 24 500 *Avena* accessions with about 240 000 characterization and evaluation observations. Considerable duplication between European, Canadian and American collections is evident from passport data.

In discussions with genebank and database managers in Saskatoon and Beltsville during summer 2000, we explored the possibility of including the GRIN data into an International *Avena* Database and implementing a regular update procedure. There are no general obstacles, but technical data-warehousing problems have to be solved. The design of US and Canadian passport data differs largely from the ECP/GR MCPD format. Identification of accessions, with the aim of identifying duplicates, was not seen as a priority task when designing the GRIN system. Some details on the comparison of the GRIN data model with our CCDB data model (EADB, IDBB) are given in Germeier and Frese (1994).

To obtain the best value from including further data, the European database should first be fully established in an agreed format and the concepts presented in points 1) and 2), including the identifying of duplication between European and American collections should be fully implemented. It is clear that to include Canadian and USDA data will need additional working capacity and needs to be funded as an international project.

9. Characterization and evaluation data

It is well known from the requirements for scientific publication that numerous details must be given for a sound description and for the interpretation of scientific results. Scientific databases have to cope with these aspects as scientific publications do in their "Materials and methods" sections. In the EADB they are represented by modules, presented in the following sections as MS Access user interfaces. The underlying data model is shown in Germeier and Frese (1994). The modules cope with:

- **Projects, participants and experiments**

The project module documents collaborative projects, their participants and the experiments undertaken in the framework of these projects (see Fig. 4).

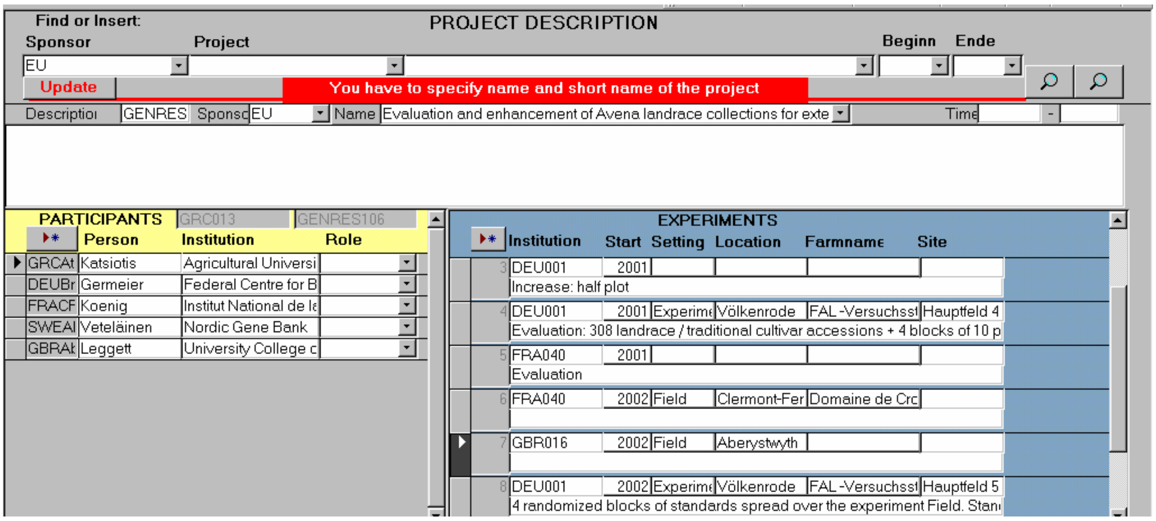

Fig. 4. Representation of project participants and experiments in the MS Access application for the EADB.

- **Experimental sites, treatments and settings**

This module allows for the documentation of experiments and experimental settings such as experimental design, experimental site and experimental treatments (Fig. 5).

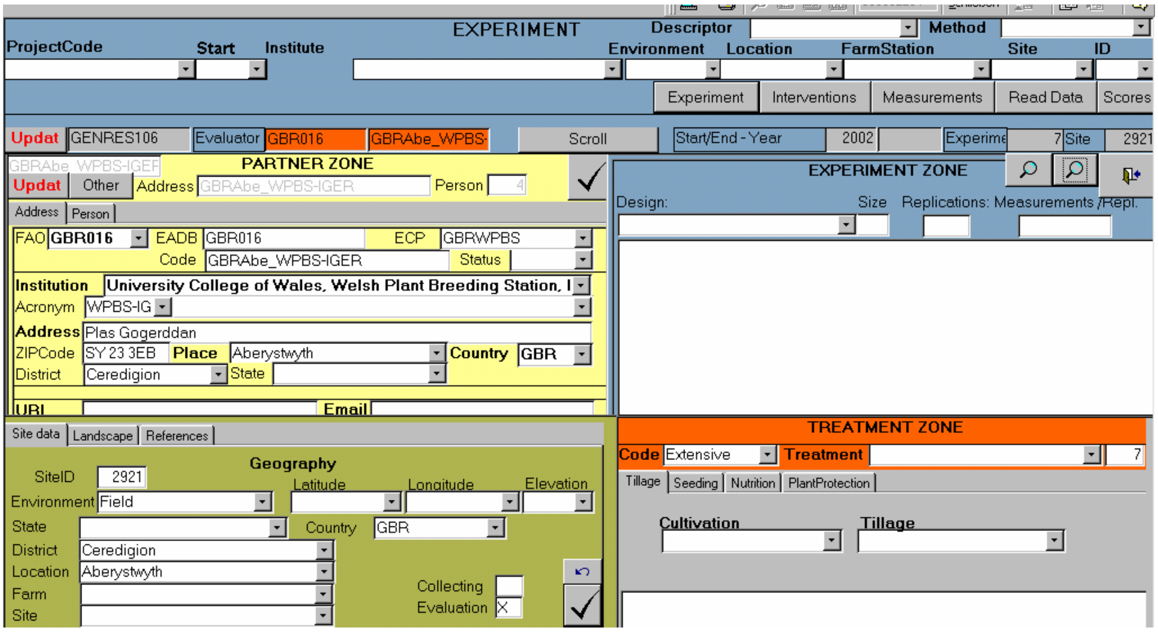

Fig. 5. Representation of experimental settings in the MS Access application for the EADB.

- **Experimental and agronomic interventions**

This module allows for a detailed and dated listing of all agronomic and experimental interventions done during the experimental cropping period (Fig. 6).

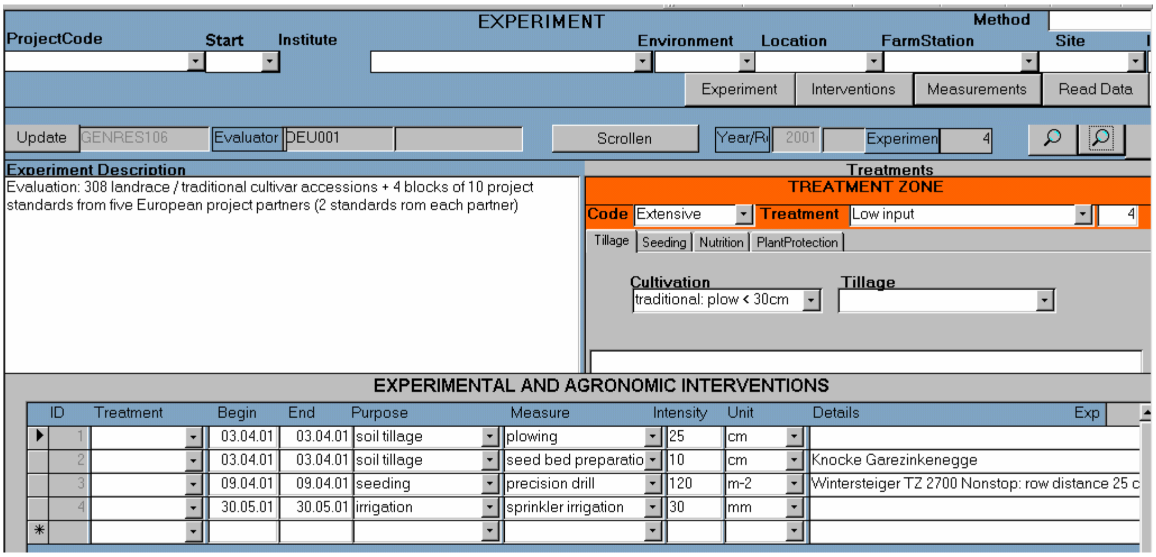

Fig. 6. Representation of experimental and agronomic interventions in the MS Access application for the EADB.

- **Descriptors and methodology**

This module allows for the relating of different methodologies (measurement procedures, rating schemes) to the descriptors given in IBPGR (1985). It also indicates which descriptors should be observed at specific developmental stages of the plant (Fig. 7). Currently, besides IBPGR (1985) descriptors, the UPOV (1976) and Bundessortenamt (1996) descriptors and methodologies are entered.

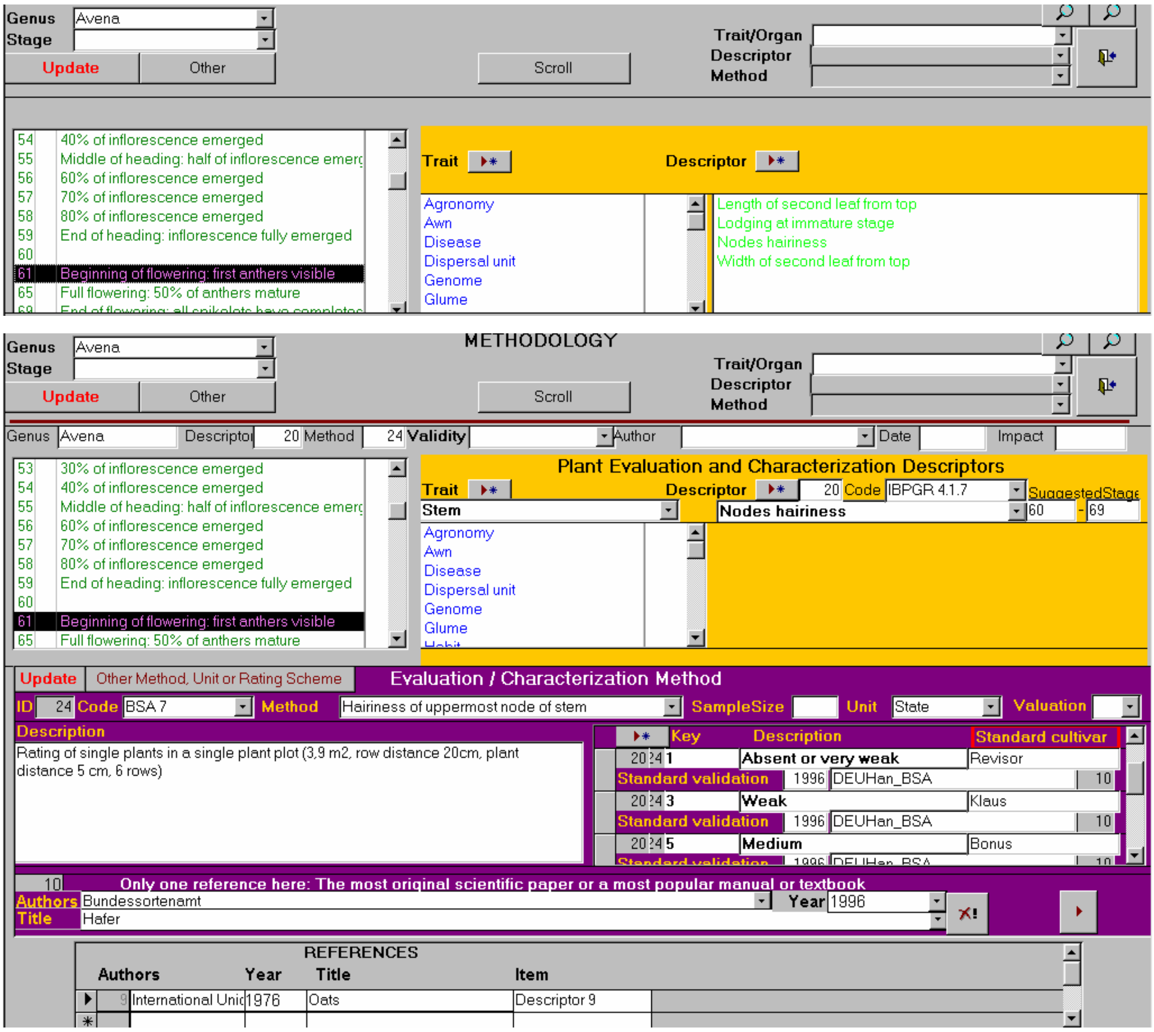

Fig. 7. Representation of descriptors and methodology in the MS Access application for the EADB.

- **Observations**

Original and harmonized data

The general philosophy used in the documentation of characterization and evaluation data in the EADB is outlined as follows:

1. Store all data as 'original', i.e. those which were first provided, as available.
2. Measurement data in SI units are generally preferred. Algorithms to generate easy-to-read scores from measurement data can be made available more or less easily. Algorithms leading back from scores to measurements will never be possible.
3. Offer the user an easy-to-read universal score (1-9) for initial guidance, but also allow him/her to access the original data.

The calculation of universal scores may be based on distribution parameters for an experiment, on regression models taking into account environmental and agronomic experimental information, or on comparisons with standard cultivars. Currently it is calculated on distribution parameters for an experiment, thus it is biased to the experimental sample and should only be regarded as applicable for experiments in which large numbers of accessions are tested.

Characterization and evaluation data are represented according to the single observation concept (van Hintum and Hazekamp 1992; Database Management Unit of the National Germplasm Resources Laboratory, http://www.ars-grin.gov/npgs/dict/prod/dd.html) in an OBSERVATION table. This allows for the unlimited representation of additional information for each single observation by the addition of further attributes within this table (e.g. date of observation, numbers and developmental stage of observed plants, number of field replications and descriptive statistics in the case of aggregated observations) and by links to other tables describing descriptors, methodology and experimental settings (Germeier and Frese 2004). This concept further allows implementing scoring for heterogeneous populations as suggested by van Hintum (1989) in an additional text format field. Details on the implementation of methods for scoring heterogeneous populations in our CCDBs (EADB, IDBB) are given in Germeier and Frese (2004).

The format to be used for communicating data on heterogeneity within a population to the EADB should follow the rules given below:

1. Put the scores of the separate fractions in decreasing order of frequency. The most frequent score(s) should stand in the first position(s), the rarest in the last position(s).
2. If there are two fractions of similar size, put an '=' sign between their scores.
3. If the ratio between a (group of) fraction(s) and the dominating one(s) is between 1.5 and 5.0 put one 'x' before this (group of) fraction(s); if the ratio is larger than 5.0, put 'xx' before it. This allows for differentiating fractions on three different levels of frequency.

Example: A=BxC=DxxE=F=G means: Two major fractions A, B (30-35%), two minor fractions C, D (5-25%) and three rare fractions E, F, G with less than 5%.

Raw data

Mechanisms for importing evaluation and characterization data from Excel spread sheets are implemented. The database application automatically generates descriptive statistics as means, standard errors, coefficients of variation, minimum, maximum etc. from raw data (Figs. 8 and 9).

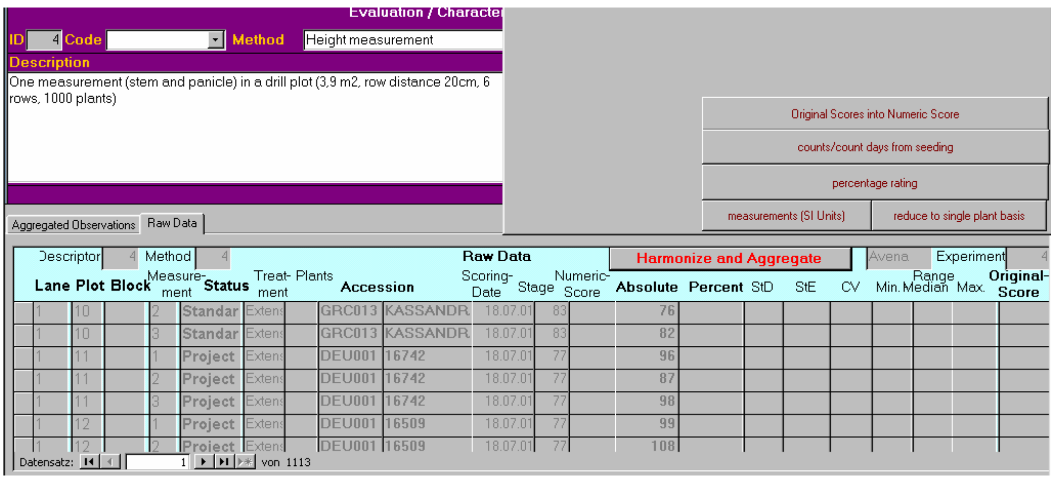

Fig. 8. Raw data and their harmonization and aggregation in the MS Access application for the EADB.

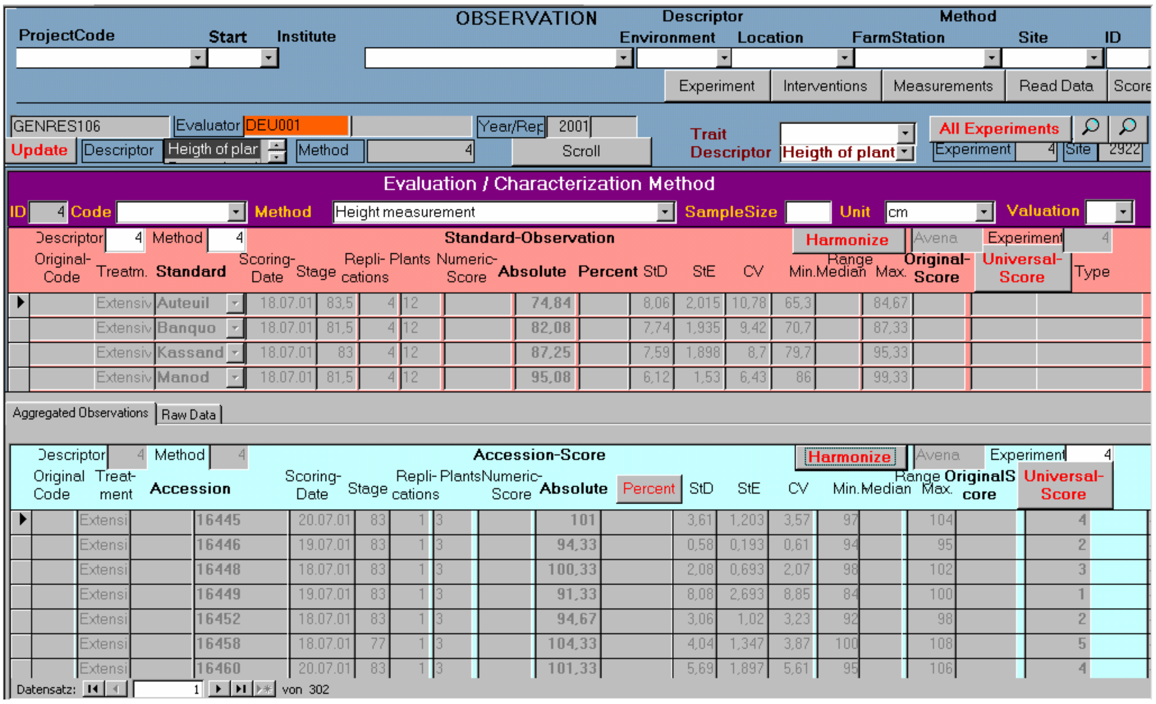

Fig. 9. Aggregated data for accessions and standard cultivars generated from raw data by the database application.

Suggestions for the transfer of future evaluation and characterization data to the EADB

It would be preferable if all raw data, not only the aggregated data (means) were delivered to the database (see above). Also, data would be better described if the respective development stages of the crop, or at least the dates of the observations, could be provided. Repeated measurements or scores can be imported from multiple columns as well as from multiple rows in the Excel sheet. Naming of columns is not of great importance (but the names should be understandable to the database manager) because the import facilities allow for separately defining the relationship of each column in an Excel sheet to the database objects. Experimental and methodological details should be provided separately to the database manager as in the "Materials and methods" section of scientific papers.

Generally providers of data are quite free in formatting their Excel sheets. However some general rules should be observed:

- Data in Excel sheets should be atomized, which means that only one number or code should be entered into one cell of the Excel sheet. All information entered within one column should relate to the descriptor represented by this column. Different information should not be merged or intermingled in one column.
- Absolute values for measurements and counts are generally preferred.
- Mixing of different data types (number, character, date) in one column should be avoided.
- Coded scores should keep to the descriptor lists (numeric scores 1-9 preferred). Additional codes like '+', '-', 'plus' etc. should be avoided. Blank (NULL) should exclusively indicate missing observations and vice versa.
- Heterogeneity in observations of one plot can be coded as described above. The database is able to store these data in original form as well as to extract mean, minimum and maximum values and to assign a universal score (rank).

Table 1 shows an example of a worksheet optimized for easy gathering of detailed data in the field and automated import into the database.

Table 1. Example of an Excel sheet easily readable by the database application

Status	Holder	Accession	Row	Plot	Date1	Stage1	Descriptors …						Date2	Stage2	Descriptors …			
Standard	BGR001	Asso	1	1	17.07.03	65							21.07.01	69				…
Accession	BEL004	125V	1	2	17.07.03	61							21.07.01	63				…
Accession	BEL004	175V	1	3	17.07.03	65							21.07.01	69				
Accession	…	…																
Accession	CHE001	80.5001	12	1	18.07.03	66							21.07.01	69				
	…	…																

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Computer-assisted search for duplicates in a medium-size Cereal Central Crop Database and an application for the sharing of responsibilities – the case of Avena *(EADB)*

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1. Some general observations on task sharing within an ECP/GR genetic resources information network

Reducing efforts and costs by the sharing of responsibilities is one of the primary tasks which the ECP/GR Programme has targeted. It has to be based on a search for duplication in the collections, which it should be possible to accomplish within the central crop databases (Gass *et al.* 1997). Searching for duplicates has to be based on a wealth of information subsuming the knowledge of the holding genebanks and international crop experts. Some more details on the discussion on sharing of responsibilities and an account of the modularization of necessary information have been given earlier (Germeier *et al.* 2003; Germeier and Frese 2004).

Up to now the ECP/GR central crop databases have primarily been lists of multicrop passport data (Hazekamp *et al.* 1997). The available working capacity of the database managers has not sufficed for much more than trying to keep the lists up to date by regularly requesting data from the holding genebanks. This function will now be taken over by EURISCO, which will be able to feed into or replace the ACCESSION table in our current central crop database (CCDB) architecture (Germeier and Frese 2004, Fig. 1).

The central crop databases will further have to play the primary role in the identification of duplicates and in the resulting activities, such as the rationalization of collections and the sharing of responsibilities within the crop working groups. They should develop into crop-specific genetic resources expert systems, primarily by advancing their functionality in relating and aggregating data. By doing this they will remain the primary user interfaces within an ECP/GR documentation network, which will be built from the following components with clearly definable tasks:

- **Genebank documentation systems / national inventories**

They provide **most original accession information** available from holding genebanks (information provided by collectors, breeders or other donors of their samples). This original information should **not be modified, 'corrected' or completed at this level** with information from other (secondary) sources.

- **EURISCO**

EURISCO centralizes the collection of passport data from holding genebank documentation systems via national inventories as the primary resource for secondary processing of the data.

- **Central Crop Databases**

They will develop into on-line available crop-specific genetic resources **expert systems**.

Based on primary data from genebank documentation and EURISCO they will additionally provide completed, harmonized and corrected passport information along with functionality for secondary data processing (**data warehousing**):

- Including additional (non-European) passport data (USDA, PGRC etc.);
- Logging changes in original data provided by the holding genebanks for their accessions;
- Providing a framework and automatic procedures to assist identification and categorization of duplicate accessions and the sharing of responsibilities;
- Providing completed, corrected, harmonized and normalized information for duplicate groups in a set of relational tables (GENOTYPE, SITE, modules for taxonomy, local names, pedigree and breeding data etc., see Fig. 1) in addition to accession-wise original passport information (MCPD zone in table ACCESSION);
- Geographical mapping of data;
- Display different taxonomic opinions;
- Allowing for calculations on pedigree data.

They centrally collect characterization and evaluation data and provide the functions which permit statistical and comparative data processing.

Although the necessary database concepts and applications should be developed on a generic level, it is advantageous to implement them on a single crop level mainly for performance reasons:

- Processing-intensive functionality and a highly interactive user interface is better suited to smaller databases;
- as there is no need to compare apples with pears, and scientific work and expertise in genetic resources is generally crop-specific, no real advantage is seen by replacing the central crop databases by a central multicrop information system.

2. Why search for duplicates? - The view of genebank and information managers (examples from the EADB)

Searching for duplication in collections has been primarily seen as an activity directed towards the rationalization of collections by the sharing of responsibilities within groups of duplicate accessions. By reducing the efforts needed for managing active available samples of duplicate accessions, this is of interest for genebank managers seeking to reduce costs and enhance efficacy.

At the data level a similar effort is targeted at reducing redundancy (Table 1). It is a basic step in the process of database normalization, which involves transferring a flat table into a relational database. This is also targeted at making work with the database more effective, especially as regards database updates and the avoidance of inconsistencies. Thus searching for duplication is a natural and necessary step in the modernization of our databases, irrespectively of the demands for the rationalization of collections.

Table 1. Motivation for searching out duplication - the views of genebank and database managers

A. View of genebank management	**B. View of information management**
Rationalization of collections	*Database normalization*
Reducing efforts for managing active publicly available samples of duplicate accessions	Reducing redundancy and inconsistency in active database modules → improving efficacy of database updates → improving performance of query response → leading to more consistent query results
Providing the user with a reduced size core collection of accessions representing most of the diversity within the whole collection	**Creating a more complete data set by compilation of information from different sources on probable duplicate accessions**

Redundant information, through the accumulation of 'mutations' (divergent interpretations, translation and transliteration, omissions and mistakes), normally undergoes a divergent evolution leading to inconsistency. This inconsistency increasingly obscures the common origin of information and of the objects described, and thus even the fact of redundancy itself. In our databases, which also have an historic aspect, accumulated inconsistency is a reality. Like duplicate accessions themselves, it cannot and should not simply be wiped out. It has something useful to tell about the history of the duplicate accessions and about the quality of the documentation. Strategies have to be developed to effectively cope with and make use of this situation.

A highly interesting result of searching for duplicates is the compilation of information from different sources for the probable duplicate accessions. This gives a more complete set of passport data (Table 4). However, it has to be kept in mind that it relies on a hypothetical compilation of the duplicate groups, which should be kept reversible in the database.

3. Lessons learned from different update strategies used by the EADB managers

Incoming updates to central crop databases normally not only contain new accessions added to the collections, but also modifications to entries already present in the database. In the worst case, modifications occur even to the accession numbers. As soon as the database develops from a single table to a set of related tables (e.g. by inclusion of characterization and evaluation data), a mere replacement of the old passport data by the new versions is no longer an option. It would greatly endanger the consistency of relationships with information held by related tables. Several strategies have been applied to cope with this problem by EADB managers:

- traditionally, incoming update lists were manually compared with the database entries. Missing data sets were inserted and modifications within the incoming data were corrected in the database entries. Data harmonization and correction, according to the opinion of the database manager, was also done within the single original passport table.
- another approach was applied from 1996-1998 within the EADB, when incoming updates were simply appended to the passport table. This led to each accession being represented by multiple and often inconsistent data sets. With this approach, the passport table also gradually became unsuited to provide a primary key for other tables, e.g. for characterization and evaluation data. Searching in such a table would be confusing. On the other hand, this procedure had the advantage that data modifications during the updates were conserved and remained transparent.

From 1999 onwards, efforts were made to overcome the shortcomings of the former approaches by new concepts (Fig. 1):

a. The simple Multicrop Passport table (ACCESSION) was embedded into a relational database design, which allows for storing unmodified original data provided by holders of the accessions together with a corrected and harmonized consistent representation of these data, normalized according to the concepts of an object relational database design. The latter is provided via a user interface to the ordinary user. Modifications to the original data provided in succeeding updates are logged in special tables (ACCESSIONUPDATE, GENOTYPEUPDATE), thus making the history of the alterations transparent.
b. Duplication and consistency checks applied manually in the traditional update procedure should be automated to a great extent by a database application, making the update process less tedious and less prone to errors. It became evident that such an application will also be applicable for computer-assisted searches for duplication in the existing data.

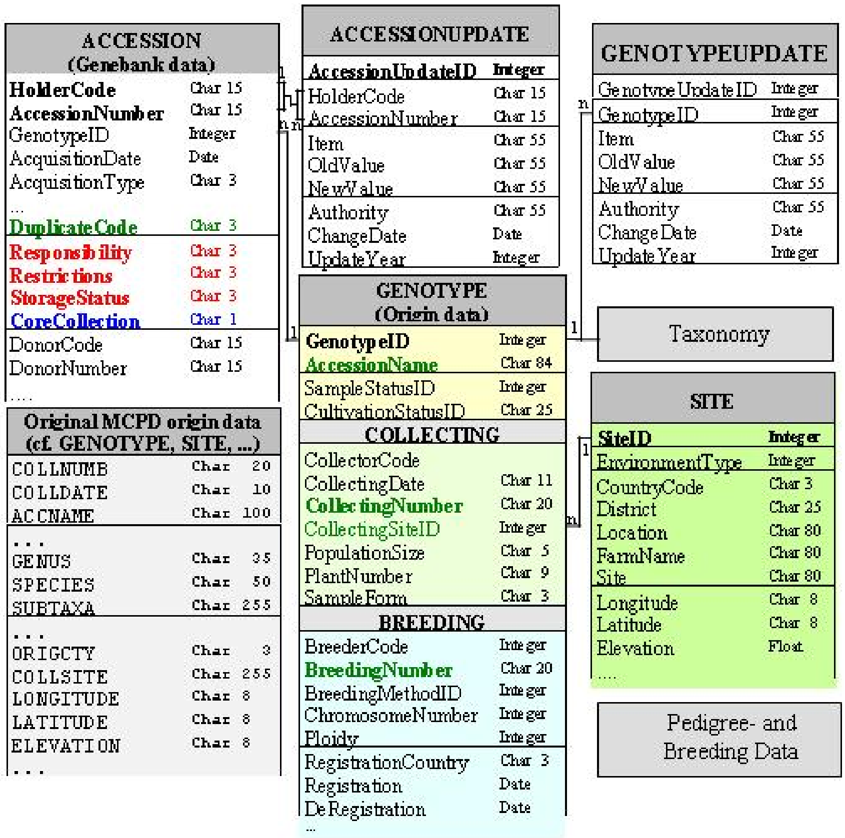

Fig. 1. Data model for the documentation of original (ACCESSION) and harmonized passport data (GENOTYPE, SITE, pedigree and breeding data) and the logging of changes on an accession and genotype (duplicate group) level (ACCESSIONUPDATE, GENOTYPEUPDATE).

4. Definition of a duplicate group (GENOTYPE) - in a strict sense and within the framework of core collection and database normalization

What we call passport data splits up in a first normalization step into two types of data, which we call ACCESSION and origin (or GENOTYPE) data respectively. They form the first pair of related tables in a relational passport database (Fig. 1). Accession data relate to a single accession held in a certain genebank. Identifiers such as accession numbers and accession-specific attributes such as donor numbers, acquisition dates and commitments regarding the status of an accession within the holding genebank, belong to them. Genotype data relate to the origin or the genotype represented by one or several duplicate accessions, which may be a collected wild or landrace specimen or bred material.

- **Redundant accessions in a strict sense**

Redundant (duplicate) accessions in a strict sense are identified by a well known or likely common origin. Identical, common, partial and compound duplicates (Knüpffer *et al.* 1996) are identified from data documenting the splitting up of accessions and their exchange between genebanks (accession information, Fig. 2B). Probable duplicates are assumed by similarities in passport data referring to the origin of an accession (collecting or breeding information/genotype information, Fig. 2A). However in many cases, the necessary information as indicated in Fig. 2, is not available.

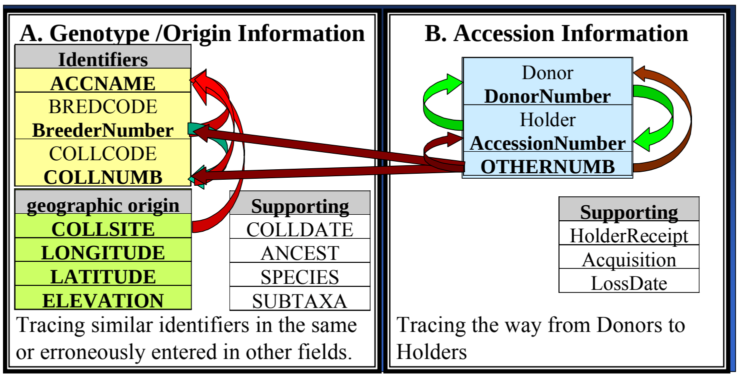

Fig. 2. Descriptors and their interrelationships, which have to be considered when searching for duplication within and between genetic resources collections.

- **Further grouping of accessions in a framework of database normalization and core collection**

From a geneticist's point of view, duplicate accessions contribute less to the value of a genetic resources collection because their genetic information is likely to be redundant. In any case, the value of an accession can be communicated to a user only as a function of the information available for it. From the view of documentation, an accession contributes to the database only by that part of its information which distinguishes it from all other accessions.

Thus a broader concept of grouping includes gathering all relevant accessions into a "duplicate" group, in cases in which they are not distinguishable by any available data other than mere accession identifiers (accession number, donor number, other number). This approach excludes, as much as possible, redundancy from the GENOTYPE table holding origin information for all accessions. It resembles the core collection concept, which tries to identify accessions representing the (known) diversity in the collection. This also implies that incoming new information will lead to reconsideration of duplicate groups, and it helps in identifying information gaps and in defining groups of accessions which should be considered for comparative research.

5. Results from searching out duplication – the case of the EADB

After the development of an application assisting the search for duplicates and based on the data taken over in 1999 (see point 3 above), one complete cycle of screening for duplicate groups has been finished for the EADB. 15 122 genotypes distinguished by data indicating their origin are represented by 32 768 accessions (some of which may still simply represent outdated accession numbers). 8131 accessions have very poor passport descriptions, and 7273 are considered unique (Table 2). The remaining 17 364 accessions represent 4223 duplicate groups with up to 39 accessions per duplicate group ("Svaloefs Oern"). On average, each genotype is represented by 2.14 accessions. Thus 53% of the well-documented accessions are considered to be duplicates (Table 2).

The extent of duplication is highest (59%) in the duplicate groups suggested by an accession or cultivar name, which is the most frequently encountered case (Table 3). It may be prone to errors by the reassignment of cultivar names. This is illegitimate according to the regulations of the International Code of Nomenclature for Cultivated Plants (Trehane *et al.* 1995), but nevertheless cannot be ruled out. In the EU it is the current practice of cultivar approval agencies to allow the re-use of names after a fixed time (N. Green, pers. comm. 2001).

Table 2. Status of information and duplication for accessions within the EADB

Total number of accessions	**32768**	**"Genotypes" distinguished by their origin data**	**15122**
Poorly defined accessions No collecting number, no collecting site + Accession name is:			
- missing	1558		(1)
- generic (Local, Taubhafer, Deutscher Hafer, Local sativa mutica, Red Rustproof, Jari Oves, Winter Turf, Avena)	4761		(1)
- an Accession number (PI, CI, CAV, pure Number)	1812		(1,2)
Total number of poorly defined accessions	**8131**	**Groups of accessions, which are not distinguishable merely because of lack of information**	**(3626)** (1)
	No. of accessions	**In duplicate groups =**	**No. of "genotypes"**
Groups of "real probable duplicates"			
>30 accessions	142	*Oern, Seger, Guldregn, Condor*	4
>20-30 accessions	481		20
>10-20 accessions	3300		241
>5-10 accessions	4574		600
>2-5 accessions	4607		1228
2 accessions	4260		2130
Total number of accessions within duplicate groups	**17364**	**Total number of groups of probable duplicates**	**4223**
"Unique" accessions	**7273**		**7273**
Total number of sufficiently defined accessions	**24637**	**Duplication: 2.14 (53%)**	**11496**

(1) Information insufficient for duplicate search in a strict sense.
(2) Lacking information could be greatly improved by integrating USDA and PGRC GRIN data.

Table 3. Extent of duplication suggested by collecting number, accession name or other collecting information

Duplication in genotypes suggested	**Accessions**		**"Genotypes"**
By collecting number	2220	Duplication: 1.24 (19%)	1797
By accession name	19500	Duplication: 2.45 (59%)	7953
Only by collecting site or collecting date	2917	Duplication: 1.67 (40%)	1746

- **Broadening the information base through the compilation of duplicate groups**

Table 4 shows the gain of information through the compilation of information available from various holders of accessions to duplicate groups. It is most evident with respect to the lifetime of accessions, which is therefore applicable primarily for cultivars. It can be estimated from the collecting dates given by some genebanks. Generally the earliest mentioned year of collection or acquisition is taken by the database as an indication of the accession's lifetime.

We frequently found that collecting numbers or collecting sites were not properly taken over, when accessions from the original holders were included into other collections. Occasionally, even some accession names and origin countries were lost. Thus considerable numbers of these descriptors can also be reassigned through the duplicate search procedure (Table 4).

Table 4. Gain on passport information through the compilation of duplicate groups

Passport descriptor	Information on passport descriptor available for accessions		
	at accession level	at genotype level	
Accession names	15674	16889	+1215 (+8%)
Sample status	14174	15903	+1729 (+12%)
Collecting number	341	697	+356 (+100%)
Collecting date, registration or **cultivar lifetime**	5990	14598	+8608 (+144%)
Origin country	16386	17052	+666 (+4%)
Collecting site	2619	4082	+1463 (+56%)

6. A database application for assisting the sharing of responsibilities on an accession basis

A framework of terms and concepts for the sharing of responsibilities has been published in Germeier *et al.* (2003), based on earlier work by van Hintum and Knüpffer (1995), Knüpffer *et al.* (1997) and Bücken and Frese (1999). Additional attributes, coping with a biologically defined duplicate type and descriptors describing responsibilities that an institution suggests or has agreed on, have been implemented into the ACCESSION table (Germeier and Frese 2004). A prototype implementation of these concepts as a MS Access application was demonstrated.

After the selection of an institution, the application displays duplicate groups involving the selected institution's accessions first on the left part of the screen (Fig. 3, left). They are identified by their collecting number, if available (e.g. AUT-82: 19), or their accession name. By selecting one of these items a full screen of passport data appears with origin data (collecting, breeding) compiled from the various data sources and a list of accession data for the accessions of the various holding genebanks in the GENEBANK ZONE. Data for the institution's own accessions, which will have to be assigned the responsibility descriptors, are further displayed for editing within a red frame at the bottom of the screen. An example is given for the Austrian collection (AUT001 BVAL-453016).

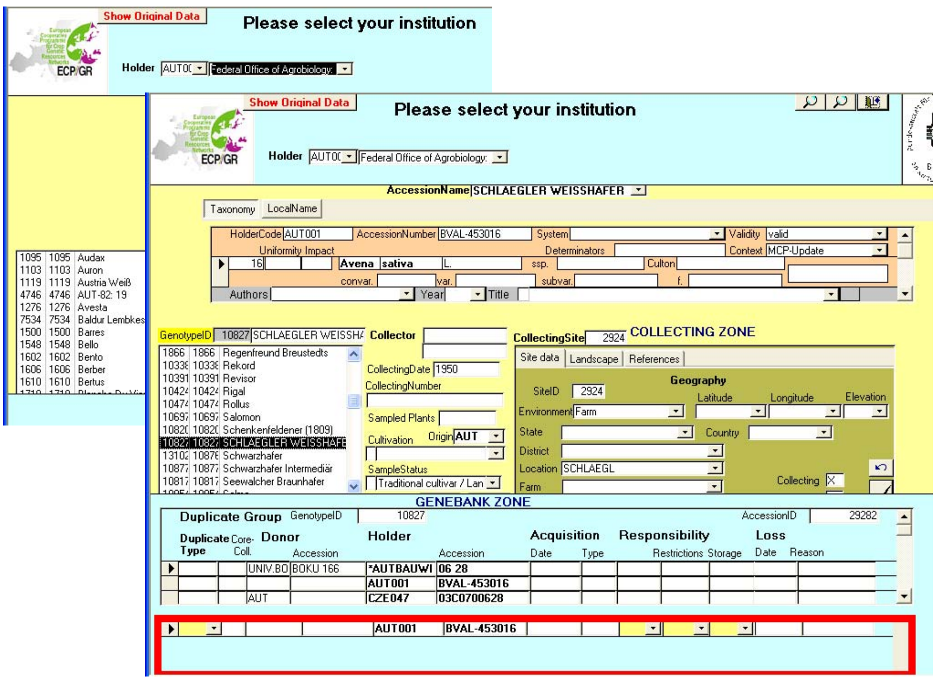

Fig. 3. Selecting duplicate groups and displaying their passport data.

By clicking the button "Show original data" it is also possible to display the (inconsistent) origin data which were provided with the original multicrop passport lists by the holders of the accessions (Fig. 4, upper screen). Clicking onto an accession within the genebank zone opens a display of detailed original data for this accession (Fig. 4, lower screen). This is intended to help curators to compare and evaluate the status of documentation for the various duplicates to their own accessions. Quality of documentation is an important criterion for selecting primary genetic resources. Therefore it is important that original documentation should remain available and transparent.

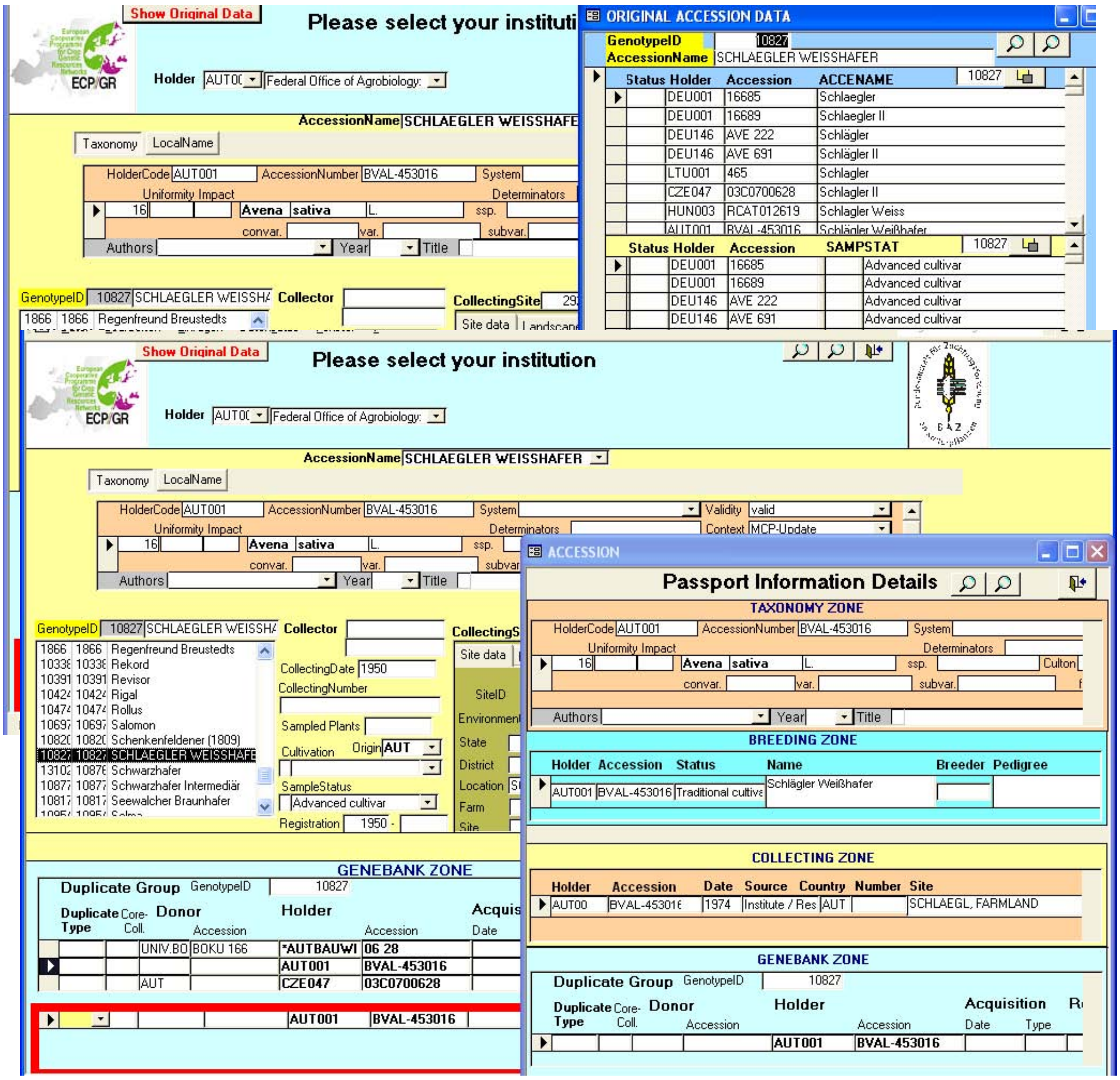

Fig. 4. Additional display of inconsistent original data provided by various holders of probable duplicate accessions (upper screen) or original details for a single accession (lower screen).

Editable fields in the frame at the bottom of the screen are displayed in Fig. 5. The application offers the values for selection (cf. Germeier *et al.* 2003) in drop-down lists.

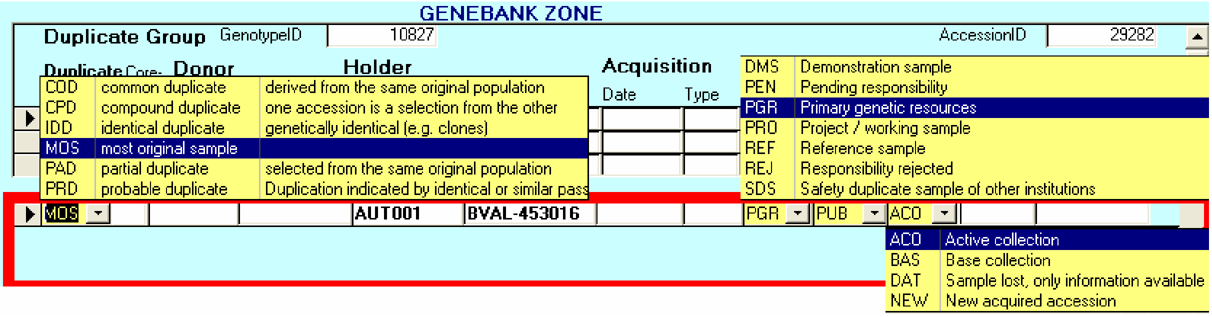

Fig. 5. Descriptors indicating the status of duplicate accessions within the holding genebank, to be filled by the curators.

Once the assigning of the assumed duplicate type has been completed and responsibility has been offered for the accessions of the respective institution, results can be exported to Excel by clicking the "Export Data" button (Fig. 6). The Excel file, which can easily be read into the ACCESSION table of the EADB can be sent to the EADB manager by email. Currently we suggest this method as the easiest to implement. Alternatively it could be implemented as an on-line Web application, but this would raise a lot of information security problems. A prototype version of the application can be downloaded from http://www.fal.de/bgrc/eadb/avena.htm.

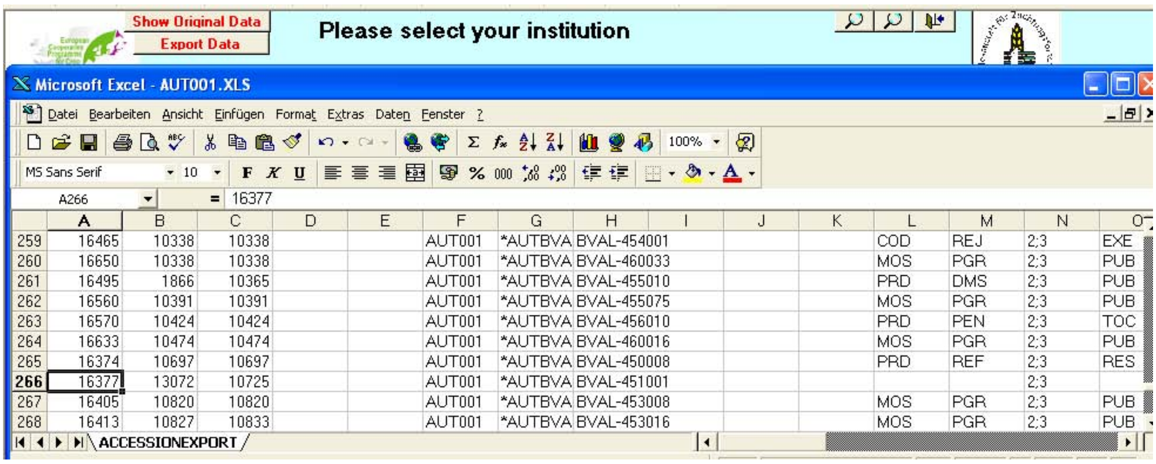

Fig. 6. Export of accession information into MS Excel.

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The Avena *collection in Bulgaria*

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Introduction

Plant genetic resources activities started in Bulgaria in 1905. The National Station holds germplasm from North-West Europe and Australia. The collection started with foreign accessions between 1905 and 1908. The varieties collected early on in Bulgaria derived from local germplasm belong mostly to var. *mutica* (Al), var. *aristata* (Körn), var. *aurea* (Körn) and var. *krausei* (Körn), and have a remarkably short vegetative period together with drought tolerance (Staneva 1965). Of the first varieties released, № 5 *A. sativa* L. var. *krausei* (Körn) was the most widely distributed variety until 1960. The cross-bred varieties with West-European germplasm arose after 1960 mainly from var. *mutica* (Al) (Staneva 1986).

Ex situ conservation

The cold stores of the genebank at the Institute for Plant Genetic Resources (IPGR) "K. Malkov", Sadovo contain the base collection (in long-term storage at -18ºC) and the working collection (in short-term storage at -6ºC). The *Avena* collection contains 3840 accessions, as shown in Table 1.

Table 1. Status of the Bulgarian *Avena* collections

Collection / origin and type of sample	No. of accessions
Long-term storage	**2384**
Origin	
Local	169
Foreign	2130
Unknown	85
Type	
Varieties	1710
Breeding lines	617
Landraces	57
Working collection	**1456**
Grand total	**3840**

Collecting *Avena* in Bulgaria

Material collected during various expeditions includes *A. fatua* L., *A. ludoviciana* Dur., *A. sterilis*, *A. clauda* Dur., and *A. wiestii* Steud. For a more detailed examination of oat diversity a specific collecting expedition is required.

Evaluation and characterization

Between 1986 and 2002, over 2000 accessions from the collection were evaluated for characteristics which would be of use to breeding programmes. Due to financial constraints, it has not been possible for these data to be computerized and thus to be made available to other genebanks.

Duplicates

We continue to identify duplicates, but now all duplicates are kept. Based on passport data and morphological inspection, after final investigations they will probably be reduced in number.

Research

The germplasm is used in research projects to:

- obtain winter hardy lines,
- breed for hull-less oats,
- screen for drought tolerance,
- screen for resistance to *Erysiphe graminis* DC. f. sp. *avenae* em. Marchal, *Puccinia coronata* Cda. f. sp. *avenae*, and *P. graminis* Pers. f. sp. *avenae* Eriks. et Henn.

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Oat genetic resources management at the Genetic Resources Centre in Clermont-Ferrand, France

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Until recently, INRA carried out a research programme on oat breeding at the Research Station in Rennes. This programme has now been stopped and responsibility for the oat collection is now shared between GEVES (Groupe d'Etude et de contrôle des Variétés et des Semences) for cultivars and landraces, and INRA Rennes for breeding lines. Clermont-Ferrand is responsible for safety-duplicates.

As the author was involved in the *Avena* RESGEN 106 evaluation programme, and because the Cereal Genetic Resources Centre has now been established in Clermont-Ferrand [56], the oat collections were moved there.

In future, safety-duplicates will be kept at GEVES Le Magneraud.

Recently, the author has received accessions from French private breeders but these were mainly recently registered varieties.

Through the RESGEN programme, accessions with the status of landraces and varieties were regenerated and a few duplicates eliminated. Seeds have been transferred from paper bags to Minigrip plastic bags as two independent stocks: a regeneration stock for the next regeneration and a distribution stock to respond to seed requests. A reference panicle is also conserved.

Passport data from all accessions have been entered into the ERGE database which uses Access software; this will make it possible to record seed stock quantity. With regard to the accessions in this collection, we will keep all samples of French origin (or which have been widely cultivated in France, such as some British, German and Swedish accessions) and also introduce some important French accessions which are missing in the collection. We have also included a few wild oats received from botanists or farmers.

Evaluation data from the RESGEN 106 programme will be entered into the database. Some evaluated traits showed good scores, such as disease tolerance – we found landraces tolerant to powdery mildew and crown rust – and high protein content. Protein content as a percentage of dry matter in evaluation year 2001 ranged from 9 to 18 and in 2002 from 11.2 to 18.2. In 2003, a heavy frost occurred in April and many accessions were destroyed by the frost and the following drought, but we were still able to score for some resistance traits.

The statistical analysis of the evaluated traits will allow us to calculate some diversity indices between all the landraces and will provide useful information for new breeding programmes.

[56] See "Building a Small Grains Genetic Resources Centre at the INRA Clermont-Ferrand Research Unit", pp. 202-204.

Collection and characterization of oats in Italy

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As oats are a minor crop in Italy, very few genotypes or cultivars have been developed in recent years. The interest in collecting and describing local populations or landraces was also quite meagre, and therefore the genetic variability available within this species remains largely unexplored.

In 1984 the Oat Section of the Istituto Sperimentale per la Cerealicoltura (Experimental Institute for Cereal Research) began collecting oat genotypes, mainly through the exchange of materials with other breeders, genebanks or research units all over the world. At present, this collection is made up of 735 entries belonging to different species, mainly *sativa* (Table 1). The duplicate samples present in the collection were identified, checked and removed. Most of the accessions are registered cultivars; a large number of breeding lines were obtained from the United States; and recently, one landrace from South Italy was added to the list.

Table 1. Taxonomic composition of the ISC oat collection

Species	Genome	No. of accessions
A. barbata	AABB	1
A. byzantina	AACCDD	9
A. nuda	AA	1
A. sativa	AACCDD	682
A. sativa var. *nuda*	AACCDD	32
A. sterilis	AACCDD	5
A. strigosa	AsAs	5
Total		**735**

The accessions originate from 38 countries, as shown in Table 2. A group of 39 entries was obtained from FAO in 1990, and their countries of origin are not known.

Table 2. Country of origin of the accessions in the ISC oat collection

Country	No. of accessions	Country	No. of accessions	Country	No. of accessions
United States	190	Norway	13	Albania	1
Italy	53	Australia	12	Argentina	1
France	50	Portugal	12	Bulgaria	1
Canada	48	South Africa	10	Greece	1
Sweden	47	Hungary	7	Ireland	1
United Kingdom	44	Spain	7	Iraq	1
Germany	35	Belgium	6	New Zealand	1
Finland	30	Denmark	5	Romania	1
The Netherlands	24	Chile	3	Slovenia	1
Russia	23	Israel	2	Tajikistan	1
Poland	17	Japan	2	Turkey	1
Austria	16	Uruguay	2	Ukraine	1
Czech Republic	14			Uzbekistan	1

Since 1998 the collection has been maintained by the Oat Section in Bergamo; a sample of each genotype (50-100 g) is kept in a cold room at 4°C. Every year a part of the collection (i.e. all the new entries and the accessions with less than 50 g stored) is regenerated in the field, and the main morphological data (plant height, earliness, panicle type, seed colour, presence of awns) are recorded.

Biochemical characterization

The accessions of the collection have been used to explore the genetic variability for specific characters. The first study was the description of 145 genotypes from the United States (cultivars and breeding lines) from the qualitative and agronomic point of view (Mascheroni *et al*. 2000). A group of 60 cultivars, bred or grown in 17 European countries, were also characterized in terms of chemical components of the kernel (protein, β-glucan and dietary fibre) and some agronomic and technological traits (Redaelli *et al*. 2003).

All these genotypes were also checked for genetic uniformity through electrophoretic fractionation (Acid-PAGE) of alcohol-soluble storage proteins (avenin). This technique is routinely carried out on the new entries, to describe the protein pattern of a specific accession, to verify its uniformity by analyzing a number of single seeds or to compare two samples of the same accession with different origins. As an example, the electrophoretic patterns of cultivars 'Creole' (France) and 'Oac Woodstock' (Canada) are shown in Figs. 1 and 2, respectively. The avenin patterns of the accessions in the collection are currently being organized in a catalogue.

Naked oat genotypes (*A. sativa* var. *nuda*) are of special interest, since they are considered a potential raw material for the production of oat-enriched foods with superior nutritional value. A preliminary chemical characterization of 23 naked oat cultivars and breeding lines (Conciatori *et al*. 2000) allowed us to choose the most suitable genotypes for this purpose.

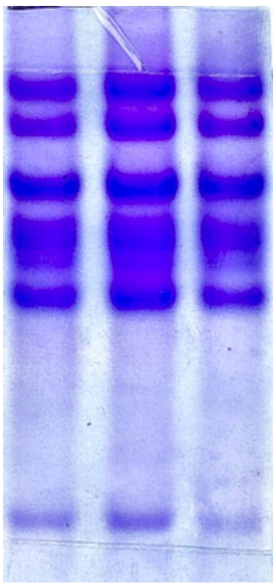

Fig. 1. Electrophoretic pattern of avenin from cultivar 'Creole' (France).

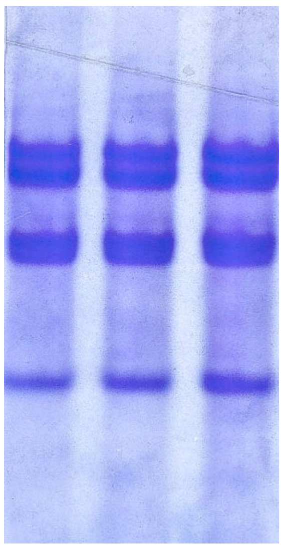

Fig. 2. Electrophoretic pattern of avenin from cultivar 'Oac Woodstock' (Canada).

Agronomic characterization: evaluation of frost resistance

In order to improve the utilization of the germplasm collection in breeding programmes, beside biochemical and molecular characterization, an extensive evaluation of important agronomic traits is also required. Resistance to biotic and abiotic stress is a crucial aspect for cultivar adaptation to agricultural environments (Boggini *et al*. 1995). Among winter cereals, oat is the most frost sensitive and its relatively poor level of winter hardiness is the most important factor limiting the sowing of winter oats in northern Italy and central Europe. Frost resistance, the most important component of winter hardiness, is an inducible process which can be promoted by cold acclimation and is associated with a number of biochemical and molecular changes (Cattivelli *et al*. 1995).

In this study we employed field testing to explore the genetic variability for cold resistance in winter and spring oats and to identify genotypes with superior frost tolerance. The experiment was carried out on a representative sampling of the oat cultivars grown in Europe and some North American genotypes, consisting of 62 oat genotypes with different origins. Frost damage was evaluated during the season 1998-99 in a nursery of small plots (1 m^2) with three replications at Fiorenzuola d'Arda (North Italy). The average minimum temperature during the first and second week of February was –5°C with a minimum temperature of -10°C without snow cover. Frost damage was scored in mid-February 1999; at this time plants were at the third leaf/initial tillering stage. Frost injury was assessed on a 0-9 scale, according to Rizza *et al*. (1994):

0 = no damage
1 = slightly yellowed leaf tips
2 = half yellowed basal leaves
3 = fully yellowed basal leaves
4 = whole plants slightly yellowed
5 = whole plants yellowed and some plants withered
6 = whole plants yellowed and 10% plant mortality
7 = whole plants yellowed and 20% plant mortality
8 = whole plants yellowed and 50% plant mortality
9 = all plants killed

Table 3 summarizes the cold damage data for the 62 genotypes tested. The average level of frost damage was 5.8, and the range was between 3 and 9, suggesting the existence of a broad genetic variability for winter hardiness in oats. Thirty-nine genotypes out of 62 (including many winter oats) showed a frost damage score equal to or higher than 6, indicating that some plant mortality occurred. On the other hand, some frost resistant cultivars with damage only on the basal leaf were also found (Rizza *et al.* 2001).

Frost heavily affects yield, reducing the expression of yield potential. When the yield potential of winter oats was assessed by comparing the same set of cultivars in winter and spring sowings in a North Italian environment, genotypes with an intermediate level of resistance (frost damage score of 5 or 6), although not completely killed by winter frost, still yielded more from spring than from winter sowings. This tends to suggest that frost resistance not only improves winter survival, but is a fundamental component of high-yielding winter cultivars: only those cultivars with a high level of frost resistance yielded more from winter than from spring sowings (Reggiani and Cattivelli 1997). The extent of the yield decrease after winter sowing was found to be related to the degree of frost injury detected in the field experiment.

Table 3. Field frost damage detected in Fiorenzuola (mid-February 1999). Growth habit indicated when known (W= winter, S= spring)

Cultivar	Country of origin	Growth habit	Field-detected frost damage (0-9 scale)	Cultivar	Country of origin	Growth habit	Field-detected frost damage (0-9 scale)
Aintree	FRA	W	3	PC 58	FAO		6
Alba	ITA		7	PC 59	FAO	W	4
Anita	BEL	S	6	PC 68	FAO		8
Argentina	ITA	W	7	Pendek	NDL	S	7
Astra	ITA	W	8	Peniarth	GBR	W	3
Ava	ITA	W	6	Pennline	USA	W	4
Bulban	AUS	S	7	Perona	ITA	S	7
Chamois	GBR	W	3	Phoenix	DEU	W	6
Coker	USA	W	3	Pinto	GBR	S	7
Coker 227	USA	W	3	Pirol	DEU	S	8
Cw 0002/18	GBR	W	4	Plata	USA		7
Cw 0002/58	GBR	W	4	Pluco	NDL		5
D'Hiver Du Prieuré	FRA	W	4	Pol	NOR	S	8
Emperor	GBR	W	3	Prevision	ITA	W	8
Flavia	ITA	W	6	Puhti	FIN	S	7
Gerald	GBR	W	6	Roar Sejet	DNK		7
Image	GBR	W	3	Rodgers	USA	W	3
Kalott	SWE	W	6	Rodney	CAN		6
Krypton	GBR	W	5	Rodney A	CAN		5
Leanda	NDL	S	5	Rodney ABHD	CAN		7
Lexicon	GBR	W	6	Rodney B	CAN		7
Manoire	FRA	S	8	Rodney D	CAN		6
Marisa	ITA	W	7	Rodney ECPG3	CAN		6
Mirabel	FRA	W	4	Rodney H	CAN		8
Nave	ITA	S	9	Rodney M	CAN		7
Noire de Moyencourt	FRA	W	4	Rogar 8	ITA	W	8
Norlys	GBR	W	4	Solva	DEU	W	6
Ombrone	ITA	W	8	Sovereign	GBR	W	4
Ondine	FRA		6	Tropicale	FRA	S	6
Origine	FRA	W	3	Weibull 17578	SWE	S	8
Park	GBR		6	Yeats	USA	W	3
Mean value = 5.8							

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Distribution and ecology of the wild tetraploid oat species **Avena magna** *and* **A. murphyi** *in Morocco*

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Introduction

Morocco is considered to be the centre of diversity of the genus *Avena*. Twenty-eight *Avena* species have been recorded in Morocco, which made Morocco a target country for collecting oat species during the last couple of decades. Oat is not a traditional crop in Morocco but was introduced by the French during the 1920s. Until now, the hexaploid (2n = 6x = 42) common oat *A. sativa* is the main fodder crop in non-irrigated lands of Morocco and is grown in pure stands or in mixtures with vetch. The present common cultivars of Morocco were selected from oat introductions from the USA and Canada. These cultivars were initially bred for the cooler climates of the USA and Canada, which explains their lack of adaptation to the Moroccan climate which is characterized by hot temperatures and drought. Therefore, in dry years, the performance of these cultivars is so poor that farmers are left without fodder and are forced to sell their animals at much reduced prices, which is disastrous for their economy. Moreover, oat cultivation faces other problems, i.e. diseases such as barley yellow dwarf virus (BYDV), crown rust and powdery mildew. These diseases are a real threat to oat cultivation in Morocco. Because of these disease problems, alternative varieties with resistance to these pathogens are required. The wild plant genetic resources which are endemic in Morocco constitute a good reservoir of resistant genes for diseases and are characterized by good adaptability to the edaphic and climate conditions of Morocco.

Two newly discovered tetraploid wild oat species (2n = 4x = 28), *A. magna* Murphy et Terell, native to Morocco (Rajhathy and Sadasivaiah 1969), and *A. murphyi* Ladizinsky, a native of southern Spain (Ladizinsky 1971), have seed groat which is exceptionally rich in protein, ranging between 25 to 30% of dry matter (Ladizinsky 1995), much higher than that of the common oat cultivars which varies between 13.4 to 22.3% depending on the cultivars (Clamot 1975, 1979, 1985). These plant species are well adapted to the Moroccan climatic and soil conditions and are genetically close to the common oat. Moreover, they have shown resistance to crown rust, powdery mildew and barley yellow dwarf virus (BYDV) (Ladizinsky 1993). Since these tetraploid oat species carry many interesting characters, they have recently been domesticated by transferring into them the domesticated complex of the common oat *A. sativa.* The transferred characters were the non-shedding spikelets, glabrous and yellow lemma, and reduced awn formation. Domestication was achieved by crossing the common oat with either of the tetraploid species and then backcrossing the pentaploid hybrids using pollen of the tetraploid wild parent (Ladizinsky 1995). The derived domesticated lines of *A. magna* and *A. murphyi* are currently being used in crosses with the aim of further developing them by transferring into them some of the diversity of the common oat cultivars of Morocco, and for transferring the protein content, disease resistance and adaptability of the domesticated tetraploid types into the common oat cultivars of Morocco. This work has been undertaken within the framework of the collaborative project between INRA-Morocco and the Hebrew University of Jerusalem under the supervision of Prof. Ladizinsky. The project was financed by USAID (United States Agency for International Development) from 1998 to 2001. The project activities are still going on and need further financial support to achieve all their objectives.

Material and methods

Since the 1980s, collecting missions in Morocco have been undertaken by international or national research institutes to gather wild genetic resources of *Avena* species. These collections were undertaken in different regions of Morocco during 1985, 1988 and 1989. From 1998 to 2001, the forage programme of the National Institute for Agricultural Research (INRA), in collaboration with the Hebrew University of Jerusalem, has undertaken four systematic collecting tours in Morocco to collect the two tetraploid oat species *A. magna* and *A. murphyi*. These collecting missions were aimed not only at gathering plant genetic material but also at identifying the areas and habitats in which these taxa grow. These data will help in locating areas which will be suggested for *in situ* conservation for the better preservation of these taxa.

- **Characteristics of the collecting years**

All four collecting years (1998-2001) were characterized by drought and erratic rainfall patterns. Most of the rainfall occurred at the beginning of the cropping season - November to second half of January. During the rest of the season, the rainfall was almost zero. This affected the growth of the wild oat plants which were short, reached maturity quickly and shattered their seeds by the beginning of May. Consequently, we did not manage to gather many seeds.

- **Surveyed areas**

The targeted sites for collecting were those with heavy black soils on which these two taxa grow. We collected during 1998 from Benslimane, the El Gara region near Machraâ Bel Ksiri to Ain Defali, and from Ouazzane to Ain Dorji, Tangier to Tetouan, Chefchaouen to Al Hoceima via Bab Taza, and from Al Hoceima to Nador via Midar and finally from Nador to Ras El Ma and back to Rabat via Taounate, Fes, Sidi Kacem towards Ouazzane. The collection trip itineraries of 1999, 2000 and 2001 concerned only the western parts of Morocco covering Benslimane, Sidi Kacem, Ouazzane, Tangier, and Khemisset (Table 1). In general, we collected from sea level to more than 350 m in altitude. The collecting strategy was to harvest one spikelet per plant of about 100 plants per population. The seeds were kept separately for multiplication and subsequent evaluation. A total of 44 accessions were gathered during the four collecting tours (Table 2).

Results and discussion

During the collecting tours, we found that the habitat of *A. magna* is characterized by a crumbling dark heavy clay soil on rolling hills and valleys with marl as parent rock. This taxon grows mainly on the edges of fields but is less common as a weed in wheat fields. In such fields, however, it can form massive stands reaching heights of nearly 2 m. A previous survey of *A. magna* in Morocco indicated that this taxon occurs South-East of Casablanca, South-East of Rabat and North of Meknès (Ladizinsky 1993). However, during our recent collecting trips we managed to discover a population of *A. magna* in the Tangier area in a mixed stand with *A. murphyi* and *A. sterilis*. In order to verify the occurrence of both taxa on the same site, we collected again in the same site in the following year (1999) and we found there a few *A. magna* plants among the *A. murphyi* populations. Therefore, it seems that the presence of *A. magna* in the Tangier area was not just accidental. Another important finding was the discovery of a weedy *A. magna* thriving in a wheat field west of Fès. During the collecting trip of 2001, we found another interesting site for *A. magna* in the Ouezzane region. At this site, the *A. magna* stands were abundant, growing in a wheat field, almost 2 m in height and producing big panicles with large seeds.

Table 1. Site description of *A. magna* and *A. murphyi* collected in Morocco from 1998 to 2001

Province	Location	Alt. (m)	Longitude	Latitude	No. of accessions.	
					A. magna	***A. murphyi***
Benslimane	5 km N of AL Aioun, N of Benslimane	180	07 05 00 W	33 42 00 N	0	1
Benslimane	11 km S Ben Slimane on road Ben Slimane to El Gara	250	07 05 70 W	33 31 63 N	3	0
Benslimane	18 km S of the site 1600 m before El Gara - Melila / Zaida junction	250	07 11 90 W	33 21 60 N	1	0
Khemisset	5 km from Sebt of Marchouch towards Rommani	360	06 38 80 W	33 32 58 N	2	0
Khemisset	1.4 km from Rommani to Maaziz	250	06 35 86 W	33 32 71 N	2	0
Khemisset	20 km from Rommani to Maâziz	270	06 27 14 W	33 34 75 N	2	0
Khemisset	At junction Rabat-Had Brachoua/Khemisset-Maâziz	380	06 36 11 W	33 33 87 N	1	0
Khemisset	7 km from Jamaat El Oued (Jamaât moule labled) to Maâziz	320	06 24 62 W	33 39 17 N	2	0
Khemisset	11 km from Jamaâ El Oued (Jamaât moule Lablade) from Rommani	220	06 22 17 W	33 40 19 N	2	0
Khemisset	200 m from the junction Rabat-Had Brachoua/Khemisset-Maâziz at the electricity station enclosed area	250	06 36 11 W	33 33 87 N	1	0
Ouezzane	4 km from junction Teroual-Mjaara, towards Teroual, on the right side, Ouezzane	250	05 16 00 W	34 49 00 N	2	0
Ouezzane	4 km S of Had Kourt (2 Km from junction Belkssiri/Had Kourt/Ain Defali on the way to Had Kourt, on the right roadside)	0	05 40 73 W	34 37 50 N	2	0
Ouezzane	2 km E of Had Kourt on the way to Ouezzane	20	05 40 66 W	34 39 21 N	1	0
Ouezzane	3 km W of Had Kourt/Ouezzane junction near the water pass.	80	05 37 74 W	34 52 01 N	1	0
Ouezzane	4 km E of Had kourt on the way to Ouezzane (on the right pathway) right roadside.	20	05 41 41 W	34 37 80 N	1	0
Ouezzane	19 km from Junction Ouezzane-Majaâra/Ouezzane-Fès towards Ain Defali (2 km before Ain Defali)		05 32 44 W	34 37 47 N	1	0
Sidi Kacem	10 km Machraa Bel Kssiri to Ain Defali	30	05 48 19 W	34 33 05 N	1	0
Sidi Kacem	4 km from junction Tetouan, Ouezzane/Fes-Meknès on P28	110	05 31 89 W	34 38 19 N	1	0
Sidi Kacem	9 km from Junction Tetouan, Ouezzane/Fès-Meknès	140	05 34 00 W	34 41 00 N	2	0
Sidi Kacem	6 km from junction Ouezzane-Tetouan/S. Kacem-Meknès towards Ouezzane	70	05 29 29 W	34 12 07 N	1	0
Sidi Kacem	At the junction coming from Moulay Driss to Sidi Kacem/Fès	100	05 31 63 N	34 10 46 N	1	0
Tangier	5.5 km from the main junction Rabat-Tetouan inside Tangier (Near Total gaz station)	60	05 51 00 W	35 45 04 N	0	2
Tangier	At Rabat-Cap Spartel junction	60	05 52 03 W	35 44 01 N	0	2
Tangier	1 km from the gaz station near junction Cap Spartel/road leading to the East.	50	05 41 19 W	35 44 67 N	0	1
Tangier	4 km from the junction to Cap Spartel, 500 m S of the left roadside, slope of a hill	70	05 53 80 W	35 45 48 N	0	2
Tangier	500 m N of the main road towards Badriouine access in front of DEWHIRST Society.	60	05 49 80 W	35 44 33 N	1	1
Tangier	1 km on the main road towards Badriouine access in front of DEWHIRST Society.	90	05 51 02 W	35 44 01 N	2	2

Table 2. Collected species and number of accessions per region

Province	Species	No. of collected accessions
Benslimane	*A. magna*	4
	A. murphyi	1
Sidi Kacem	*A. magna*	5
Ouezzane	*A. magna*	9
Tangier	*A. magna*	3
	A. murphyi	10
Khemisset	*A. magna*	12

For *A. murphyi*, it was reported by Ladizinsky (1971) that this species is a native of southern Spain. It has an affinity for dark heavy alluvial soils and is encountered in field edges and undisturbed patches. In Morocco, this taxon is restricted to some areas in Tangier with an exceptionally large population at the junction of the road from Tangier to the airport at Cap Spartel. But in 1999 we found another area where *A. murphyi* grows near Benslimane. This site was a marsh with black clay soil on which *A. murphyi* grows together with *Juncus* plants. In both sites, the altitudes did not exceed 100 m.

Throughout the collecting trips, we noticed many habitats with soil types appropriate for finding additional populations of *A. magna* and *A. murphyi*. For example, from Ouezzane to Tangier and also south of Settat we spotted some habitats which can be potential targets for further exploration for *A. magna*. For *A. murphyi*, we could not find any more populations in the Benslimane region, but further exploration of the marshes in this region will be of great importance to define the distribution of this species.

In general, during the collecting trips, we collected more *A. magna* populations (33) and a few *A. murphyi* populations (11). This indicates that *A. murphyi* is undergoing genetic erosion, since in most of the reported sites where this taxon had previously been collected we could not find *A. murphyi* populations. In general, both taxa are highly threatened by genetic erosion due to rapid urbanization, especially in the northern region, as well as by overgrazing, cultivation and drought during the last few years. Clearly, measures need to be taken to protect these two species before they vanish completely. It is also clear that further systematic exploration is necessary to determine the areas where these species are still abundant so that sites for *in situ* conservation can be selected.

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The Romanian oat collection

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General information for the years 1998-2000

Land area under cultivation:

Total	8 498 830 ha, of which
Cereals	5 655 188 ha, of which
Oats	232 316 ha
Oat production (total)	243 830 tonnes
Oat average yield/ha	1050 kg/ha

The largest area of oat cultivation is in western and northern Romania. Four spring varieties of *Avena sativa* L., three of Romanian origin, and one of French origin, were included in the Romanian Official Catalogue of Agricultural Plant Species for the year 2001.

Composition of the oat collection

The national oat collection comprises 187 accessions of the species *Avena sativa* L. This small collection is maintained at the Suceava Genebank (166 accessions) and at the Agricultural University, Timisoara (21 accessions).

The composition of the collection according to the status of the samples is given in Table 1, and according to country of origin in Table 2.

Table 1. Status of samples in the Romanian oat collection

Status of sample	No. of accessions (%)
Local landraces	170 (91%)
Breeders' lines	4 (2.1%)
Advanced cultivars	1 (0.5%)
Unknown	12 (6.4%)

Table 2. Country of origin of the Romanian oat collection

Country of origin	No. of accessions
Romania	181
Moldova	1
Poland	1
Russian Federation	1
Unknown	3

Collecting activities of the Genebank

Recent additions to the collection by collecting year are given in Table 3.

Table 3. Number of oat accessions entering the collection by year

Collecting year	No. of accessions	Collecting year	No. of accessions
1988	2	1994	18
1989	2	1995	8
1990	13	1998	1
1991	26	2001	31
1992	18	2002	31
1993	6		

Characterization and evaluation

Of the total collection only 44 accessions have been characterized and 36 evaluated biochemically. The descriptors used are those formulated by IBPGR (1985) with traits which are of interests for Romanian breeders. The crude protein, lysine and tryptophane content have been analyzed.

For the protein content determination the classic Kjeldahl method was used, employing an intermediate step based on a biuret method variant. The results varied from 9.79% to 13.75% of protein based on dry matter, with an average value of 11.44%.

A method based on the reaction between aminoacids and a ninhidrin reagent was applied to assess the lysine content, which ranged between 1.10% and 2.64% of the total protein content. The average value for the lysine content was 1.84%.

The tryptophane content was analyzed colorimetrically based on reactions between tryptophane and a mixture of reagents, heating to 65°C for colour development and on reading the extinction at 550 nm ± 10 nm. The minimum and maximum values obtained for the accessions studied were 0.49%, and 1.24% respectively, while the average value was 0.82%.

Storage

In the Suceava Genebank the oat collection is kept as follows:

- base collection: long-term conservation at -20°C; seeds packed in aluminium foil bags;
- active collection: medium-term conservation at +4°C; seeds kept in glass jars.

Documentation

The following information is documented at the Genebank:

- passport data (according to FAO/IPGRI *Multi-crop Passport Descriptors*);
- characterization and evaluation data;
- collection management data;
- on-farm data for Romanian landraces.

Reference

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Conservation activities carried out with the oat collection at CRF-INIA, Spain

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The Spanish Plant Genetic Resources Centre of the National Institute for Agricultural and Food Research and Technology (Centro de Recursos Fitogenéticos, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria - CRF-INIA) maintains a collection of cultivated oats made up of 1600 accessions, the majority of which are Spanish landraces.

The main conservation activities carried out at the CRF-INIA with this collection are the acquisition of new samples, multiplication, characterization and exchange of material. These activities mainly involve the following oat species: *Avena sativa* L., *A. byzantina* C. Koch and *A. strigosa* Schreb. This paper summarizes the work we have carried out within these activities since the last meeting of the Working Group on *Avena* in 1998 (Pérez de la Vega *et al.* 1998).

Collection of new oat samples by CRF-INIA

The CRF-INIA has organized five expeditions since the last meeting. The expeditions were undertaken during September-November 1998, July-August 1999, November 1999, October-December 2001 and October-November 2002. The expedition in July-August 1999 was organized by IPK (Institute for Plant Genetics and Crop Plant Research, Germany) in collaboration with CRF-INIA and other members of the National Network of Plant Genetic Resources.

During the expeditions the following data were collected:

- Local name
- Collection date
- Region
- Province
- Locality
- Latitude
- Longitude
- Altitude
- Type of material

Moreover, we include in the expedition data all the information provided by the farmer with regard to sowing dates and utilization of the crop.

During the expeditions listed above, 31 samples were collected (Table1):

Table 1. Species collected during collecting expeditions in Spain, 1998-2202

Species	No. of samples
Avena sativa	19
Avena strigosa	9
Avena fatua	3

Clearly the greatest number of samples was of *A. sativa*. All these accessions are Spanish landraces and they were collected in eight different provinces in western Spain. The collecting sites ranged from 250 m to 1082 m in altitude and between 35º02'20''N and 43º22'17''N in latitude.

Multiplication of oat accessions at CRF-INIA

The criteria for the multiplication of the oat accessions maintained at CRF-INIA are: to have a germination above 80% in the active and base collections, and/or to conserve a number of seeds greater than 2000 in the active collection. Based on these parameters we have achieved the multiplication and/or regeneration of the following accessions (Table 2):

Table 2. Number of oat accessions multiplied/regenerated at CRF-INIA

Species	1997-1998	2000-2001	2001-2002	2002-2003	Total
A. sativa	14	92	66	75	247
A. byzantina	1	7	31	0	39
A. strigosa	0	4	3	2	9
Total	**15**	**103**	**100**	**77**	**295**

Characterization of the oat accessions at CRF-INIA

The distribution by species and number of the accessions characterized at the CRF-INIA since 1998 are shown in Table 3.

Table 3. Number of oat accessions characterized at CRF-INIA

Speices	1997-1998	2000-2001
A. sativa	14	92
A. byzantina	1	7
A. strigosa	0	4
Total	**15**	**103**

These accessions were characterized for 16 agromorphological traits following the IBPGR (1985) descriptors with minor modifications. Eleven traits are qualitative variables and five are quantitative. We have analyzed these characterization data for the 92 accessions of *Avena sativa* studied in 2001. The results of frequency for the qualitative data and means for the quantitative characters are shown in Tables 4 and 5. According to these data there is little variation in these Spanish landraces for the following characters: nodes' hairiness, angle of flag leaf to culm, erectness of panicle, shape of panicle and kernel covering. We found higher variation for the quantitative data, mainly for plant height and number of spikelets in the panicle.

Table 4. Class partition and frequencies of each qualitative agromorphological character for 92 Spanish accessions of *Avena sativa* L.

Qualitative character	Frequency
Nodes' hairiness	
1 Glabrous	90.2
3 Slightly pubescent	7.6
5 Moderately pubescent	1.1
7 Highly pubescent	1.1
Angle of flag leaf to culm	
3 Acute	95.7
5 Intermediate	4.3
7 Obtuse	0.0
Hairiness of leaf sheath	
1 Glabrous	85.9
2 Border presence	14.1
Erectness of panicle	
3 Drooping	0.0
5 Semi-erect	0.0
7 Erect	100.0
Erectness of spikelets	
3 Drooping	66.3
5 Semi-erect	33.7
7 Erect	0.0
Shape of panicle	
1 Unilateral	3.3
2 Equilateral	96.7

Qualitative character	Frequency
Awnedness	
1 No awns	7.6
2 Few awns	9.8
3 Weak awns	16.3
7 Strong and many awns	66.3
Awn type	
1 Straight	55.4
2 Geniculate	39.1
Hairiness at basal part of the primary grain	
1 Glabrous	60.9
3 Slightly pubescent	6.5
5 Moderately pubescent	15.2
7 Highly pubescent	17.4
Kernel covering	
1 Grains naked	0.0
2 Grains covered	100.0
Lemma colour	
1 White	43.5
2 Yellow	23.9
3 Grey	0.0
4 Red	0.0
5 Black	18.5
6 Other	14.1

Table 5. Mean and standard deviation of each quantitative agromorphological character for 92 Spanish accessions of *Avena sativa* L.

Quantitative character	Minimum	Maximum	Mean	Standard deviation
Days to flowering	157	203	184.34	11.412
Days to maturity	201	226	214.75	5.107
Plant height (cm)	91	174	129.14	18.386
No. of grains in spikelet	1	3	1.96	0.306
No. of spikelets in panicle	38	168	77.28	27.438

Utilization of the oat collection maintained at CRF-INIA

Another service provided by the CRF-INIA is to respond to requests for material by the users. In the last six years we have received the following requests for oat accessions (Table 6).

Table 6. Utilization of the CRF-INIA oat collection

User	Objective	No. of accessions
Farmer	Growing in field	8
Research Centre	Teaching activities	4
	Research activities	50
	Growing in field	15
Firm	Breeding	1150
Others	Teaching activities	3
Total		**1230**

Based on the number of samples requested, the most important area of utilization of the oat collection was by a Spanish firm which required material for fodder breeding.

Acknowledgements

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Update of the Avena *core collections – Landraces*

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Avena landraces and traditional cultivars are being characterized and evaluated within the EU-funded project GENRES CT99-106 "Evaluation and enhancement of *Avena* landrace collections for extensification of the genetic basis of *Avena* for quality and resistance breeding". The project is managed with the help of a project database which complements the European *Avena* Database (EADB) for project purposes. Project results will all be entered into the EADB. Initially 2548 accessions were selected from the EADB and included in the project database. They were selected according to the following criteria:

Identification of landraces and traditional cultivars

1. **Landraces as indicated in the field SAMPSTAT: 7398 accessions are recorded as landraces/traditional cultivars at an accession level (Table 1).**

Table 1. Accessions indicated as landraces/traditional cultivars and their origin

ORIGCTY	Accessions SAMPSTAT 30	ORIGCTY	Accessions SAMPSTAT 30	ORIGCTY	Accessions SAMPSTAT 30
RUS	2262	ARM	88	SWE	38
ESP	1309	GEO	82	LVA	37
UKR	351	ITA	77	FRA	35
KAZ	226	MNG	75	NLD	27
GBR	217	AUT	74	LTU	26
TUR	215	BEL	71	CZE	23
BYS	208	ROM	51	CYP	18
DEU	185			FIN	9
YUG	163			DNK	8
BGR	157			CHE	7
MDA	133			BNL	6
HUN	112			IRL	3
PRT	109			NOR	2
GRC	105			ALB	1
POL	100				

The reliability of the SAMPSTAT data is questionable. The EADB update initiated in 1998 during preparation of the project proposal showed considerable changes in the SAMPSTAT field: for 223 accessions it has been changed from 3 to 4, for 341 from 3 to 5, for 241 from 5 to 3. In several cases the accession name does not indicate a landrace, while SAMPSTAT does; 41 accessions with SAMPSTAT 3 (now 30) are even shown as hybrids in the SPECIES field. Thus many entries in SAMPSTAT need to be reconsidered. From Table 1 it is evident that the origins of accessions shown as landraces/traditional cultivars are very unevenly distributed among European countries. Large numbers originate from Russia, Spain, some eastern European countries, the UK and Germany. The sample status is not defined at all for 13644 accessions (about 40%).

Another source of probable landraces is the group of 3500 *A. sativa* accessions which have collecting information (collecting number, collecting site), if it can be assumed that besides wild material, only landraces were collected, while advanced cultivars and breeders' lines are normally not collected but donated. Of these, 961 have no indication of SAMPSTAT (mainly IPK accessions), 1276 are recorded as landraces/traditional cultivars and 1232 as advanced cultivars. Table 2 indicates their origins.

They are clearly the best documented accessions currently available. Unfortunately, as most of them lack the proper indication in SAMPSTAT and have no accession names, they are not very well represented in the project (Table 2), which has a collection of accessions that is biased towards SAMPSTAT and accession name information.

Table 2. Accessions of *Avena sativa* with collecting information

ORIGCTY	SAMPSTAT	***Avena sativa* collected (with collecting number or collecting site information)**	
		Total	**In project**
ESP	Advanced	1197	
ESP	Landrace/traditional	1131	
CZE	-	671	
POL	-	75	
HUN	Landrace/traditional	67	
AUT	Landrace/traditional	64	26
ITA	-	60	
GRC	-	26	
GEO	-	20	
AUT	-	19	
ROM	-	14	
ITA	Wild	14	
EST	Advanced	12	
ALB	-	9	
GRC	Advanced	8	
TUR	Landrace/traditional	6	3
KNI	Wild	6	
DEU	Breeders' lines	6	
PRT	Advanced	6	
ALB	-	6	2
TUR	-	5	
PRT	Landrace/traditional	5	
ESP	-	4	
GRC	-	4	
ITA	-	4	

2. Accessions known to exist earlier than 1950

Furthermore, accessions about which information could be found in older literature (Anonymous 1952, 1961, 1966; Hillman 1910; Moule 1964; Zade 1918a, 1918b) have also been selected. The EADB was supplemented with the necessary modules for the documentation of information on pedigree and cultivar history. Table 3 shows the number of accessions now assigned in the EADB to the year of first mention in these references.

Table 3. Cultivars with existence indicated from literature

Year of first mention found in the literature	No. of cultivars / genotypes	No. of genebank accessions
1880-1899	46	121
1900-1910	20	64
1911-1920	96	263
1921-1930	6	27
1931-1940	19	91
1941-1950	21	83
1951-1966	71	487
Total	**279**	**1136**

3. Accessions indicated by an accession name such as "*local*", "*land*" or "*lant*" or having a regional connotation within their accession or cultivar name

Identification of duplication and information gaps as a precondition for establishing a core collection

The EADB has been completely checked for duplication. The procedures used identify probable duplicates; they also point out the accessions which are only similar in the lack of information available about them. Larger groups of accessions with identical (incomplete) passport data are designated with generic names such as "Local", "Taubhafer", "Deutscher Hafer", "Prostoi Mestnyi" etc. 3227 groups including 8131 accessions have been found with an accession name "Local" or none, and characterized only by country of origin, collecting year or botanical name. As many of these accessions have an accession name "Local", they are relevant for the landrace collection and it is questionable whether the information provided is sufficient for setting up a core collection. Most of these accessions were contributed by VIR. In a collaborative project funded by the ECP/GR the situation will be considerably improved as additional passport data will be digitized and transliterated from old catalogues currently only available on paper at VIR.

Field and molecular characterization of accessions

2290 accessions have now been selected and entered into the project database for GENRES CT99-106 from the EADB. An additional 283 accessions have been suggested by the project partners. 1041 accessions will be characterized and evaluated in the field and also with AFLP marker technology. Table 4 shows the origin and approximate dates of these accessions. It can be seen that compiling information for duplicate groups considerably improved the information about the dates of usage of the project accessions.

Table 4. Origin of accessions characterized and evaluated in project GENRES CT99-106 and approximate dates when in use

Origin	Accessions selected	Accessions selected			Reference to singular very old material
		Dates earlier than	Accession Information	Duplicate Group Information	
DEU	247	Not indicated	917	312	
GBR	222	1810-19		1	Schenkenfeldener 1809
FRA	183	1820-29		5	Sandy
RUS	51	1830-39		7	Nuernberg 1832
POL	48	1880-89	11	15	
SWE	39	1890-99	17	21	
AUT	38	1900-09	8	16	
GRC	32	1910-19	19	34	
NLD	27	1920-29	38	55	
BGR	10	1930-39	1	38	
FIN	10	1940-49	14	45	
YUG	10	1950-59	10	64	
ALB	8	1960-69	2	22	
ROM	7	1970-79	4	23	
BEL	6	1980-89		52	
TUR	6	1990-99		35	
CZE	5				
IRL	5				
HUN	5				
SPA, DNK, UKR, LVA, CHE, LTU, SVK	<5				

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Avena landrace AFLP reactions

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A significant part of the EU-funded project GENRES CT99-106 "Evaluation and enhancement of *Avena* landrace collections for extensification of the genetic basis of *Avena* for quality and resistance breeding" is the use of molecular markers to characterize genetically the *Avena* landraces. Molecular markers have proved to be extremely useful tools, not only for the detection and evaluation of the genetic variation of germplasm collections, but also in generating unique profiles for genebank entries. Nowadays, a wide range of molecular marker generating techniques is available. The choice depends on the skills and technical knowledge of the people involved, and on the availability of funds and laboratory equipment. For this project the AFLP (amplified fragment length polymorphism) technique was selected, as it is a fast, more informative and less labour-intensive method than the widely used RFLP (restriction fragment length polymorphism), and AFLP profiles are highly reproducible as opposed to RAPDs (random amplified polymorphic DNA). Furthermore, availability of the 310 ABI Genetic Analyzer (Applied Biosystems), supplied with GeneScan and Genotyper software, allowed automation for running the AFLP reactions and analyzing the results.

The AFLP method consists of three major steps:

1. a restriction-ligation reaction, during which total genomic DNA is double digested with restriction enzymes *Eco*RI and *Mse*I, in the presence of adapters and T4 ligase;
2. a pre-selective PCR (polymerase chain reaction), during which a subset of DNA fragments is amplified; and
3. a selective PCR, during which a further selection of fragments is achieved and a fluorescently labelled primer is used.

Out of the 64 primer pair combinations tested, the one producing meaningful and informative patterns was selected. The use of the ABI 310 Genetic Analyzer allowed us to run about 40 reactions per day. Each unique profile is stored as an electrophenogram, where peaks correspond to the presence of a PCR product and the height of the peak corresponds to the quantity produced. All electrophenograms have to be aligned in order to make comparisons for the presence/absence of the peaks (polymorphisms) among the entries. AFLP profiles for about 800 entries have been created using a single primer pair, with more than 200 polymorphic bands obtained. These are considered sufficient to differentiate the entries. At present, different combinations of the 800 entries are tested (250 at a time), in order to create 0/1 (absence/presence of the peaks) matrices. These matrices will be used with common software (NTSYS) to calculate genetic similarities and clustering methods will be applied to derive dendrograms. Preliminary results support the close genetic relationships of landraces with a common geographical origin. Furthermore, germplasm exchange and movement can be traced among the oat producing areas.

Classification and diversity of the genus Avena *L.*

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The systematic position of the species in genus *Avena* L. still remains disputable among researchers. Two tendencies are obvious in the modern classifications of *Avena* L.: an expansion of the volume of species, and the subdivision of species into smaller ones on the basis of morphological characters.

Comparative analysis of the whole specific diversity among oats was encouraged by the profound interest in the use of these forms in taxonomy and breeding practice, and reinforced by the recent development of plant immunological, biochemical and other techniques. The practical importance of interspecies hybridization lies in combining properties of different species that have drifted apart in the process of evolution. With this, the cultivated species in most cases, have lost numerous traits initially inherent in their wild ancestors, e.g. resistance to unfavourable environmental factors, adaptation to diverse soil and climate conditions, resistance to pathogens, and a number of characters involved in increased productivity and quality – all of these characters can be found in the oat genepool and can be utilized for oat improvement.

This is one of the objectives pursued by the Vavilov Institute of Plant Industry (VIR) in studying its global germplasm collections (Loskutov *et al.* 1999; Loskutov 2002).

In the last decades, *Avena* collections have been increased through the addition of new accessions and newly described species from all regions of the Mediterranean and Black Sea regions. At present the VIR stores an oat germplasm collection of 10 000 accessions of 4 cultivated species and 2000 accessions comprising 22 wild species, which comprehensively reflects the whole spectra of intra- and interspecific diversity of the genus *Avena* L. (Loskutov 1993, 1998).

The main objectives of this research are:

- analysis of the specific diversity of 26 *Avena* species for morphological and agronomic traits on the basis of characterization and evaluation data in computerized databases;
- revision of phylogenetic relationships and the pathway of specific evolution of the genus *Avena*;
- improvement of species classification;
- selection of wild species accessions with valuable characters for use in oat breeding.

The study of a representative set of accessions of the genus *Avena* L. with different ploidy levels has made it possible to discover intraspecific diversity for all the characters involved in the research, which will contribute to a targeted search for the best breeding sources and broaden the genetic base of the eventual oat cultivars to be released.

A molecular approach was used to study the phylogenetic relationships of *Avena* diploid and polyploid species based on RAPD markers analyses (random amplified polymorphic DNA). In this investigation genetic variability in RAPDs was studied in 74 accessions (mostly of Mediterranean origin) representing 20 species with different ploidy levels.

After a complex study of major morphological characters and utilization of the karyotype structure data confirmed by the results of RAPD and avenin spectrum analysis, we have confirmed the identification of two basic genomes, which most likely participated in the formation of species in *Avena* L., namely the A and C genomes. As for the B and D genomes, they seem to be derivatives of the A genome. In addition to the data obtained during the study of the species containing these genomes, clear-cut differences have been discovered in their distribution areas (Fig. 1).

The species with A and AB (AA′) genomes have a biaristulate lemma tip and in most cases floret disarticulation. Some of them have cultivated analogues with the same ploidy level (*A. wiestii*, *A. hirtula* – *A. strigosa*; *A. vaviloviana* – *A. abyssinica*) and wider areas of distribution (*A. wiestii*, *A. hirtula* and *A. barbata*), being segetal or ruderal weeds (*A. clauda*, *A. pilosa*, *A. damascena*, *A. longiglumis* and *A. barbata*). Obviously, this group seems to have reached its evolutionary climax, and none of these species had any part in the development of hexaploid oats.

In our opinion, the species with the C and AC genomes, whose characteristic feature, i.e. the presence of a bidentate lemma tip, which is typical for hexaploid species, are transitional ancestral forms in the evolution of hexaploid oats. This group includes the diploid species *A. ventricosa*, *A. bruhnsiana*, and *A. canariensis* as well as tetraploid species *A. agadiriana, A. magna*, *A. murphyi* and *A. insularis*, where the spikelet disarticulates as the unit of seed dispersal, and does not have direct cultivated analogues.

We also found that all those with the C and AC genomes are most closely related to hexaploid species in their karyotype, avenin spectra, RAPD-analysis and other parameters. Some of them are strictly endemic or have a very limited area of distribution, being typical wild representatives of natural undisturbed habitats but never weeds in cultivated crops. It seems that in the past all of the above-mentioned species occupied vast areas. However, as the inhabitants of entirely undisturbed habitats, when these habitats became disturbed by cultivators, the areas in which they are found became more restricted, which is characteristic of such transitional forms. Hexaploid species with the ACD (ACA″) genome occupy considerable areas, unmatched in size with other groups of species, because of their allopolyploid nature and probably the existence of two (modified) A genomes.

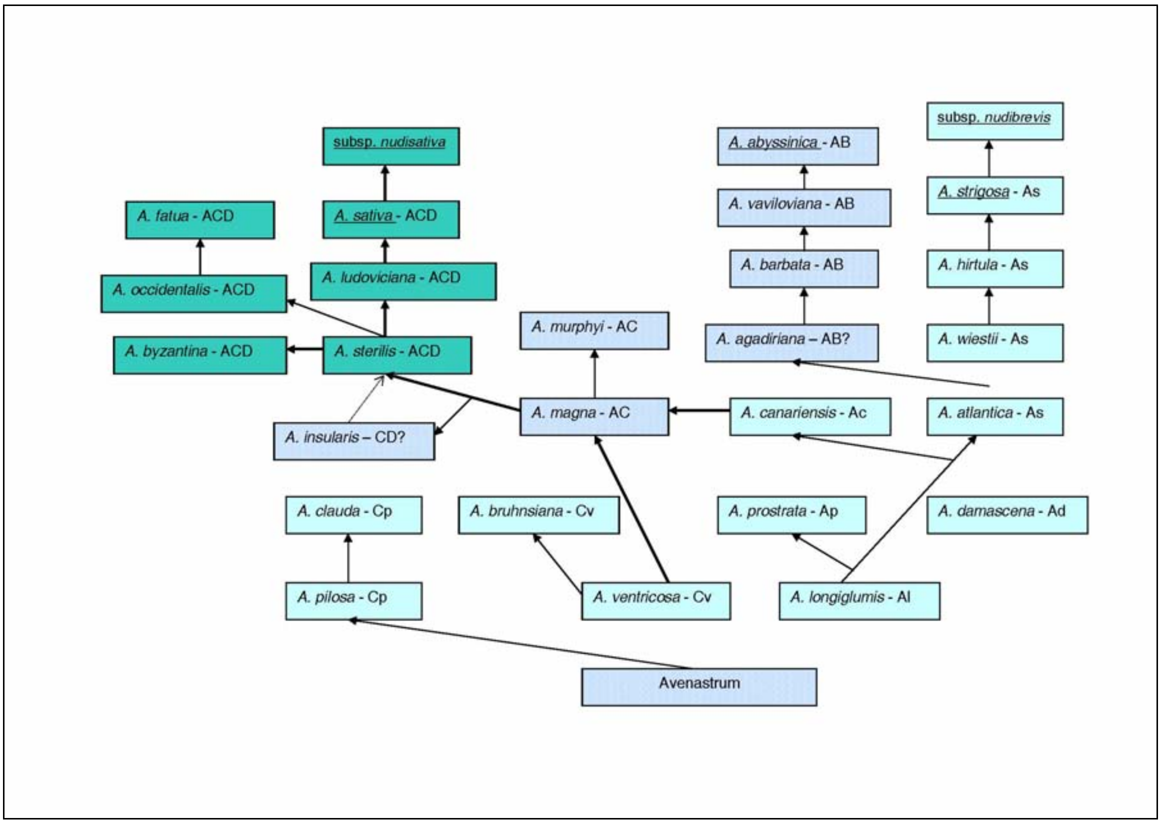

Fig. 1. Phylogenetic relationship of *Avena* species.

The analysis of intraspecific diversity helped to identify centres of morphogenesis for all cultivated oat species. The centre for the diploid species *A. strigosa* is Spain with Portugal, for the naked forms designated by Linnaeus as *A. nuda* L. it is Great Britain, for the tetraploid species *A. abyssinica* it is Ethiopia, for the hexaploid species *A. byzantina* it is Algeria and Morocco, for the hulled forms of *A. sativa* it is Iran, Georgia and Russia (Tatarstan), for its hull-less forms it is Mongolia and China (Fig. 2).

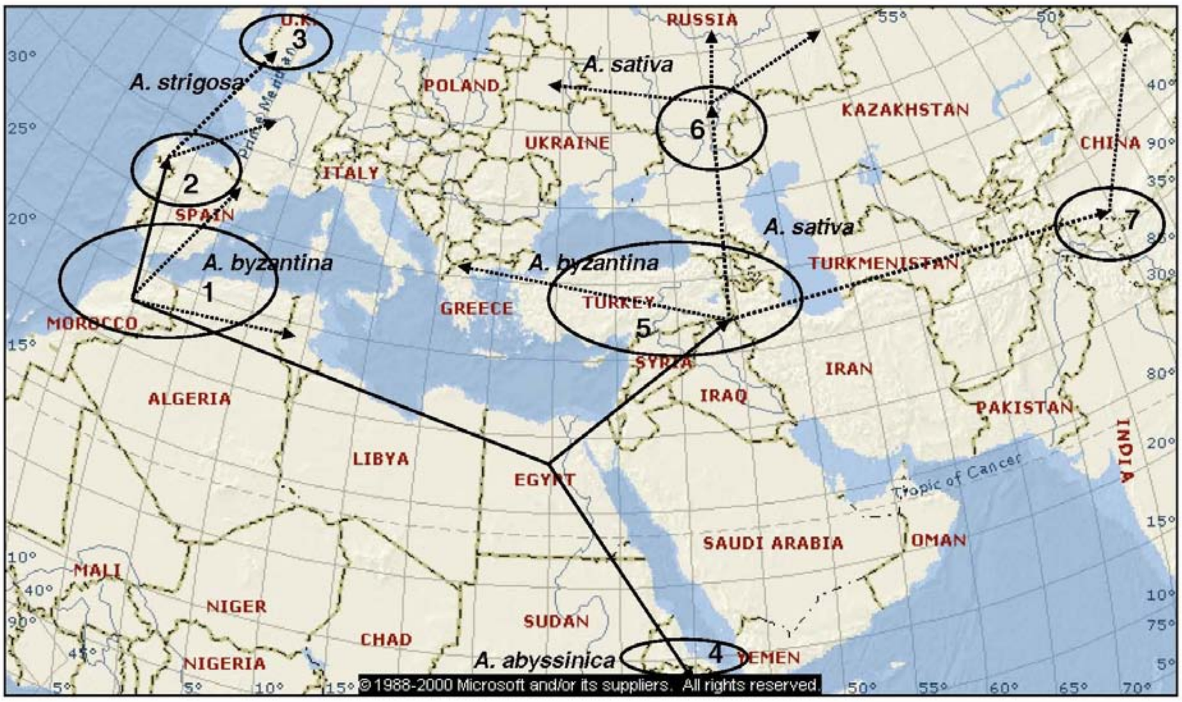

Fig. 2. Evolution pathway of *Avena* species.

Most likely the formation of the progenitor of hexaploid species (*A. sterilis*) was in the western part of the Mediterranean region, where the species *A. byzantina* originated, and then all species moved to the East and began to cover large territories in the region of the Asia Minor centre. Here more adaptive hexaploid forms of wild species (*A. ludoviciana*) appeared, which began to distribute itself in all directions by evolving high intraspecific diversity with wild and transitional weedy forms co-evolved with cultivated species (*A. sativa*) of hexaploid oat.

Complex study of specific diversity and analysis of geographic distribution of the habitats of oat forms and species confirmed that the centre of origin of *Avena* L. lies in the western part of the Mediterranean region, while the secondary centre of formation of *Avena* species and the origin of the cultivated oat (*A. sativa*) is situated within the Asia Minor centre of crop origin.

Based on the recent literature concerning oats and the evaluation of 26 species of the VIR world collection of genus *Avena* L. under field conditions and different laboratory methods, we have suggested an adjusted classification of the species in *Avena* L. genus. We have divided this genus into two subgenera, subgen. *Avenastrum* and a typical subgenus *Avena* which, in its turn, is subdivided into two sections, *Aristulatae* Malz. and *Denticulatae* Malz. Such divisions have been made according to the character of the lemma tip – biaristulate or *Aristulatae* and bidentate or *Denticulatae* (Table 1).

Table 1. Speciation in the subgenus *Avena* L.

Section	Species			2n	Genome
	Wild		Cultivated		
	Floret disarticulation	Spikelet disarticulation			
Aristulatae Malz.	*A. clauda* Dur.	*A. pilosa* M.B.		14	Cp
	A. prostrata Ladiz.				Ap
	A. damascena Raj.et Baum				Ad
	A. longiglumis Dur.				Al
	A. wiestii Steud.	*A. atlantica* Baum			As
	A. hirtula Lag.		*A. strigosa* Schreb.		
	A. barbata Pott.			28	AB
	A. vaviloviana Mordv.		*A. abyssinica* Hoch.		
Denticulatae Malz.		*A. ventricosa* Bal.		14	Cv
		A. bruhnsiana Grun.			
		A. canariensis Baum			Ac
		A. agadiriana Baum et Fed.		28	AB?
		A. magna Mur. et Terr.			AC
		A. murphyi Ladiz.			
		A. insularis Ladiz.			CD?
	A. fatua L.	*A. sterilis* L.	*A. byzantina* Koch	42	ACD
	A. occidentalis Dur.	*A. ludoviciana* Dur.	*A. sativa* L.		

Section *Aristulatae* includes diploid species *A. clauda*, *A. pilosa, A. longiglumis, A. prostrata*, *A. damascena*, *A. wiestii*, *A. hirtula*, *A. atlantica* and cultivated *A. strigosa*; tetraploid species *A. barbata*, *A. vaviloviana* and cultivated *A. abyssinica.*

Section *Denticulatae* includes diploids species *A. bruhnsiana*, *A. ventricosa*, *A. canariensis*; tetraploid species *A. agadiriana*, *A. magna*, *A. murphyi, A. insularis*; hexaploid species *A. fatua*, *A. occidentalis*, *A. sterilis*, *A. ludoviciana* and cultivated *A. byzantina* and *A. sativa.*

It is suggested that the evolutionary pathway of species of section of *Aristulatae* Malz. with cultivated species *A. strigosa* and *A. abyssinica* apparently reached their evolutionary climax. On the basis of detailed morphology, distribution and ecology we concluded that diploids and tetraploids of *Denticulatae* were involved in the evolution of hexaploid wild and cultivated oats.

A revised taxonomic system for the species in the genus *Avena* based upon the degree of relationship with hexaploid species has been developed (Loskutov 1999).

For breeding purposes some agronomic characters were evaluated in oat species. The wide diversity in response to photoperiod and vernalization illustrated the level of polymorphism for these characters within the cultivated and wild genepools of the genus *Avena*. The results of this study demonstrated that for the majority of the wild species evaluated, cold requirements have more influence on heading date and the duration of the vegetative period than daylength. It has also been shown that the response of wild *Avena* species to vernalization is to some extent linked with the geographic distribution of the accession, while the response to daylength is species-dependent. No strict correlation between species, their geographical origins and response to photoperiod was observed although several daylength-insensitive forms of various species originated from latitudes south of 40°N.

The results of a study assessing resistance to crown rust (caused by *Puccinia coronata* Cda. f. sp. *avenae* Faser et Led.) at the species level showed that most diploid wild species do not have this character. Among the tetraploid species, resistance was observed in most species. Hexaploid species *A. sterilis* was the most resistant and promising for character-targeted breeding. *A. ludoviciana* and *A. occidentalis* may also be regarded as promising. Resistance was most clearly expressed in the hexaploid accessions from Spain, Italy, Turkey, Israel and

Iran. Resistant forms for all groups of species came mostly from North African countries such as Tunisia, Algeria and Morocco.

While assessing stem rust (caused by *Puccinia graminis* Pers. f. sp. *avenae* Eriks.) resistance, the variation of responses in the wild species studied was wider than in cultivated oats. At the same time, among a few diploid species, medium resistance to this disease was identified. Tetraploid wild species were characterized as strongly susceptible to this pathogen. All hexaploid wild species, on the average, demonstrated medium resistance to the agent of stem rust. Resistant forms were identified among the accessions from Italy, Iran, Iraq, Israel, Tunisia, Algeria, Morocco and Ethiopia. Group resistance to major obligate fungal diseases (crown and stem rust) was observed in the forms belonging to species *A. longiglumis*, *A. canariensis*, *A. hirtula*, *A. barbata*, *A. agadiriana*, *A. magna*, *A. insularis*, *A. macrostachya*, *A. occidentalis* and *A. sterilis*.

Medium tolerance to BYDV (barley yellow dwarf virus), caused by *Hordeum virus nanescens* Rademacer et Schwarz.) was observed in the diploid species with A genome variants. An overwhelming majority of tetraploid species with different genomes had medium tolerance to this virus, except for the highly susceptible *A. agadiriana* and *A. murphyi*. All hexaploid species basically demonstrated medium tolerance to BYDV, with *A. occidentalis* having the highest percentage of resistant accessions. Strong and medium tolerance was typical of the oat forms from Greece, Turkey, Syria, Israel, Morocco, Algeria and Tunisia. Comparing the data of BYDV resistance and strong aphid colonization enabled us to ascertain the identification of BYDV resistant accessions belonging to diploid species *A. clauda*, *A. pilosa*, *A. damascena*, *A. canariensis* and *A. hirtula.*

Resistance to powdery mildew (caused by *Erysiphe graminis* D.C. f. sp. *avenae* em. March.), oat leaf blotch (caused by *Helmithosporium avenae* Eidam.), oat leaf blight (caused by *Septoria avenae* Frank.) and oat necrotic mottle (caused by *Mirothecium verrucaria* Ditmar. ex Fr.) were demonstrated by the accessions collected in various regions and belonging to different ploidy levels.

Our field researches enabled us to find great diversity in the structure and separate elements of the panicles. Variation for these descriptors was insignificant throughout the years of the study. Analyzing the panicle structure at species level confirmed that parameters such as panicle length, number of spikelets and panicle density varied more in the diploid wild species than in other groups of species.

Field evaluation of wild oat species cast light on the rich diversity in kernel characters. Analyzing the percentage of husk and size of kernels at the species level helped to determine that diploid wild species had greater variation for these characters than did the other groups of species. On the whole, it was ascertained that diploid species had the highest values of husk percentage and the lowest kernel size. Two tetraploid species, *A. magna* and *A. murphyi* were also distinguished for the large size of their kernels, since their 1000-grain weight (23.5-23.8 g) reliably exceeded maximal average values of all species studied. Hexaploid species demonstrated less variation in the structure of kernels than the tetraploids. *A. fatua* was reported to be among the species with the lowest (38.5%) percentage of husk (on the level of *A. sativa*, 31.7%), while *A. sterilis* had the highest values (53.2%) among this group of species. Variation for kernel size (15.1-17.1 g) was insignificant among these species, being comparable with *A. sativa* (15.9 g).

The data from biochemical research on wild and weedy field oat species showed the highest groat protein content (over 20% of protein) in the accessions of diploid *A. longiglumis* and *A. atlantica*, tetraploid *A. magna* and *A. barbata*, and hexaploid *A. sterilis*. Potential sources of high protein content would be *A. murphyi* and *A. occidentalis* (over 19.0%). High nutritive value of protein was notable in tetraploid *A. barbata* (5.6% of lysine in protein). Hexaploid species appeared to have a percentage content of lysine and other essential aminoacids in protein comparable with the level of *A. sativa.* Noteworthy for high groat oil content (7-10%)

were some accessions of diploid *A. pilosa* and *A. canariensis*, tetraploid *A. murphyi* and *A. magna*, hexaploid *A. fatua, A. ludoviciana* and *A. sterilis*. The quality of oil in oat may be determined by the content of monounsaturated fatty acids, such as oleic acid, which are capable of prolonging oil preservation time during storage. The highest content of oleic acid (over 46% of the sum of acids) was detected in the forms of diploid *A. hirtula, A. longiglumis* and *A. wiestii*, tetraploid *A. barbata, A. vaviloviana* and *A. magna*, hexaploid *A. fatua* and *A. ludoviciana.* At the same time, the biological activity of such oil is determined by the ratio between linoleic and oleic acids that should be equal to one. This ratio was also observed in the accessions of diploid *A. ventricosa*, *A. clauda*, *A. pilosa* and tetraploid *A. vaviloviana.* This research allowed us to map the geographic distribution of intraspecific diversity with regard to all oat species and forms. It appeared that accessions with high groat protein content had originated mainly from Israel, Morocco and Azerbaijan, while those with high groat oil content were from the Ukraine, Azerbaijan, Georgia and Morocco.

These studies confirmed that the species *A. sterilis* and *A. ludoviciana* are the most promising and important both in terms of grain quality and in terms of the potential for transferring this trait into cultivated oat. The research resulted in finding intraspecific variation in the biochemical parameters under study, which opens the possibility of searching for forms with a complex of commercially valuable properties and high grain quality.

Increasing abiotic resistance of the released cultivars, to a great extent, provides for conservation of the biodiversity of major agricultural crops. In view of this, specific priority should be given to research aimed at seeking new sources of edaphic resistance among wild relatives of cereal crops, since cultivated species in the process of evolution have in most cases lost the characters that initially belonged to their wild ancestors.

Evaluation of aluminium tolerance has shown that the wild species (diploid and tetraploid ones) carrying a C genome have low levels of resistance to the excessive content of aluminium and hydrogen ions in the nutrient media, while the carriers of A and B genomes were more frequently characterized as having high aluminium resistance. The analysis has made it clear that some accessions that we have identified as resistant originated in environments with excessive moisture or in mountainous areas. It seems very likely that the long-term life of plant forms under soil and climate environmental stress has led to the development of efficient protective mechanisms against unfavourable edaphic factors in these genotypes. All the forms of cultivated oats identified in the process of this study may be recommended for utilization in breeding.

The analysis of evaluation data used in this research was made with Corel Paradox9 for Windows software. The database amounted to 1680 Kb and contained over 5800 records in 48 fields. It includes evaluation data for 26 oat species during 1987-2001.

The study of such a representative set of accessions of genus *Avena* L. with different ploidy levels made it possible to display intraspecific diversity for all the characters involved. Some of the tetraploid species and more especially the hexaploid ones identified as sources of the valuable characters descriptors may be directly included in the breeding process for resistance to biotic and abiotic factors, for agronomic traits, and grain quality for feed and food. Numerous research projects in this direction and the practical results of oat breeding have provided evidence that the utilization of wild species along with the cultivar diversity of cultivated forms is the most promising trend for oat breeding, capable of broadening the genetic base and reducing genetic erosion of this crop.

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The identification of duplicates within and between germplasm collections

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The problem of conservation and identification of plant genetic resources (PGR) is directly linked with the necessity for optimizing and systematizing the existing collections, and therefore duplicate identification in collections held by genebanks is an aspect of special importance. Creation and the appropriate use of passport, characterization and evaluation databases for the *ex situ* collections should be among the priorities of any genebank. The value of any collection strictly depends on the completeness of information about each accession. An accession of a collection in any genebank is a botanical form which must be registered and precisely identified (Table 1). Unfortunately, due to the gaps in our knowledge, there is still a debate regarding the ploidy level and taxonomic position of the Linnaean species *A. nuda* L., most of non-Russian authors regarding the diploid species *A. strigosa* and *A. nuda* as synonyms and some using the term var. *nuda* for *A. sativa* (Table 2).

Unfortunately most specialists use the principles of biological species in their work with PGR. They combine the whole diversity of forms in a number of composite, so-called biological species. The remaining species are defined as taxonomic species and are incorporated in the former ones without being divided into cultivated and wild forms. And so if you take for example oat landraces from Turkey, all of them appear to be duplicates (Table 3).

Table 1. Wrong identification of oat cultivated species

No.	Species	Accession number	Accession name	Country of origin
53	fatua	400940	Mindo Ci 4328	USA
54	fatua	400941	Primus I	SWE
56	fatua	400943	Roxton	CAN
57	fatua	400931	Zalahashagyi S Tf	HUN
58	fatua	400932	Bonda	USA
59	fatua	400933	Detenicky Bily	CSK
61	fatua	400935	Exeter Can 342	CAN
62	fatua	400936	Fulwin	USA
63	fatua	400937	Sirius Ii	SWE
64	fatua	400938	Zalalovoi Sz Tf	HUN
65	fatua	400939	Marion	USA
66	fatua	400920	Jindrichovsky	CSK
67	fatua	400921	Milton B Feher	
68	fatua	400922	Orion Iii	SWE
69	fatua	400923	Perle	NOR
70	fatua	400924	Record	NLD
71	fatua	400925	Pobjeda	
72	fatua	400926	Slapsky Polorany	CSK
74	fatua	400928	Abudance Can 333	GBR
75	fatua	400929	Ajax	CAN
76	fatua	400930	Aristata 0339	
77	fatua	400918	Hatvani 117	HUN
79	fatua	400908	Minor	DNK
80	fatua	400913	Eszterhazi 103	HUN

Table 2. Wrong identification of naked oats

No.	Species	Accession number	Accession name	Country of origin
81	nuda	03C071263	Vir K 2468 Local	MNG
82	nuda	03C071264	Vir K 2472 Local	MNG
83	nuda	03C071265	Vir K 1929 Local	CHN
84	nuda	03C071266	Vir K 1932 Local	CHN
85	nuda	03C071267	Vir K 11014	CHN
86	nuda	03C071258	Liberty	CAN
87	nuda	03C071139	Rhea	FRA
88	nuda	03C071049	Glabrata	USA
89	nuda	03C070987	Caesar	DEU
90	nuda	03C070911	Urcar	CAN
91	nuda	03C070873	Vicar	CAN
92	nuda	03C070840	Laurel	CAN
93	nuda	03C070844	Brighton	CAN
94	nuda	03C070644	Nos Nackthafer	DEU
95	nuda	03C070240	Ljubimec	SUN
96	nuda	03C070212	Vir K 2301	SUN
97	nuda	03C070219	Litevsky Nahy	SUN
98	nuda	03C070182	Holden	USA
99	nuda	03C070164	James	USA
100	nuda	03C070056	Mongolia	

Table 3. Use of different taxonomic approaches to identify hexaploid cultivated species of oat

CATNUM	ORIGCTY	ACCENAME	BIOL_CONC	SPECIES	SCINAM	LEMMA COLOUR
1903	TURKEY	LOCAL	A.SATIVA L.	A.SATIVA L.	A.SATIVA L. VAR.MUTICA, ARISTATA	WHITE
4636	TURKEY	LOCAL	A.SATIVA L.	A.BYZANTINA C. KOCH.	A.BYZANTINA C. KOCH. VAR.ANOPLA	RED-BROWN
4637	TURKEY	LOCAL	A.SATIVA L.	A.BYZANTINA C. KOCH.	A.BYZANTINA C. KOCH. VAR.SOLIDA	RED-BROWN
4639	TURKEY	LOCAL	A.SATIVA L.	A.BYZANTINA C. KOCH.	A.BYZANTINA C. KOCH. VAR.CULTA	RED-BROWN
4676	TURKEY	LOCAL	A.SATIVA L.	A.SATIVA L.	A.SATIVA L. VAR.ARISTATA	WHITE
5419	TURKEY	LOCAL	A.SATIVA L.	A.BYZANTINA C. KOCH.	A.BYZANTINA C. KOCH. VAR.ALBOMUTICA	WHITE
5420	TURKEY	LOCAL	A.SATIVA L.	A.BYZANTINA C. KOCH.	A.BYZANTINA C. KOCH. VAR.MONATHERA	RED-BROWN
6535	TURKEY	LOCAL	A.SATIVA L.	A.SATIVA L.	A.SATIVA L. VAR.GRISEA	GREY
6538	TURKEY	LOCAL	A.SATIVA L.	A.SATIVA L.	A.SATIVA L. VAR.MUTICA, GRISEA	WHITE, GREY
6550	TURKEY	LOCAL	A.SATIVA L.	A.SATIVA L.	A.SATIVA L. VAR.MUTICA	WHITE
6722	TURKEY	LOCAL	A.SATIVA L.	A.SATIVA L.	A.SATIVA L. VAR.ARISTATA, CINEREA	WHITE, GREY
7693	TURKEY	LOCAL	A.SATIVA L.	A.SATIVA L.	A.SATIVA L. VAR.ARISTATA, MUTICA	WHITE
7704	TURKEY	LOCAL	A.SATIVA L.	A.SATIVA L.	A.SATIVA L. VAR.AUREA, MUTICA	YELLOW, WHITE
11641	TURKEY	LOCAL	A.SATIVA L.	A.BYZANTINA C. KOCH.	A.BYZANTINA C. KOCH. VAR.NIGRA	BLACK

Rationalization of terminology and classification between genebank collections is one of the most significant problems. This is very important to improve the efficiency of PGR conservation in our continent. Quite often, accessions of national collections have been received from other genebanks. When comparing collections for possible duplication, it is desirable to have the most complete information about the origin of an accession, that is, the original name of the accession, catalogue number from the donor genebank, catalogue numbers for this accession in other genebanks of the world, the place of origin and reproduction of the accession. In the case of cereals, the botanical infraspecific taxonomy component is an extremely important part of cereals collection activities. Another problem of not using infraspecific taxonomy is contamination of accessions during maintenance. In the Vavilov Institute of Plant Industry (VIR) the majority of botanical criteria systems were created under the guidance of N.I. Vavilov in the 1920s and 1930s and later developed and refined on the basis of new data from studies of plant diversity.

At the end of 1999, VIR, BAZ (through ZADI), IPK and NGB agreed on the implementation of a pilot project on the comparison of *Avena* collections conserved in Russia, Germany and Sweden. In total, over 17 100 entries have been analyzed, which is equivalent to 62% of the European *Avena* Database and 18% of the total world *Avena* collection.

In VIR duplicate identification within germplasm collections of particular crops is undertaken by an expert or curator specializing in the relevant crop species, as these are the people who can, thanks to their knowledge and experience, understand the value and significance of a duplicate and come to a well-weighed decision in each particular case. For such purposes we carefully collect information from the accession origin or donor country. There may be different numbers or names and pedigree information.

We used the following principles in our work to compare all passport databases between collections. For the analysis of passport data, a special structure for a joint database has been developed to make possible the comparison of named accessions and additional information for each individual. For analyzing and identifying duplicates, the most important fields are ACCNAME, DONORNUM, OTHERNUM, as well as the SCINAM field for determining identity in terms of classification units (i.e. genus, species, subspecies, etc.).

The analysis of passport data showed 464 oat accessions in the joint database to have some confusing information. These accessions required additional checking and consultations between genebank experts (Table 4).

Table 4. Duplicates within and between cultivated oat collections

VIR	BAZ	IPK	NGB	ACCENAME	SCINAM	OTHENUM	DONONUM	ORIGCTY	DONORCTY
	52939			ACACIA	Avena sativa L.		PI220867	AUS	USA
11300				ACACIA	A.BYZANTINA C.KOCH.	PI 220867		AUS	
		AVE 1319		ALAMO	A. saliva L. var. montana Alef.			USA	USA
		AVE 975		ALAMO	A. saliva L. var. aurea Koern.		CI 5371	USA	USA
10300			NGB 9798	ALGERIBEE	A.BYZANTINA C. KOCH.			AUS	
		AVE 1156		ALGERIBLE	A. sativaj, var. mutica Alef				HUN
		AVE 901		ANDERS	A. saliva L. var. aristata Krause		6-149		HUN
13498				ANDERS	A.BYZANTINA C. KOCH			SWE	
		AVE 606		ANTHONY	A. saliva L var mulica Aiof	CI 7001	BBA 2627	USA	DEU
		AVE 781		ANTHONY	A saliva L var. mulica Alef.		BBA 2556	USA	DEU
8665	16815	AVE 231		ANTHONY	A.SATIVA L. VAR.UUTICA	C.I. 2143		USA	
		AVE 679		APPLER	A. bvzantina Koch subsp. bvzantina	CI 7003	BBA 2629	USA	DEU
1874	52328	AVE 786		APPLER	A.BYZANTINA C.KOCH.	C.I. 0775	BBA 2607	USA	USA
	41660			ARTEMOWSK	Avena saliva var. mutica ALEF.		94	SUN	DEU
	41700			ARTEMOWSK. KRIM 90	Avena sativa var. aurea KOERN.		106	SUN	DEU
12239				AVE 0448/63	A:STRIGOSA SCHREB.	AVE 0448		URY	GERMANY
			NGB 4726	AVOINE NUE GROSSE	Avena nuda L.			DNK	
2122				AVOINE NUE GROSSE	A.SATIVA L. VAR.INERMIS			FRA	
	52566			BAGE	Avena sativa L.		PI 185657	ARG	USA
	52581			BAGE	Avena sativa L.		PI 189625	BRA	USA
10881				BAGE SEL. KLEIN	A BYZANTINA C.KOCH.	D.I.V 040		ARG	
	52931		NGB 9795	BALLIDU	Avena sativa L.		PI 193031	AUS	USA
11305		AVE 876		BALLIDU	A.BYZANTINA C. KOCH.	PI 193031		AUS	
		AVE 651		BAMBO II	A. sativa L. var. obtusata Alef.				HUN
		AVE 600		BAMBU	A sativa L. var. mutica Alef.			SWE	DDR
	16631			BAMBU 1	Avena sativa var. mutica ALEF.		11 12 42	SWE	DEU
	52423			BANCROFT	Avena sativa L.		CI 04468	USA	USA
	51440			BANCROFT (OW03)	Avena sativa L.		CI 04468	USA	USA
		AVE 1232		BEEDEE	A. sativa L. var brunnea Koern.		CI 6752	USA	USA
11210				BEEDEE	A.SATIVA L VAR.MUTICA	C.I. 6752		USA	
			NGB 6356	BELAR	Avena sativa L-			AUS	
		AVE 1158		BELAR	A. bvzantina Koch subsp. bvzantina			IND	DDR
		AVE 227		BELAR	A. sativa L. var. aurea Koern.			GER	DEU
		AVE 877		BELAR	A. bvzantina Koch subsp. bvzantina			AUS	AUS
8669		AVE 1159		BELAR	A.BYZANTINA C. KOCH.	C.I. 2760	BBA 2559	USA	

The conclusion from the analysis of the four databases shows that 90% of the VIR database has unique accessions between the four collections compared, while the IPK database has 70% and the BAZ and NGB databases have 50-60%. The number of unique entries was analyzed by using the DONORNUM and OTHERNUM fields, when there was available information about identification numbers from different genebanks and especially from the USDA GRIN database. This analysis showed that the proportion of unique accessions compared to other genebanks was lower: VIR – 80%, IPK – 60%, NGB – 45% and BAZ – 25%.

From the analysis of databases, 1276 accessions have been found to have the same scientific name and be duplicated in two (1034 entries), three (207 entries), or sometimes four (35 entries) genebanks at a time (Table 5).

Table 5. Structure of duplicates in joint database

Genebank				No. of duplicates
VIR	**BAZ**	**IPK**	**NGB**	
VIR	BAZ			409
VIR		IPK		414
VIR			NGB	87
	BAZ	IPK		93
	BAZ		NGB	18
		IPK	NGB	13
Double duplicates				**1034**
VIR	BAZ	IPK		153
VIR	BAZ		NGB	23
VIR		IPK	NGB	23
	BAZ	IPK	NGB	8
Triple duplicates				**207**
VIR	BAZ	IPK	NGB	35
Total duplicates				**1276**

It was found that some collections are contaminated, some accessions are misidentified, but most often the accessions are not comprehensively determined taxonomically. This shows that some genebanks have not maintained the original samples of seeds or herbarium seeds which could be compared with reproduced accessions and checked for contaminated material. Some accessions have been found to have the same scientific name and to be duplicated in two, three, or sometimes four genebanks at a time.

Also, some accessions have been revealed to coincide by their accessions names and all other numbers, but to differ considerably by the scientific name (botanical varieties). These accessions require additional checking and the consultation of genebank experts. Our opinion is that some formal approach targeted at revealing similarly sounding or spelling names should be used by the crop expert with utmost care.

These examples demonstrate the importance of consistent taxonomic approaches in working with PGR. Interspecific and especially infraspecific classification is becoming more and more important, not only in botanical, breeding and plant science research, but more especially in genebank activities related to the proper preservation of plant genetic diversity

Avena murphyi: ***Genetic variability in Spanish populations***

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Avena murphyi Ladiz. (2n=4x=28, AACC) is an annual species which has a very restricted area of distribution in the province of Cádiz (southern Spain) and near Tangier (Morocco). It grows in heavy alluvial soils, a habitat which is quickly disappearing due to human activities and there is a real threat of extinction of this species.

In order to protect this species, the Andalusian Government included *A. murphyi* in the local Red List in 1994, and a proposal to establish a genetic reserve has been made by Valdés *et al.* (2000).

In the collecting expeditions we carried out during 1995-96, only one population was found and, as reported at the fifth meeting of the *Avena* Working Group (Pérez de la Vega *et al.* 1998), the isozymatic analysis showed very low levels of genetic variability. This low genetic variability represents an additional threat to the survival of this species in Spain.

In 1999, we started a new programme which included four additional populations. The study on the genetic variability of these samples is presented in this work.

The geographical location and sample size of the populations are shown in Fig. 1. As can be observed, the samples were relatively small, which reflected the small population sizes.

Fig. 1. Geographical location and sample size of the Spanish populations of *Avena murphyi*.

A single panicle of each plant was collected and stored separately; when multiplication was required, one seed per plant was sown and the descendant seeds were again stored separately. In this way and due to the high levels of self-fertilization, the genetic integrity of the samples is being maintained.

The genetic variability of the populations has been assessed using four different types of markers: isozymatic loci, seed storage proteins loci, RAPDs (random amplified polymorphic DNA) and ISSRs (inter-simple sequence repeat). All individuals in each population sample were analyzed for isozymes and storage seed proteins, and 10 plants per population were analyzed for RAPD and ISSR loci.

In order to describe the level and structuration of the genetic variability, several parameters were assessed in each population: number of alleles per locus (A), percentage of polymorphic loci (P) and Nei's gene diversity (H). The values for each population are shown in Table 1.

Table 1. Genetic variability in *A. murphyi* populations (A = mean number of alleles per locus; P = percentage of polymorphic loci at 99% level; H = Nei's gene diversity; n = sample size)

Method	Parameter	Population				
		La Negra n = 25	**Facinas n = 18**	**Bolonia n = 81**	**Tahivilla n = 108**	**A393 n = 25**
Isozymes 12 loci	A	1.16 (1.16)*	1.33 (1.25)	1.58 (1.25)	1.58 (1.22)	1.25 (1.16)
	P	16.67 (16.67)	33.33 (25.00)	58.33 (25.00)	58.33 (33.33)	25.00 (16.66)
	H	0.093 (0.101)	0.148 (0.146)	0.154 (0.084)	0.217 (0.137)	0.167 (0.076)
Seed storage proteins 9 loci	A	1.44 (1.44)	1.55 (1.33)	1.77 (1.55)	1.88 (1.22)	1.33 (1.11)
	P	44.44 (44.44)	55.55 (11.11)	77.78 (55.55)	88.88 (22.22)	33.33 (11.11)
	H	0.153 (0.125)	0.085 (0.045)	0.212 (0.229)	0.138 (0.076)	0.104 (0.052)
RAPDs 64 loci	A	1.53	1.26	1.79	1.62	1.59
	P	53.12	26.56	79.68	62.50	59.37
	H	0.150	0.110	0.248	0.195	0.224
ISSRs 59 loci	A	1.27	1.01	1.45	1.47	1.22
	P	27.11	1.69	45.76	47.45	22.03
	H	0.083	0.004	0.166	0.151	0.065

* Values obtained for the sub-sample used for analysis of DNA markers are shown between parentheses.

The analysis of genetic diversity within and among populations was carried out using Nei's method, in which the total diversity in the species (H_T) is the result of average diversity in the populations (H_S) plus the average gene diversity among populations (D_{ST}). The relationship $D_{ST}/H_T = G_{ST}$ measures the relative magnitude of differentiation among populations (Table 2).

Table 2. Variability parameters for the four types of markers used (A = mean number of alleles per locus; P = percentage of polymorphic loci at 99% level; H_S = average diversity in the populations; H_T = total diversity in the populations; D_{ST} = average gene diversity among populations; G_{ST} = coefficient of differentiation among populations)

Method	Parameters					
	A	**P**	**H_S**	**H_T**	**D_{ST}**	**G_{ST}**
Isozymes	1.38 (1.23)*	38.33 (23.33)	0.155 (0.109)	0.254 (0.239)	0.099 (0.130)	0.389 (0.546)
Seed storage proteins	1.59 (1.33)	59.99 (28.88)	0.138 (0.105)	0.210 (0.219)	0.072 (0.114)	0.344 (0.520)
RAPDs	1.55	56.24	0.185	0.300	0.115	0.383
ISSRs	1.28	28.80	0.093	0.265	0.172	0.646

* Values obtained with the sub-sample used for analysis of DNA markers are shown between parentheses.

The data show that a substantial amount of genetic variation is present in *A. murphyi* populations, in spite of their small number and size. This fact is even more remarkable when this species is compared with *A. barbata*, another tetraploid species which is very common and which generally occurs as large populations. For isozymes, Spanish populations of *A. barbata* presented the following values of the diversity parameters: A=2.0, P=43.3, H_S=0.17, and for RAPD markers, in a study carried out in 12 Argentinean populations, the values were A=1.54, P=40.30, H_S=0.14.

The fact that the few and small *A. murphyi* populations contain genetic variability at the same level as the large and abundant *A. barbata* populations suggests a recent reduction in the number of individuals, probably due to human activities.

Most estimates of the genetic variability in populations using the four types of markers did not show any significant correlations; therefore, we can consider that these markers provide independent estimates of variation.

The coefficient of genetic differentiation (G_{ST}) indicates an important contribution of the diversity in and between populations to the global variability; thus, efforts should be made to conserve all five populations, and not only the largest one.

So as to evaluate whether the use of markers yielded similar relationships between populations, we estimated the Nei's identity for all pairs of populations, and a Pearson correlation (r) was obtained. The correlation was significantly positive for isozyme and storage protein loci ($r=0.93$, $p<0.001$) whilst it was almost zero for the rest of the comparisons. We can therefore consider that protein and DNA markers provide independent estimates of the genetic relationships.

In summary, our results indicate that Spanish populations of *A. murphyi* cannot be considered as depleted of genetic variation as previously assumed. However, the patterns of variation are clearly influenced by the genetic markers used. This could be due to the fact that different markers reveal the genetic characteristics in different regions of DNA (protein-coding genes in isozymes and storage protein loci, and mainly non-coding areas in RAPD and ISSR loci) which are influenced by distinct evolutionary forces.

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Wild Avena *genetic resources for breeding and research*

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Mildew resistance from wild *Avena* (see also EU Project below)

Around 900 accessions of *Avena sterilis* and *A. fatua* which originated from 15 different countries were challenged with race 5 of *Blumaria graminis* f. sp. *avenae* which causes powdery mildew in oat.

Inoculations were carried out in the glasshouse during the early seedling stage, and both seedling susceptible and resistant plants were allowed to continue growth to adult plants.

Several potentially resistant plants were recorded and hybrids between the potential resistors and elite cultivated germplasm were made in order to shorten the time of introgression of the resistance into the cultivated oat.

Among the F2 progeny, three different lines expressed very good adult plant resistance, though each had a degree of seedling susceptibility. The inoculum level in the glasshouse was extremely high, much greater than would be expected under normal field conditions, and it therefore seems probable that these lines would be extremely resistant under normal cultivation.

During an unrelated experiment involving the diploid species *Avena strigosa,* two accessions, one from Portugal, the other from Uruguay (kindly supplied by Wiesław Podyma at the Plant Breeding and Acclimatization Institute (PBAI, Poland), were also noted to have some resistance to *Blumaria graminis*. However, as introgression from diploid to hexaploid is more protracted than hexaploid to hexaploid introgressions, these have not been pursued further.

Genetic relationships within the wild diploid *Avena*

Of the wild weedy diploid species of oat, 13 have been designated as A genome species. These have been further assigned to one of two groups based on karyotype, morphology, chromosome pairing of their hybrids and genomic *in situ* hybridization. Four, *A. longiglumis*, *A. prostrata*, *A. canariensis* and *A. damascena* have been assigned the genomic designations AlAl, ApAp, AcAc and AdAd respectively based on these criteria, whilst the remaining species have been assigned to the 'strigosa' group with the genomic designation of AsAs.

However, the three species *A. hispanica*, *A. lusitanica* and *A. hirsuta* (the latter also known as *A. matritensis*) have been historically assigned to the AsAs genome group based on very scant evidence. Interspecific hybrids between these three species and the purportedly closely allied As and other A genome species have now confirmed that in terms of reproductive compatibility based on chromosome pairing and seed set, all these taxa belong within the AsAs genome '*A. strigosa*' group.

EU Project GENRES CT99-106 "Evaluation and enhancement of *Avena* landrace collections for extensification of the genetic basis of *Avena* for quality and resistance breeding" - Years 1–3

Preliminary observations of genetic variation and breeding prospects

From the observations already made, the genetic variation present in the landraces observed during Years 1, 2 and 3 may be of direct use to the breeding programme at IGER and elsewhere. Differences in floral morphology in terms of open and compact panicle types (particularly the latter) may be useful as well as the shorter growing accessions. The variations in heading date (30 days from earliest to latest in Year 2 and 27 for the main but 52 for the whole including the very late types) may also be of value to breeding programmes. The later flowering accessions are almost certainly winter forms and it is likely that these require vernalization at low temperatures and/or short day length in order to flower during a normal growth period. These observations may indeed be of value in selecting further genes for cold tolerance.

During Year 1 there was a heavy natural infection of crown rust (*Puccinia coronata* f. sp. *avenae*) and a number of accessions were recorded as resistant or partially resistant. Some of these accessions were also observed to be resistant in the laboratory tests conducted by the Swedish partner (partner 5) in the project.

During Years 2 and 3 heavy natural infection of powdery mildew (*Blumaria graminis* f. sp. *avenae* [formerly *Erysiphe graminis* f. sp. *avenae*]) came into the plots and all plants were scored for resistance. In Year 2, 15 lines were recorded as displaying some level of resistance whilst one seemed to be completely immune. In Year 3, a further 19 accessions were scored as possessing some resistance to mildew, and these data will be compared with the glasshouse evaluations conducted by the Swedish partner (partner 5) when the data are complete. It is of particular interest that of the potential mildew resistant/tolerant plants recorded in Year 2, ca. 50% were late flowering (possibly winter) types.

When all the data have been collected and analyzed there will doubtless be numerous characteristics which will be of value to plant breeders, not least the protein analyses being undertaken by the French partner (partner 4).

From molecular analyses being undertaken by the Greek partner (partner 1), it is also hoped that the physiological/morphological/pathological data will yield markers for some of the important traits which have been identified during the course of the project.[57]

[57] See report by A. Katsiotis, "*Avena* landrace AFLP reactions", p. 83.

Using molecular mapping to access and understand valuable traits in wild relatives of oats

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Wild relatives of crop species are a rich source of valuable traits from which currently only a small fraction have been exploited for crop improvement. One of the fundamental problems of crop improvement is how to successfully transfer valuable, novel genes from wild relatives belonging to the secondary or tertiary genepools to polyploid food crops. In this project, diploid and hexaploid relatives of the cultivated oat are being assessed for a wide range of agronomic characters. We are also producing a genetic map at the diploid level using RFLP (restriction fragment length polymorphism), microsatellite and other markers. The two parental lines chosen for mapping show contrasting performance for a wide range of traits (e.g. height, flowering time, tillering, naked character of grain, grain type and composition, the domestication syndrome) and the two reciprocal F_2 mapping populations which have been developed segregate for these traits. Phenotypic data gathered until now indicate a wealth of genetic variation in many aspects of plant phenotype, not least spikelet morphology which has produced a number of novel variants not reported in the literature. Molecular markers identified in this project will not only enable the precise transfer of beneficial genes from wild diploid relatives to hexaploid cultivated oats but will also make possible selection against the simultaneous transfer of adversely linked genes such as shedding grain base, awns and hairy lemmas, which have in the past often reduced the potential of such introgressions in plant breeding programmes. An increased understanding of the molecular genetic basis of grain composition will provide tools that will enable the production of premium value grain designed to meet the specific needs of the end user.

Phylogeny of ACCase in Avena

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Analysis of a 1.4 kb region of the plastidic acetyl CoA carboxylase (ACCase) gene suggests that different lineages of the *Avena* A/D genome progenitors may have been involved in the creation of the *A. sterilis* and *A. sativa* hexaploids. Our starting point was the cloning and sequencing of PCR (polymerase chain reaction) products from two parents used in a cross to map groat oil content QTLs (quantitative trait loci). Polymorphisms in the clones were assigned to particular genomes based on similarity to diploid and tetraploid species, the sequences of which were obtained directly from genomic PCRs. The C genome sequence from both parents is identical, and divergent from the extant diploids *A. ventricosa* and *A. eriantha*. Alleles from one of the A/D genomes appeared to differ slightly in each parent, with two small deletions and two single nucleotide polymorphisms (SNPs) being specific to the high oil parent. The progenitor of these two alleles appears to be ancestral to the closest extant lineage of diploid species, *A. prostrata*, *A. canariensis* and *A. damascena*, which share common features, such as small deletions, not seen in the *A. sativa* sequences. Finally, the alleles from the remaining parental genomes appeared to derive from two separate lineages, with the high oil parent sequence being identical to that of *A. strigosa* while the low oil parent appears to be closely related only to genomes in other polyploids. Specifically, there is only a single nucleotide difference with the non-C genome of *A. insularis*, which in turn is closely related to one of the alleles in *A. barbata* and more distantly to one in *A. maroccana*. In contrast, the high oil parent equivalent is more closely related to an allele in the second genome of *A. barbata* and to a sequence in *A. agadiriana*, and is almost identical to one of the *A. sterilis* sequences, which lacks an *A. insularis*-like allele. It is likely that *A. sterilis* is the source of the high oil parent gene as the latter was derived from a long-term breeding experiment by the University of Iowa which used a high proportion of *A. sterilis* lines as the initial parents.

We therefore suggest that, for this region of the genome at least, *A. sativa* and *A. sterilis* share a common A and C genome, but a lineage including *A. insularis* may have given rise to the *A. sativa* D genome, and a lineage including *A. strigosa* has given rise to the *A. sterilis* equivalent. Tetraploids containing relatives of these two lineages include *A. barbata*, where both are present, and *A. insularis, A. murphyi* and *A. maroccana* where each is present in combination with the common C genome. Polyploidization of any of these could have created the current hexaploids, however it is tempting to speculate that *A. sterilis* has arisen relatively recently by the addition of an *A. strigosa* genome to those of *A. murphyi*, while *A. sativa* seems more likely to contain DNA which is also found in *A. insularis* and *A. murphyi*.

Barley

Perspectives for a modern use of barley germplasm – ECP/GR Barley Working Group Chairman's Report

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Introduction

Plant genetic resources can be regarded as the keystone of the arch between famine and plenty (Fig. 1), within the development of agriculture in the past ten thousand years. Barley, as a major crop of early agriculture, played an important role in human development. After early pioneering work, sources of wild barley have been well collected with major *ex situ* collections available for use by breeders. It is unlikely that any wild accession could be directly used as a crop so it is necessary for a breeding programme to identify new alleles to be incorporated into cultivars. Breeding programmes should feed new cultivars back into genebanks, as arranged between the British Association of Plant Breeders and the John Innes Centre. However, this is not a process that can continue indefinitely and while the concept of the Core Collection is useful it needs to be updated by the incorporation of novel molecular genetic data. In this scenario a genebank acts as a "time buffer" allowing different generations of cultivars to be compared in a single experiment (Ellis *et al*. 2000).

A review of the ECP/GR programme in relation to barley genetic resources has to take account of developments such as the Barley Core Collection (BCC), the European Barley Database (EBDB) and the GENRES project. In addition, it is important to find a vision for the future and not to stagnate because we are shackled by the routine responsibilities that fill every day. In this context the GRACE project offered a major opportunity to bring all aspects of genetic resources into the 21st century. The refusal of the EU to fund any plant research in Framework 6 is a neglect of an important part of the EU science research community. The EU neglect is reflected at the national level in that the UK Government has made it clear that no extra funding will be made available for genetic resources (GR) research. A meeting was held in Birmingham, England in September 2002 with the aim of defining all the *ex situ* collections of plant, animal, microbial and virus. While collections of plant species are well set up and documented – even on a shoestring as the case of the cereal collections – other species are not. This process is still on-going as the Minister then responsible made it clear that the UK Government took its GR Treaty responsibilities very seriously.

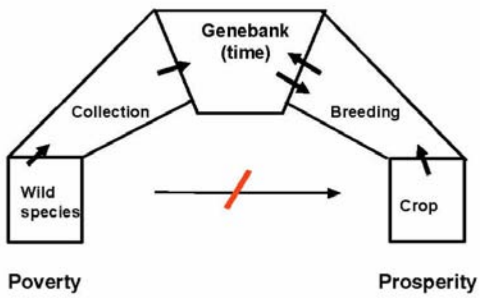

Fig. 1. Hypothetical relationships between wild species and a crop mediated by human activities.

Barley Core Collection

The concept of core collections originated with Frankel (1984) as a means of managing large collections of germplasm. The identification of a set of germplasm based on distinctions such as origin, morphological features and, later, genetic markers could permit the maintenance and assessment of a manageable subset of the whole collection. The European subset of the BCC is currently represented by 298 genotypes. The International Barley Core Collection (BCC) is at present made up of 1338 genotypes (Knüpffer and van Hintum 2003), documented on the European Barley Database (EBDB).

For the concept of the Core Collection to work effectively outside genebanks, it has to be accepted by barley researchers as a valuable contribution to their own science. This is often out of the question, as for many purposes the Core Collection is simply too big. Plant breeders, pathologists, geneticist and many other groups use germplasm collections for their own particular purposes. The methods that may be used range from phenotype assays through to assessment of DNA-based markers. Collection curators have no obvious means by which to rationalize these competing aims. Material transfer agreements, which oblige researchers to acknowledge the use and origin of particular germplasm, do not ensure that data are deposited in a public database. If it were possible to link, seamlessly, collections with evaluation data and DNA sequence data, then germplasm collections would immediately become highly relevant to modern research aims.

An example of the use of germplasm in experimentation is a study that used SSRs (simple sequence repeats) to assay the genetic variability in the pedigrees of 101 spring barley cultivars (Russell *et al*. 2000). The grain was initially obtained from the Biotechnology and Biological Sciences Research Council (BBSRC) collection, maintained at the John Innes Centre by Dr Mike Ambrose. Historically, in the UK the cereal collections of the Plant Breeding Institute, Cambridge (PBI); the Welsh Plant Breeding Station, Aberystwyth (WPBS) and the Scottish Plant Breeding Station, Edinburgh (SPBS) (Table 1) were centralized at the Plant Breeding Institute. This resulted from the 1979 review of UK cereal research that *inter alia* led to the amalgamation of the Scottish Plant Breeding Station with the Scottish Horticultural Research Institute to form the Scottish Crop Research Institute.

Table 1. Original distribution of cereal collections in the UK

	PBI Cambridge	Scottish PBS	Welsh PBS
Barley	+	+	+
Hordeum spontaneum	+	(+)	(+)
Oats	+	+	+
Wheat	+	+	+

The sale of the PBI plant breeding programme in 1987 to Unilever PLC resulted in the move of the (now) BBSRC Cereal Collections to the John Innes Centre, Norwich (JIC). Access to the collection is possible by consulting a catalogue produced by the then AFRC (Agricultural and Food Research Council) Institute of Plant Science Research, but this has not been updated since 1989, or for barley through the European Barley Database (EBDB) currently hosted at the Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany. Distribution of material in the collection is excellent, if slow, but the level of duplication, implicit in the triplicate origin of the collection, is problematic.

The cultivars studied by Russell *et al.* (2000) were commercialized between 1894 and 1998 and they found that 72% of the alleles could be traced back to just 19 "foundation cultivars". Of these cultivars only eight were included in the European Barley Core Collection (Table 2). At the same time the occurrence of rare alleles was scored and EU Core Collection accessions accounted for only 27 of 81 examples. So in this study the strict application of the Core Collection concept would have resulted in the loss of more than half the genetic variation deployed by the breeders during the breeding of current spring barley cultivars.

Table 2. SCRI "Foundation cultivars" found in the Barley Core Collection EU. Cultivar names were modified from those used by Russell *et al*. (2000) by the bracketed additions to restrict the level of duplication after searches on the European Barley Database

Cultivar	Duplicates	BCCEU
Balder	5	-
Bavaria	10	+
(Abed) Binder	23	+
Criewener	2	-
(Heils) Franken	17	+
Gotlands	2	-
Gull	2	-
Haisa (II)	19	+
Hanna	24	-
(Pflugs) Intensiv	11	+
Irish Archer	2	-
Isaria	20	+
Kenia	13	+
Kneifel	3	-
Krim-mesni	5	-
Opal	15	-
Valticky	14	+
Vollkorngerste	1	-
Weihenstephan II	1	-

Duplication of accessions

A point that emerged clearly from the interrogation of the EBDB was, especially if the "less precise" mode is used, that there are a very large number of putative duplicates. The occurrence of duplicate accessions can be viewed as a blessing or a curse. Before the use of precise cultivar maintenance methods, i.e. before commercial breeding, the majority of cultivars were heterogeneous. In this case duplicate samples may help to maintain the heterogeneity. Recent work at SCRI has shown that, while earlier cultivars used to show higher levels of heterozygosity this can still be detected in modern cultivars. However, in many cases duplication can arise accidentally and is a problem that needs resolution. There may be no simple cost free method of removing true "duplicates". One suggested solution has been the use of genetic markers (Lund *et al*. 2003) but there has to be careful consideration of the objectives before appropriate techniques can be selected.

Use of core collections

There are a few examples in the scientific literature of the use of the core collection concept in barley. Bowman *et al.* (2001) report feed quality variation in the USDA National Small Grains Collection. Some 1480 accessions from Afghanistan to Zimbabwe were grown near Bozeman, Montana and dry matter digestibility, morphological traits and starch production were measured. The lowest level of digestibility was found in 'CIho-3709', a landrace from the Nile delta region of Egypt, while a landrace from Macedonia, 'IV/192', had the highest levels. Among the cultivars tested the Swedish 'Green No. 296' from Lulea had the lowest level of dry matter digestibility while 'MCU 3876', from Colombia, had the highest.

Another example is a survey of grain silicon content (Ma *et al*. 2003) who found one hundred fold higher levels in husked by comparison to naked grain. Six-row grain had only slightly higher silica levels than two-rowed.

Origin and use of wild barley in crop improvement

Barley as a crop originated in the Fertile Crescent as a successor crop to wheat because of its greater tolerance to the soil salinity accidentally induced by irrigation. The main uses of barley are for animal feed and beverage production. As the processes of domestication were succeeded in turn by "involuntary" breeding, to produce landraces, and then by deliberate breeding, to give highly bred cultivars, so important traits of wild barley were lost. A large body of work has developed based on the use of disease resistance and the wider genetic variation in wild barley for cultivar improvement. The SCRI programme explored the use of mildew resistance from wild barley (Thomas *et al.* 1991) in a backcross programme that produced resistant lines. Even although these lines were later tested in Egypt, Morocco and Tunisia in an EU-funded project (Forster 1988), they did not achieve commercially acceptable performance there or in the UK.

Other examples of work with wild barley at SCRI concerned the improvement of tolerance to physiological stress. A useful discovery was the stable isotopic changes that related to stress reactions in avoidance rather than stress tolerance (Handley *et al*. 1984). Drought avoidance is enhanced by the development of high levels of post-harvest dormancy and this trait can be problematic for *ex situ* collections. Among the largest collections of wild barley is the BBSRC collection (25 000 samples) held at the John Innes Centre (JIC). Professors Hayes (Welsh Plant Breeding Station) and Dinoor (Hebrew University of Jerusalem) jointly organized the collection of these 230 Israeli populations in 1977. The original material was jointly multiplied, on a single plant basis, in the UK by workers at PBI, Cambridge, SPBS and WPBS and then deposited in a well-maintained seed store at PBI, later moved to JIC. It is important to remember this historical context when considering UK action in the ECP/GR context. When samples were tested in 1999, following a recent multiplication cycle at JIC, dormancy was found in all samples with germination ranging from 0% to 80%. This effect must relate to the interaction of the genotypes with the glasshouse environment. In commercial crops in Northern Europe the abiotic stresses tend to be at lower levels than those in the Middle East and are less predictable, e.g. rainfall does not follow any seasonal pattern. Therefore, in this context high post-harvest dormancy does not have any adaptive significance and is antagonistic to good malting quality. The use of wild barley accesses wide genetic diversity between wild and cultivated barley parents but requires a stricter selection programme than cultivar inter-crosses, perhaps offering the ideal opportunity for marker-assisted selection in early generations.

Use landraces – not wild barley!

It is interesting however, that perhaps the most important single gene for Northern European agriculture, the *mlo* mildew resistance, was discovered in Ethiopian landraces rather than in wild barley (Jorgensen 1992). Landraces may be genetically closer to modern cultivars than wild barley, but even so, extensive breeding through several cycles of re-crossing were necessary to assemble favourable alleles in appropriate linkage blocks (Thomas *et al*. 1998). Landraces have existed worldwide and represent a resource, closer to cultivars than wild barley, that may possess useful alleles. An interesting example is the tolerance of acid soils through limiting uptake of heavy metals (Al, Fe, Mn) into the cytoplasm. Barley is less tolerant of acid soils than wheat or oats so a major transformation of Scottish soils, by the practice of liming, started as barley crops replaced 'Bere', particularly in the 19th and early 20th century. It would be possible to reduce the costs of liming if barley were as tolerant as other crops, but at the risk of increasing aluminium concentrations in animal diets.

When trial plots were established on soil that was still highly acidic despite liming after the removal of woodland, 'Golden Promise' was highly susceptible and few seedlings survived. In contrast, 'Scots Bere' was more tolerant and produced a grain yield equivalent to 1 t/ha. Oats surrounding the trial grew well and produced a higher yield. The overall impression of the site was that high inputs were necessary to produce economically acceptable grain yield at the expense over overall biodiversity. The trial plots resembled a desert while the mixed woodland (oak, birch, pine) hosted a range of plant and animal species. The "desert" feel of the site was emphasized by the removal of stones from the soil, a common feature leading to the degradation of Mediterranean soils. Stones protect the soil surface from rain-induced erosion and act as "magnets" for moisture with the consequence that individual plants may escape the effect of soil acidity as their roots encase stones.

Given that modern agriculture is based on high inputs, the application of fertilizer, herbicide and fungicide permits higher and more reliable yields from 'Golden Promise' than from 'Scots Bere'. 'Golden Promise' with short straw is well suited to combine harvesting and has small grains that germinate very evenly in maltings. In particular, the weak straw of 'Scots Bere' (lodging lowers yield) obscures the merits of the landrace. This is well illustrated by the results from a large diallel experiment carried out at the SPBS in the early 1970s. 'Scots Bere', 'Golden Promise' and 'Ymer' were adapted to Scottish conditions with an early heading date but are not as excessively early as 'Olli' and 'Pirkka'. 'Scots Bere' was tallest, its straw being 40 cm longer than that of 'Golden Promise' and was the highest yielding line. An additional point of interest is that 'Scots Bere' had the highest level of diastatic power despite having lower alpha-amylase. Diastatic power is the sum of the starch degrading enzyme activity in the malt and is made up of limit dextrinase, alpha-amylase and beta-amylase components. Alpha-amylase is synthesized *de novo* in the aleurone layer in response to a gibberellic acid signal from the embryo at the start of germination. In contrast, beta-amylase is synthesized during grain development and is a component of the albumin proteins of the grain. Albumins have a higher content of the aminoacid lysine than the hordeins, the major storage proteins of the grain. High beta-amylase has the corollary of higher lysine content in the endosperm. If re-investigation confirms these results then a major objective, of improving grain nutritional quality, could finally be achieved. It is important to ensure that yield and grain components are compared under carefully controlled conditions, as high grain nitrogen may simply be the corollary of low yield. It is very important to conserve and encourage the use of landraces in barley breeding programmes. However, it would appear that this group of materials is the most difficult to conserve.

The development of simple sequence repeats (SSRs) in barley (Ramsay *et al.* 2000) has speeded up the process of mapping phenotypic traits (Ellis *et al*. 2002). In a particularly useful exercise, a range of germplasm (some 900 genotypes) has been scanned for 50 SSRs chosen to give the widest possible coverage of the genome. The genetic factor responsible for acid soil tolerance was mapped originally to chromosome 4H with morphological markers (Stølen and Andersen 1978). A scan of the SSR allele variation for the SSRs scanned on chromosome 4H showed a number of alleles unique to particular genotypes. However, work in Australia (Raman *et al*. 2003) indicated close linkage between *alt*, the gene responsible for acid soil tolerance, and the SSR Bmag353. As the same allele is also present in 'Maythorpe', this marker cannot be considered as a diagnostic tool although it can be used in routine screening of breeding lines.

Conclusions

The development of molecular markers has transformed views of germplasm with the deficiency of pedigree analysis underlined by the high level of genetic relationship detected between unrelated lines (Ellis *et al*. 1997). The use of SSRs to analyze germplasm from which modern cultivars are descended shows how the current EU Core Collection needs to be overhauled. SSRs also indicate that even modern germplasm has a degree of residual heterozygosity and they have been demonstrated to be a useful method in analyzing collection duplicates. Current DNA-based methods have developed considerably from the initial attempts to use markers for barley breeding. There is reason to think this rate of development will continue and that in the next few years high throughput techniques will make possible the screening of large bodies of germplasm. In the meantime it is important that existing material is conserved and new lines are well documented. At SCRI the Genome

Dynamics Programme, headed by Dr Robbie Waugh, aims to play a vigorous part in the development of the role of DNA markers in genetic conservation.

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The barley collection in Bulgaria

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Introduction

The Institute for Plant Genetic Resources (IPGR)-Sadovo is located in the Thracian Plain of South Central Bulgaria, 20 km from Plovdiv, at an elevation of 141 m asl, latitude 42°07′N and 24°56′E. The average temperatures are as follows: average annual temperature +12.3°C; average maximum temperature in July +30.8°C; average minimum temperature in January -3.2°C. The average annual rainfall is 410 mm, although a tendency to drought should be pointed out. The above factors determine Sadovo as a place of transitional continental climate. The predominant soil texture type in the experimental field is sandy loam with pH 7.84 (Stoyanova 2002).

Status of the barley seed collection

We described in previous publications (Popova *et al.* 1997, 2000) how the barley base collection is maintained in IPGR–Sadovo. There is also a small new collection in the State Agricultural Institute-General Toshevo.

Regarding the status of the collection and the evaluation data, some changes have taken place in the period 2000-2002. The total number of evaluated accessions has increased by 338 and is now about 3380. Every year the working collection rises by approximately 70-80 samples, mainly of Ethiopian "landraces"; it now comprises 1625 accessions.

Evaluation

Barley selection in Bulgaria started in 1915, when the principal method was the individual selection of local barley forms. This was followed by the use of hybridization methods, and the current period is characterized by the application of new selection methods. Local forms, old varieties and modern varieties of the intensive cultivation type have been evaluated and preserved in the genebank's barley collection in IPGR-Sadovo. There are over 100 accessions.

Table 1 lists a selection of Bulgarian barley varieties, providing additional data on accessions which are already included or will be included in the *Index seminum,* freely available for exchange.

The table includes both two-row and multi-row varieties of winter and winter-spring growth habit, which allow a longer period of sowing from October till the end of February.

As for height, in general varieties are of medium height, but the majority are less than 100 cm high.

The ear length, an important structural element of the crop, is greatest for two-row varieties - 'Oglon', 'Korten' and 'Perun'.

As far as earliness is concerned, varieties belong to the early biotype compared to standards 'Hemus' (multi-row) and 'Obzor' (two-row), although there are also varieties earlier by 3-4 to 5 days than standards. This is valid especially for two-row varieties.

The weight of 1000 grains varies from 37-40 to 48-52 g for two-row varieties, while for multi-row ones it is lower because of the ear structure.

The content of raw protein does not vary much; however it is lower in two-row varieties, which explains their use in brewing. Multi-row varieties are used as forage plants and their raw protein content is higher.

The varieties tabulated here are considered to show comparatively high biological potential (Popova *et al*. 2003).

The short descriptions of varieties in Table 1 will give the opportunity to users to order what is of interest for them.

Table 1. Pedigree and basic characteristics of Bulgarian barley varieties

Varieties	Year of cross-fertilization and registration	Pedigree	Growth habit*	Plant height (cm)	Spike length (cm)	Earliness	Weight of 1000 seeds (g)	Crude protein (%)
A. Two-row								
Obzor (standard)	1975/1984	28H-46-10 x Trumpf	WS	89	7-8	Early biotype	45-47	11-12
Ruen	1974/1984	Tripoli Tripolitani x Alpha	W	100-110	7-8	Early biotype	48	12.8
Yubilei 100	1974/	Markelli 5 x Malta	W	100-110	5-8	Early biotype	48-52	13.2
Krassi 2	1975/	Markelli 5 x Trumpf	WS	80	5-7	Average early	37-40	12-13
Oglon	1975/	28H-46-10 x U613/72	W	68-70	9-10	Early biotype	40-42	13
Perun	1978/1996	Alpha x Mer	W	95	6-7	3-4 days before St	48-49	11.5
Aster	1981/1994	(Novi Sad-183 x M-20-H) x 22FG-29	W	80	9	3-4 days before St	42-45	11.2
Emon	1981/1998	137 HS-2/M-21-71/3/Malta (M-20-71)x (M-21-71/4/ 111G-65)	W	88	7-8	2-3 days before St	47-48	11-12
Korten	1983/1993	Oglon 31T-23 x 111G-65	W	85	9	4-5 days before St	48-49	11.5
B. Multi-row								
Hemus (standard)	1976/	Robure x Mirage	W	100	6	early biotype	38-40	12-13
Karnobat	1974/	№234 x №468	W	70-80	5.5-6	early biotype	36-38	
Jerun	1974/1991	(№190/17989) x №468	WS	97	6.5-7	early biotype	37-39	12.5-13.5
Zenit	1977/1987	(№411/37 x 32478) x №468	WS	92-100	5.4-6	early biotype	36-39	12.5-13-5
Izgrev	1978/1990	(№42-66-6-4 x Miraj)x Kamchia	W	88-101	5.5	early biotype	36-39	12.5-13.5
Diana	1979/	An x-ray mutant of the Miraj	W	82-90	6.5-7	early biotype	32-36	12.5
Panagon	1980/1994	4074/79 x 22 FG-29	W	90	7-7.5	early biotype	34	13
Vesletz	1982/1994	№102/121 x Karnobat	WS	91	5.5-6	early biotype	37-39	11-14
Aheloj	1982/1996	KT/2023 x Productiv	W	90-97	7	Early biotype	36-38	13.3

* W= Winter; S =Spring

Exchange

1. Aegean Agricultural Research Institute, Izmir, Turkey: 5 accessions.
2. Institute for Wheat and Sunflower "Dobrudja", Dobrich, Bulgaria: 13 accessions.
3. Agrarian University, Plovdiv, Bulgaria: 12 accessions.

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The collection of spring and winter barley genetic resources in the Czech Republic [58]

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Introduction

Barley is a traditional and important crop in the Czech Republic. Both forms of the crop are grown: spring barley on ca. 400 000 ha and winter barley on ca. 180 000 ha. Barley breeding has a very long and successful tradition in the country (Lekeš 1997; Bareš *et al.* 1998).

Evaluation and documentation of plant genetic resources (PGR) in the Czech Republic are carried out in the framework of the "National Programme on Plant Genetic Resources Conservation and Utilisation" that was launched by Ministry of Agriculture in 1994. The Genebank in the Research Institute of Crop Production (RICP), Prague-Ruzyne was assigned the task of project coordination and is also responsible for other activities – evaluation of wheat, triticale and winter barley collections. The winter barley collection consists of 1894 accessions, including mainly cultivars, advanced lines and landraces, together with 80 wild relatives.

The Agricultural Research Institute Kroměříž Ltd. is responsible for the development and evaluation of the rye, oat and spring barley collections. These crop collections contain nearly 5351 accessions. The spring barley collection with 2662 accessions is considered to be a large and important Czech cereal collection.

Methods of evaluation

Evaluation of barley genetic resources is carried out according to the methodology given by Stehno *et al.* (2004). New accessions are evaluated each year on 2.5 m^2 plots. Two check cultivars that are included after each tenth plot enable better comparisons of evaluation data from different years, i.e. from different conditions. Registered cultivars with high yield potential, acceptable yield stability and good grain quality are used for this purpose. In the case of winter barley, both types (six-row and two-row) are used simultaneously as the check cultivars.

Morphological characters, growth and development phases and canopy characteristics are evaluated during the growth period. Spike samples are taken from each accession for spike analyses and for the spike collection. Seed samples taken from each plot after harvest are analyzed from the point of view of quality.

The descriptor list for genus *Hordeum* L. (Lekeš *et al.* 1986) is used to score the properties and characters.

Documentation of the barley collection

- **Sub-database of passport data**

Passport data represent the basic information on particular accessions. They are gathered regularly, completed and entered in the Czech database of genetic resources EVIGEZ. A unique accession number is given to each entry separately for spring (C06-xxxxxx) and winter (C05-xxxxxx) barley accessions. Passport data are maintained under the special EVIGEZ software, based on FoxPro, and they are linked with other sub-databases

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[58] (updated December 2005)

(description data, monitoring of the seed store). The same passport data are available in another system on the Internet (http://genbank.vurv.cz/genetic/resources).

- **Evaluation data**

Evaluation data represent important information for the utilization of genetic resources in breeding or further research. The data from former years of evaluation are still kept in field notebooks and are being progressively converted into the scoring scales and entered into the database.

Each year, the recently obtained description data are prepared and entered into the database. This activity is one of our priorities. Recently description data for 1402 barley accessions were entered.

- **Monitoring of seed store**

Pre-dried seed samples of barley are maintained in the same way as samples of other cereals in the store, at –5°C for the active collection and -18°C for the base collection. Where to find the seed sample in a cold chamber, seed amount and seed viability are monitored in this part of the information system.

"Core" collection

The core collection of spring barley genetic resources maintained in the Czech Republic has been prepared. Pedigree analysis was used as the first step of the procedure. The core collection of winter barley is under process of preparation.

Information and material exchange

Passport data of the Czech barley collection are freely available on the Internet and can be obtained as a file or hard copy. Availability of description data depends on the collection holder.

Most seed samples are available freely, but some accessions can be provided only upon agreement of the owner. Seed samples are submitted on the basis of a Material Transfer Agreement (MTA).

Utilization of barley genetic resources

Barley accessions are used in breeding programmes within the country because the spring barley collection is connected very closely with the breeding programmes. The winter barley collection is also tightly linked to the breeding of new winter barley cultivars (Špunar *et al.* 1996, 1999).

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Barley germplasm collections in France

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National Collection

The maintenance of the national barley *(Hordeum vulgare* L.) collection in France is now shared between several kinds of participants and users: both public institutions such as INRA (Institut National de la Recherche Agronomique) and private breeders are involved. The seeds are kept in cold stores according to international standards. Duplicates are kept.

INRA barley collections

In 2001 the INRA barley collection in Clermont-Ferrand received the barley germplasm previously maintained at INRA-Montpellier. The number of accessions is now about 6500. A new store was built and all the cereal collections were transferred there in 2002. The present facilities are improved in that they have a better and safer power equipment to ensure a lower moisture level in the rooms. The pre-conditioning of the seeds is also improved, as a special room is devoted to this step prior to medium-term storage.

Barley evaluation networks

French barley breeders continue to take part in barley evaluation and regeneration, as during previous years, led by the coordination unit (for small seed cereal genetic resources) which itself is overseen by a steering committee. The seed samples are divided between two conservation sites at INRA-Clermont-Ferrand and GEVES (Groupement d'Etude et de contrôle des Variétés et Semences)-Le Magneraud. Data are recorded in the centralized database "ERGE" using the FAO/IPGRI *Multi-crop Passport Descriptor List* and other descriptors for evaluation.

Participation of INRA and GEVES in the recent European project GENRES CT98-104 has generated a large amount of information on very large series of barley accessions from diverse origins. After the confidentiality delay existing in the project contract has elapsed, a significant number of promising sources of resistance to diseases, in particular, are expected to be tested on a wider scale and eventually to become available to breeders.

In the recent period, the main points of interest for the barley breeders have been mainly focused on new resistance sources such as tolerance to barley yellow mosaic virus (BaYMV), barley mild mosaic virus (BaMMV) and barley yellow dwarf virus (BYDV), and to some extent also on the diversity of β-glucan content in the barley kernel.

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Status of barley germplasm collections in Israel

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The barley germplasm collections in Israel contain mainly accessions of wild barley (*Hordeum spontaneum)* collected from natural populations in the Fertile Crescent. Out of 13 519 accessions in these collections, 12 344 are wild accessions of *Hordeum spontaneum* and 186 accessions of other wild *Hordeum* spp. (mainly *H. bulbosum*). Only 989 accessions are cultivated forms of *Hordeum vulgare* (Table 1).

Table 1. Collections of barley germplasm (*Hordeum* spp.) in Israel

Institute	*H. spontaneum*	*H. vulgare*	*Hordeum* spp. (mainly *bulbosum*)
Institute for Cereal Crops Improvement, Tel Aviv University	6500	500	143
Institute of Evolution, University of Haifa	3390	0	0
Israeli Gene Bank for Agricultural Crops (IGB), Agricultural Research Organization	2210	480	33
Faculty of Agriculture, The Hebrew University of Jerusalem	200	0	0
Department of Plant Sciences, Weizmann Institute of Science	44	9	10
Total	**12344**	**989**	**186**

Beside the collection of the Israeli Gene Bank for Agricultural Crops (IGB), other collections are maintained by Israeli researchers in their respective institutions as part of their research programmes. The following are the reports on the status of the collections in these institutes provided by the contact person in each institute.

Israeli Gene Bank for Agricultural Crops (IGB)

Contact person: Dr Rivka Hadas (email: rihadas@volcani.agri.gov.il).

The IGB collections include 2210 accessions of *H. spontaneum*, 480 *H. vulgare* and 33 *Hordeum* spp. All accessions are fully documented.

Institute for Cereal Crops Improvement (ICCI), Tel Aviv University

Contact: Dr Jackob Manisterski (email: cereal@post.tau.ac.il).

The barley collection in the Lieberman Germplasm Bank in the Institute for Cereal Crops Improvement includes 6500 *Hordeum spontaneum* and 143 *Hordeum* spp. accessions collected in Israel and 500 *H. vulgare* varieties. Some of the *H. spontaneum* are single lines collected randomly; some are selections for disease resistance made in natural habitats and most lines belong to transects sampled in different *Hordeum spontaneum* populations. The collection has been evaluated for leaf rust of barley (*Puccinia hordei),* and for powdery mildew (*Erysiphe graminis hordei)*. The *H. vulgare* accessions in the collection are differential varieties and varieties from different international nurseries. The collection is preserved at 5°C with 35% relative humidity.

Institute of Evolution, University of Haifa

Contact: Prof. Eviatar Nevo (email: nevo@research.haifa.ac.il).

The collection of wild barley, *Hordeum spontaneum*, in the Wild Cereal Genebank at the Institute of Evolution consists of 3390 accessions from various sources used for macro- and microgeographic studies of natural populations:

1. The Macrogeographic collections contain 33 populations from Israel (1371 accessions), 20 populations from Iran (327 accessions), 20 populations from Turkey (313 accessions) and 27 populations from Jordan (646 accessions);
2. The Microgeographic collections (733 accessions) contain 392 accessions from Nahal Oren ("Evolution Canyon"), 286 accessions from Tabigha (soil type: basalt vs. terra rossa) and 55 accessions from Neve Yaar (sun vs. shade).

The collections were evaluated for various agronomic traits. Out of the 3390 genotypes, 2200 genotypes were evaluated for all or some of the following traits: multiple disease resistances (e.g. powdery mildew, leaf rust, septoria, net blotch, spot blotch and stem rust); abiotic stress (e.g. drought tolerance and salt tolerance); agronomic traits (e.g. germination, biomass, earliness, yield, grain protein content and milling energy); genetic diversity studies using various molecular markers (e.g. allozymes, RAPDs, SSRs, AFLPs, sequence-tagged-sites, retrotransposons and rDNA). A list of publications describing the evaluation of these collections can be found on the Web site of the Institute of Evolution (http://research.haifa.ac.il/~evolut/). The collection is preserved at 5°C with 35% relative humidity.

Faculty of Agriculture, The Hebrew University of Jerusalem

Contact: Prof. Amos Dinoor (email: dinoor@agri.huji.ac.il).

The active collection of *Hordeum spontaneum* contains over 200 entries, collected at five locations in Israel. They were collected at a variety of niches, as single-spike entries and were then propagated several times over the years. These entries were tested for resistance to selected collections of powdery mildew cultures both in the Czech Republic and in Israel, in cooperation with Dr A. Dreiseitl. Quite a number of entries were resistant to many fungal cultures. The data are not yet published.

Department of Plant Sciences, Weizmann Institute of Science

Contact: Prof. Moshe Feldman (email: lpfeld@wiccmail.weizmann.ac.il).

This small collection was collected 25 years ago in Israel and was preserved at -18°C. This collection contains 44 *Hordeum spontaneum* accessions, 9 cultivated *H. vulgare* accessions, 9 *H. bulbosum* accessions and one accession of *H. muritanum*.

Status and development of the national spring barley germplasm collections in Lithuania

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Introduction

Activities related to spring barley genetic resources were initiated in Lithuania in 1994, together with the Baltic project on plant genetic resources conservation funded by the Nordic Council of Ministers and carried out in close cooperation with the Nordic Gene Bank. The National Plant Genetic Resources Programme for cultivated plants "Genefund" was launched in 1998 by the Lithuanian Ministry of Education and Science. It was subsidized by the Lithuanian Science and Studies Foundation and coordinated by the Lithuanian Institute of Agriculture (LIA). The Programme encompasses conservation and research on genetic resources of agricultural and horticultural plants and domesticated animals. Eight research and educational institutions which had earlier been involved in the conservation of genetic resources joined the programme (Būdvytytė 1998). The exploration, collecting, conservation and evaluation of spring barley plant genetic resources are conducted within the framework of this programme.

The national barley collections

Three institutions are responsible for the maintenance of cereal collections: the Lithuanian Institute of Agriculture (LIA, Dotnuva), Vilnius University (VU, Vilnius) and the Lithuanian University of Agriculture (LUA, Kaunas). All spring barley accessions are kept in the active collections of these institutions. The type of material and the numbers of accessions are shown in Table 1.

Table 1. Lithuanian spring barley collections, 2003

Institution	No. of accessions			
	Total	**Varieties**	**Breeding lines, mutants, genetic stocks, intraspecific taxa**	**Varieties of Lithuanian origin**
Lithuanian Institute of Agriculture	831	599	232	14
Vilnius University	336	10	326	7
Lithuanian University of Agriculture	23	5	17	1
Total	**1190**	**614**	**575**	**22**

The Lithuanian barley breeding programme includes only spring barley. It was started in 1924. The collection currently contains 14 spring barley varieties of Lithuanian origin: all these are maintained at the LIA spring barley collection, and only duplicates in the other two locations. Thirteen spring barley accessions of Lithuanian origin have already been placed in long-term storage (10 000 seeds per accession) at the Lithuanian Genebank (Table 2).

Table 2. Spring barley varieties of Lithuanian origin stored at the Lithuanian Genebank, 2003

Variety	Pedigree	Year of release	No. of accessions in storage
Auksiniai	Individual selection from Gull	1927	13
Dotnuvos ketureiliai	Individual selection from landrace	1930	17
Džiugiai	Individual selection from landrace	1947	18
Auksiniai II	Abed Kenia/Ackerman Isaria	1947	14
Gausiai	Auksiniai II/Viner+Abed Archer+Bigo	1961	20
Gintariniai	KM 1081252/Pallas	1973	19
Dainiai	Gausiai/Gaaselle//Abed 3371	1981	16
Auksiniai 3	Carina/Tarra 26	1983	15
Vilniečiai	Mutant from Pallas	1986	-
Aidas	KM 1192/Ofir//Effendi	1990	11
Ūla	Roland/Ca 33787	1992	23
Alsa	Mirena/mutant from Gintariniai//Abava/Emir	1993	12
Aura	Mirena/mutant from Gintariniai//Lina	1997	344
Luokė	Vega//Ofir/Berenice/3/Flare	1999	683

The Lithuanian Genebank is located at the Lithuanian Institute of Agriculture. It currently maintains 117 accessions of spring barley. There are 33 varieties and breeding lines from LIA and 84 mutants and genetic stocks from VU collections. Twelve spring barley accessions of Lithuanian origin have been placed in the long-term safety-duplication collection in the base collection of the Nordic Gene Bank (Table 3).

Table 3. Number of spring barley accessions stored at the Lithuanian Genebank, 2003

Institution	1997	1998	1999	2000	2001	2002	2003	Total	Safety-duplicated at NGB
Lithuanian Institute of Agriculture	13	5	2	3	4	3	3	33	12
Vilnius University	11	40	19	0	7	7	0	84	0
Lithuanian University of Agriculture	0	0	0	0	0	0	0	0	0
Total	**24**	**45**	**21**	**3**	**11**	**10**	**3**	**117**	**12**

Evaluation and utilization of the collections

The possibilities for enriching the national spring barley genetic resources with local diversity are very limited. Therefore we are concentrating on the evaluation and investigation of the genetic resources already accumulated, because only after detailed evaluation and investigation can we determine their real value, their possibilities for future use and the relevance of further preservation of such material. The evaluation of collections is carried out according to the national barley descriptors, prepared on the basis of IPGRI descriptors (Leistrumaitė 2002).

The Lithuanian Institute of Agriculture has an active spring barley collection, which is mainly used for breeding purposes. It is not stored in the long-term seed store. The number of accessions in it varies. Since 1989 all spring barley varieties received by the Lithuanian Institute of Agriculture have been collected and maintained. The number of accessions collected at the LIA currently amounts to 831. Most of the accessions (410) were received from the Vavilov Institute of Plant Industry (VIR) (Anonymous 1922-2003). Table 4 lists the numbers of spring barley accessions according to their countries of origin (29 countries).

Table 4. Number of accessions and countries of origin of the Lithuanian Institute of Agriculture's spring barley active collection

Country of origin	No. of accessions	Country of origin	No. of accessions
Australia	2	Italy	7
Austria	8	Former Yugoslavia	4
Belgium	4	Kazakhstan	2
Belarus	26	Lithuania	36
Canada	8	Latvia	28
Former Czechoslovakia	28	Netherlands	29
Germany	97	Norway	4
Denmark	95	Poland	36
Estonia	12	Portugal	1
Finland	64	Russia	57
France	52	Sweden	95
United Kingdom	62	Ukraine	60
Georgia	1	United States of America	7
Hungary	3	Uzbekistan	2
Iceland	1		
Total = 831			

In order to maintain high viability of the seed the varieties must be regenerated every three years. About 300 accessions are planted and investigated in the experimental fields annually. The main tasks of this work are evaluation and characterization, documentation and preparation of seed samples for conservation in the long–term store at the Lithuanian Genebank.

The Lithuanian PGR Barley Database was developed in 2002. Passport data of 647 spring barley accessions are available on the home page of LIA (http://www.lzi.lt/, subsection Lithuanian PGR). The passport data for other accessions are not complete. The database is constantly updated with new material.

At Vilnius University the spring barley collection is used for genetic research. They have an original collection of induced barley mutants and revertants - about 300 accessions. It includes several genetically unstable loci: *be (branched ear), tw (tweaky spike)* and others. Among the latter the most promising for plant morphogenetics and immunogenetics are homeotic *tw* type mutants with lodicules converted ectopically to stamens and/or pistils. The barley collection also includes genetic stocks, cultivars and mutants with marker genes for barley chromosomes, genes determining high resistance to fungal infection or high lysine content. Over 10 generations of these have been multiplied under Vilnius conditions. Therefore they might be considered as new, partially adapted local accessions. This is evidenced by a new allelic variant of the gene *Hooded* (Rančelis *et al.* 2001). DNA polymorphism analysis by PCR (polymerase chain reaction) using random primers and amplified microsatellites was applied to about 80 barley mutants, hybrids and cultivars originating from Lithuania or neighbouring countries. At present the nucleotide sequence analysis of homeotic loci is still being carried out.

The spring barley collection of the Lithuanian University of Agriculture is used exclusively for educational purposes. It consists mostly of morphologically different lines representing different intraspecific taxa.

Perspectives for the future

The following activities are planned using the spring barley genetic resources:

- To continue the evaluation of breeders' and mutant active collections for the identification, characterization, documentation, preservation and utilization of the most valuable accessions;
- To provide additional passport information and complete the Lithuanian Barley Database with evaluation and characterization data;
- To extend cooperation and exchange of genetic material with other holders of plant genetic resources.

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The Romanian barley collection

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Introduction

Barley is traditionally an important crop in Romania, occupying over 7% of the total cultivated area of cereals (Fig. 1). In the last seven years the barley growing area has varied between 1 017 000 and 412 000 ha (Fig. 2). Grain yields recently ranged from 2.6 to 3.0 t/ha and the average national production of barley reached nearly 867 000 t in 2002.

The Romanian National List of Released Varieties includes 13 registered spring barley varieties for 2002, 7 local and 6 foreign varieties, and 20 winter barley varieties.

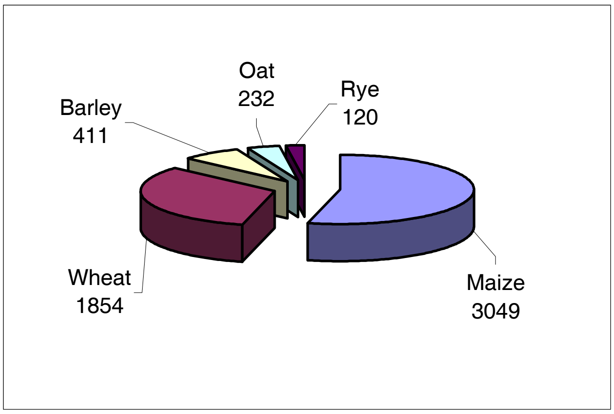

Fig. 1. Areas cultivated under cereals in Romania (in thousands ha).

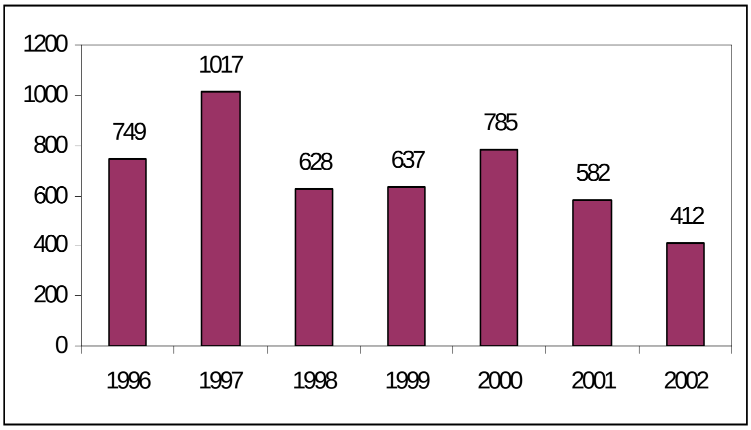

Fig. 2. Evolution of the area cultivated under barley in Romania, 1996-2002 (in thousands ha).

Description of the Romanian barley collection

The barley collection is divided into three sub-collections according to crop growth characteristics.

The winter barley sub-collection at the beginning of 2002 consisted of 1728 samples. Brewing accessions dominate the barley collection with 1942 spring accessions and 155 intermediate accessions.

The national barley collection is currently held by five Romanian institutes (Table 1).

Table 1. Romanian institutes holding the national barley collection

Institute	No. of accessions
Institute for Cereals and Industrial Crops Fundulea	2096
Agricultural Research Station Suceava	845
Suceava Genebank	851
Agricultural Research Station Simnic	25
Agricultural University Timisoara	8
Total	**3825**

Concerning the subspecies of *Hordeum vulgare*, the entire collection consists of var. *distichon* (1942 accessions), var. *hexastichon* (1580) and var. *tetrastichon* (300).

The institutes involved in the breeding of barley are:

- The Institute for Cereals and Industrial Crops (ICCPT Fundulea),
- The Agricultural Research Station Suceava (SCDA Suceava), and
- The Agricultural Research Station Turda (SCDA Turda).

Description of the Suceava Genebank collection

The Suceava Genebank has a working collection and a base collection. As indicated above, the total number of accessions is 851, including 183 indigenous, 511 foreign (Russia, Germany, USA) and 152 of unknown origin (Table 2).

Regarding the status of the accessions, the collection consists of 280 advanced cultivars, 523 breeding lines, 44 local varieties and 4 accessions of unknown status.

Table 2. Countries of origin for the Suceava Genebank collection (only countries with more than 10 accessions are listed)

Country of origin	No. of accessions
Argentina	10
Canada	23
China	15
Former Czechoslovakia	11
Germany	44
Moldova (Republic of)	19
Poland	34

Country of origin	No. of accessions
Romania	183
Russia	64
Sweden	13
Turkey	72
USA	55
Yugoslavia	17
Unknown	152

Evaluation of barley genetic resources

Breeders interested in the programmes for the management of genetic resources can maintain the collections if the established germplasm offers enough material which can be used as parents for breeding.

In Romania, the barley breeder programmes have the following objectives:

1. For fodder: high productivity, precocity, resistance to diseases, higher protein contents (more than 16%);
2. For brewing: high productivity, precocity, resistance to diseases, lower protein contents (less than 13%).

Evaluation of barley germplasm in the Suceava Genebank involves three steps:
1. Characterization and preliminary evaluation of barley accessions;
2. Secondary evaluation;
3. Selection of sources resistant to diseases for potential users.

1. Characterization and preliminary evaluation of barley accessions
The characterization descriptors have to achieve quick and easy differentiation between phenotypes. These descriptors contain information on hereditary traits which may be dependent or independent of climatic factors. It is also possible to include a minimum number of descriptors which are needed for potential users.

Up till now, the Suceava Genebank has carried out the characterization and preliminary evaluation on 293 barley samples.

The barley collection is currently evaluated according to the following IPGRI barley descriptors:

- Sowing date
- Germination date
- Growth rate
- Tillering capacity
- Total number of tillers
- Number of fertile tillers
- Growth habit
- Earing date
- Plant height
- Days to flower
- Spike length
- Number of spikelets per spike
- Number of seeds per spikelets
- Number of seeds per spike
- Number of seeds per plant
- Weight of seeds per spike
- Weight of seeds per plant
- 1000-seed weight

2. Secondary evaluation
Genetic resistance to biotic stress is a decisive factor in determining the productive value of cultivars. For precise determination of barley resistance to diseases, a standardized evaluation methodology was used, presented in the context of the EU GENRES CT98-104 project in which Romania was a partner.

In this area there are two distinct activities:
a. Evaluation of genetic resistance to biotic stress, and
b. Evaluation of fungi in seed germplasm before and after long-term storage.

3. Selection of sources resistant to diseases for potential users
Genetic diversity is the most valuable factor for the development of new cultivars that will be able to withstand biotic and abiotic stress and will have high grain yield and good quality.

Our work focuses on the evaluation of accessions and selection of the most resistant ones with potential for breeding. At present, our genebank holds many samples very resistant to one, two ore more diseases (Table 3).

Table 3. Disease resistance of the barley material held at the Suceava genebank

Disease	No. of samples
Septoria tritici	114
Erysiphe graminis	56
Puccinia graminis	25
Helminthosporium sp.	3
Helminthosporium graminearum	117
Helminthosporium tritici	142
Helminthosporium sativum	89
Ustilago hordei	126
Rhinchosporium secalis	124
Erysiphe and *Puccinia*	39
All analyzed diseases	1

Maintenance of seed samples

Barley seed samples are maintained in the Suceava Genebank as part of the active collection at +4°C (851 samples). The most valuable accessions are duplicated in the base collection kept at -20°C (185 samples). An important part of the barley accessions (3061 samples) is still kept in the research institutes as working field collections.

Documentation of the Romanian barley collection

Data on barley genetic resources represent an important part of the BIOGEN database (the Romanian documentation system for plant genetic resources consists of passport, characterization and evaluation data and genebank management data). The Suceava Genebank Web page will be available in future on Internet at www.svgenebank.ro.

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Report on the barley collection in Slovakia

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Characteristics of the Slovak barley collection

Conservation of the cultivated plant genepool in the Slovak Republic is funded and supported by the Ministry of Agriculture. The mandate for coordination was given to the Research Institute of Plant Production (RIPP) in Piešťany. RIPP has been working with plant genetic resources (PGR) systematically for 52 years. The barley collection was one of the first collections created in our institute. The Slovak National List of Released Varieties for 2002 recorded 24 spring barley and 14 winter barley varieties.

The RIPP barley collection currently includes 1717 accessions (376 winter barley and 1341 spring barley). The base collection, which includes only domestic accessions, contains 21 accessions of Slovak origin. The current composition of the barley collection in the genebank is presented in Table 1.

Table 1. Barley accessions in the Slovak genebank

Type of barley	Collection			Total
	Base	Active	Working	
Spring barley	21	802	518	1341
Winter barley	0	356	20	376
Total	**21**	**1158**	**538**	**1717**

The composition of the barley collection is shown in Fig.1. Nearly 25% of the material originates from the Slovak and Czech Republics.

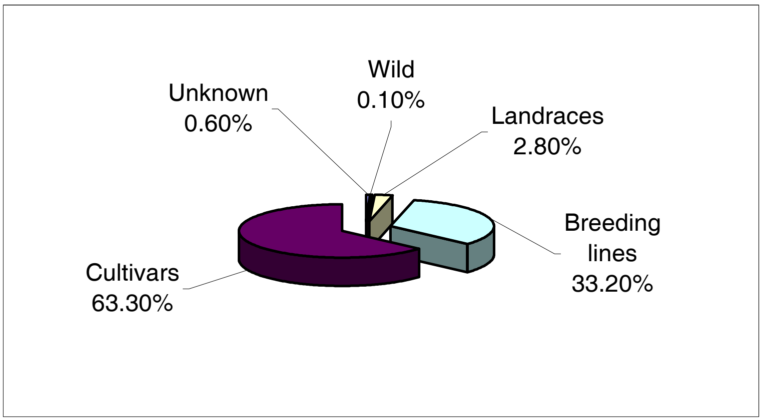

Fig. 1. Composition of the Slovak barley collection.

Study of genetic resources

The barley accessions are evaluated under field conditions on the RIPP experimental fields. The aims are collecting and conservation (varieties, old historical material, landraces, breeding material, wild species, etc.) and evaluation for all selected aspects (morphological characteristics, phenological stages, evaluation of yield characters, disease resistance and postharvest quality analyses) according to the descriptor list for Barley, developed on the basis of UPOV, IPGRI and EVIGEZ Descriptor Lists. At present about 30 morphological characters are studied.

Resistance to diseases – powdery mildew (*Erysiphe graminis)*, leaf rust (*Puccinia hordei*), net blotch (*Phyrenophora teres*) and scald (*Rhynchosporium secalis*) – is evaluated in field conditions and will also be tested in the laboratory. In 2003 we evaluated about 400 accessions, including 356 of spring barley and 51 of winter barley.

Reproduction and storage

Genetic resources of barley are stored in the base collection at –17°C with a 10-year cycle of germination monitoring, and in the active collection at 2–5°C with a 5-year cycle of germination monitoring. Accessions stored in the active collection serve for distribution and regeneration. A safety collection is established for the accessions stored in the base collection. Safety-duplicates are located in the genebank of the Research Institute of Crop Production (RICP)-Prague according to a reciprocal cooperation agreement.

Documentation and database structure

The genebank information system is based on the database management system FoxPro. The structure of the passport data follows the principles of the FAO/IPGRI *Multi-crop Passport Descriptor List.* The documentation status for passport and description data is presented in Table 2.

Most of the description data are not stored electronically yet. After harvest the new evaluation data obtained for this growing period will be entered.

Table 2. Documentation status of the Slovak barley collection

No. of accessions	Spring barley	Winter barley
Passport data	1376	421
Description data	369	207

Evaluation activities on barley

In the period 2001–2002 we were included in the project GENRES CT98–104 "Evaluation and Conservation of Barley Genetic Resources" as a non EU-member. This project, which lasted three years for the EU partners, was coordinated by Dr Helmut Knüpffer (Genebank Department, IPK Gatersleben, Germany).

During the last year of the project, the Research Institute of Plant Production carried out the following activities: computerization of existing evaluation data for 300 accessions; field evaluation of 100 accessions of spring barley for resistance to powdery mildew (*Erysiphe graminis*) and of 100 accessions for resistance to rust (*Puccinia hordei*). All results have been recorded in Excel and transmitted to the project coordinator.

Priorities for the future

The objectives of the research in future are to assess the genetic diversity of spring barley genotypes grown in Slovakia (historical and most frequently grown varieties originating from Slovak and former Czechoslovakia). One hundred barley genotypes will be evaluated and analyzed with molecular markers. Simple sequence repeats (SSRs) analysis has several advantages over other markers. These include a high level of polymorphism, co-dominance, simplicity and marker stability. A majority of SSR-derived primer pair amplified length variation in SSRs. Null alleles and heterozygous genotypes at the SSR loci are also detected. We plan to include the results of this analysis into the barley database.

International Barley Genes and Barley Genetic Stocks Database

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Background

The request for an International Database for Barley Genes and Barley Genetic Stocks was already discussed in 1989 at an FAO Working Group on Plant Genetic Resources in Lund, Sweden. At the IBPGR Workshop in Helsingborg, Sweden, in 1991, Sigfus Bjarnason, then director of the Nordic Gene Bank, demonstrated a proposed database for Barley Genes and Genetic Stocks (Bjarnason 1992). In his proposal he stressed the importance of gene, allele, synonym, stock and reference tables.

At the 15th North American Barley Researchers Workshop in Guelph, Canada, 1993, Dave Matthews and co-workers (Altenbach *et al.* 1993) introduced the Triticeae Genome Database "GrainGenes", developed under the Plant Genome Research Program of the US Department of Agriculture at Cornell University, with additional support from the International Triticeae Mapping Initiative, USA.

The GrainGenes and its software, ACeDB, were later to become the model for the BGS (Barley Genetic Stocks) database.[59] Since ACeDB has several important advantages over conventional relational database systems in handling biological information, and because a usable data model already existed for wheat mutants at GrainGenes, the decision was natural. Dave Matthews of Cornell University kindly worked as an advisor and support person throughout the project, for example by adapting the data model for barley and providing the GrainGenes model for linking data to references.

The Barley Genetics Newsletter and Barley Genetics Stock Descriptions

The task of compiling a database for barley genes and genetic stock took a new turn in 1997 when the format for describing morphological mutants in the Barley Genetics Newsletter (BGN) changed.

The overall structure of the descriptions was made more consistent, with special paragraphs dedicated to cover previous nomenclature, inheritance, locus location, descriptions of physiological and morphological characters, mutational events, mutants used for description, parent germplasm and references.

The descriptions include information about gene expression and its locus name with the use of three-letter symbols in all descriptions. These recommended locus symbols are based on the utilization of a three-letter code for barley genes as approved at the business meeting of the Seventh International Barley Genetics Symposium at Saskatoon, Saskatchewan, Canada, on 5 August 1996.

The chromosome numbers and arm designations are based on the Triticeae system. The utilization of this system for barley chromosomes was recommended at the 1996 Saskatoon meeting.

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59 *"ACeDB is a genome database system originally developed for the* C.elegans *genome project, from which its name was derived (**A C. e**legans **D**ata**B**ase). However, the tools in it have been generalized to be much more flexible and the same software is now used for many different genomic databases from bacteria to fungi to plants to man. It is also increasingly used for databases with non-biological content" (see http://www.cbi.pku.edu.cn/Doc/Databases/AcedbManual/)*

Each gene is associated with a stock number. This BGS-number corresponds to an accession in the Barley Genetic Stock Collection (GSHO, Aberdeen, USA), and contains one of the alleles used for the description. In many cases the stock allele, and sometimes other alleles used for the description, have been backcrossed into near-isogenic lines with the two-rowed Bowman cultivar as common background by Dr Jerome D. Franckowiak, Fargo, USA. The Bowman back-crossed lines can also be found in the Aberdeen collection.

The Barley Genetics Stocks ACeDB Database

Thanks to the BGN coordinators' well formatted descriptions in the Barley Genetics Newsletter (vol. 26 and later issues), it was possible to convert the enormous amount of information into a database system that allows field-based searches, e.g. by gene or allele names.

The BGS database now includes more that 500 genes with descriptions, over 3700 alleles, and over 1700 references. Almost 4000 germplasm objects are referenced (mutant and parents). Many of the germplasm accessions are hyperlinked to Web pages of the holding genebanks (ARS/GRIN/NSGC or NGB) in order to facilitate easy ordering of material containing interesting alleles.

Many of the genes are illustrated with images, both overviews and detailed close-up character photographs. Most of them are taken in Bowman backcrossed derived lines and compared with the normal cultivar. There are more than 900 digitized images in the database.

The database is easy to handle; it starts with Basic and Simple Search, and it is possible to select the object you are looking for. The entered text is searched across the entire database. During the coming year this International Database will get included into the Triticeae Database "GrainGenes" after some remaining problems are solved and the Germplasm part is revised.

The database is available at http://www.untamo.net/bgs.

The aim of this International Database for Barley Genes and Barley Genetic Stocks is to maintain the knowledge and its distribution to the barley community, and it will be updated continuously.

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Wheat

The European Wheat Database (EWDB) – status in June 2003[60]

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Introduction

The data structure of the EWDB was agreed in September 1996 according to the existing IPGRI standards, but only a few months before the appearance of the first version of the FAO/IPGRI *Multi-crop Passport Descriptor List* (MCPDL), which was issued in February 1997. As the previous IPGRI passport standards were known and widely used in the 1990s, the EWDB structure was for the most part compatible with the new MCPDL with only slight differences. The EWDB structure consisted of 36 passport descriptors, of which 19 were included in the later MCPDL; the others were 14 additional wheat database descriptors or 3 descriptors with an internal information value for the database managers. Characterization and evaluation descriptors were included in the set of the 20 most important descriptors, which were developed in discussion with members of the Wheat Working Group (WWG) in 1996 by referring to the revised descriptor list for wheat (IBPGR/CEC 1985) and other known descriptor lists. At the beginning of the EWDB project, passport data were collected to obtain an inventory of the documented accessions in European wheat collections.

Most data were collected during the first two years, amounting to nearly 90 000 records, which represented about 40% of all estimated European wheat accessions. After 1998 the data increase was slower. The first EWDB on-line application was ready in June 1998, just before the official establishment of the Wheat Working Group, and at that time it consisted of 74 000 records. The first ECP/GR WWG meeting took place in November 2001 in Prague, and at this event workplans for the future were developed.

Activities since November 2001

Participants in the first WWG meeting agreed on the basic rules for the further progress of work with the database. A search for unique accessions started, and selection of the first set of characterization data was carried out as the prerequisite for data delivery to the database.

The Web application that was developed resulted from the joint voluntary activities of the WWG members. Altogether 25 national reports were presented during the meeting and this allowed us to proceed with the refining of the estimate of the total number of wheat accessions in Europe. The overall sum of the wheat data consists of information received from 50 contributing institutions representing 35 European countries.

The following plan of activities for the EWDB future was agreed for the next working period:

1. To harmonize the EWDB passport database with the new version of the MCPDL (MCPDLv2, December 2001)[61];
2. To enter all passport data already collected by database managers into the EWDB structure;
3. To deliver missing data ;
4. To supply characterization data to EWDB for the six descriptors agreed upon at the first WWG meeting (awnedness, grain colour, glume colour, glume hairiness, spike density and plant height); so far only data from RICP have been included;
5. To establish links to Web pages with characterization and evaluation data;

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[60] See also updates provided at the Second Meeting of the Working Group on Wheat, September 2005 (this volume, pp. 238-239 and 299-304).

[61] http://www.ipgri.cgiar.org/publications/pdf/124.pdf

6. To enable EWDB downloading from the Web;
7. To continue working on procedures for the inclusion of evaluation data: the list currently includes 20 characterization and evaluation descriptors; scales need to be confirmed for 14 descriptors (nos. 7 to 20), and the list should be extended by adding other important descriptors.

During the relatively short period since the last WWG meeting, many activities concerned with developing the EWDB have been carried out, but some tasks still remain. The following overview reports on recent changes and improvements in the EWDB with regard to the points listed above.

1. New EWDB structure

The new improved version of the MCPDL (MCPDLv2) was issued in December 2001.

Harmonization of the EWDB data structure with the MCPDLv2 took place at the end of 2002 and at the beginning of 2003. It involved updating the passport descriptor list, the database structure, some coding tables and the adjustment of all related data in the main table.

The current database structure consists of 38 passport descriptors, of which 26 are in standardized form, i.e. consistent with the MCPDL; 9 are additional wheat descriptors and 3 are hidden internal data with technical value.

Coding tables for "biological status" and "collecting source" have been changed completely: formats of the geographic coordinates (latitude, longitude) were enlarged to include seconds; all dates were converted to the format [YYYYMMDD]; changes were carried out in the field "other number" (inclusion of information on the institutes). The structure of the table with taxon information was changed – i.e. splitting merged fields "species"/"species author" and "subtaxa"/"subtaxa author". However, the EWDB structure was ready from the beginning to include the new MCPDL fields such as "institution of breeder", "acquisition date", "ancestral data" and "collecting institute" in the basic set of passport descriptors.

The coding table for institutions, FAO INSTCODE, which had been extended with some further wheat institutions in the EWDB, was updated to reflect the current status. This file is downloadable from the EWDB page and it is used in all related fields (DONORCODE, BREDCODE, DUPLSITE, COLLCODE, INSTCODE and part of institution within OTHERNUMB).

The country table was updated according to the current ISO-3166 extended list. As the international code for Romania has been changed recently from ROM to ROU, the new code is not fully compatible with the FAO INSTCODE file, which uses the abbreviation "ROM" for all Romanian institutions. This inconsistency among standards should be solved at the international level by FAO.

The current list of EWDB passport descriptors with indication of the corresponding MCPD is available on the Web at http://genbank.vurv.cz/ewdb/pass_des.htm.

The Web page also includes a link to the official MCPDLv2 (http://genbank.vurv.cz/ewdb/default.htm → information → background).

For easier orientation or searching in the database, the prefixes used in accession numbers (abbreviations for the institutions/data contributors) are provided in a table (http://genbank.vurv.cz/ewdb/ → on-line access → quick overview → contributor). WWG members are requested to provide comments on the usage and correctness of these prefixes.

2. Inclusion of all collected passport data

The current status of records included in the EWDB is shown in Table 1. Data sources include 28 contributors representing 25 European countries. The right hand column shows the numbers of accessions declared in the respective collections according to information available by November 2001.

Table 1. EWDB content (June 2003) and estimated number of wheat accessions (November 2001)

INSTCODE	Contributor	No. of EWDB records	No. of accessions 2001
AUT001	AGB Linz AAHF	1214	1214
AUT005	GB Tyrol, Rinn	222	231
AUT011	IPP Vienna	640	640
AUT025	RSSC Wies	1	*1
BGR001	IPGR Sadovo	10034	10329
BLR011	AFF Zhodino-Minsk	19	*19
CHE001	SFRAC Nyon	4362	8681
CHE071	Schweizer Bergheimat Lucerne	4	4
CYP004	ARI PGRH Nicosia	80	*80
CZE122	RICP Prague-Ruzyne	10259	10886
DEU001	BAZ Braunschweig	8737	11118
DEU146	IPK Gatersleben	16757	17821
ESP004	CRF Alcalá de Henares	2814	2906
FRA051	GEVES Surgères	1949	1949
GBR011	JIC Norwich	9461	9461
GRC035	NAGREF Athens	170	240
HUN003	IA Tápiószele	5461	9869
HUN020	ARI Martonvasar	839	*839
LTU001	LIA Dotnuva Akademija	7	201
LVA010	PGLIB Salaspils	566	*566
NLD037	CGN Wageningen	5315	5475
POL003	IHAR Radzików	10397	*10397
RUS001	VIR St. Petersburg	34808	>44000
SVK001	RIPP Piešťany	2616	3475
SWE002	NGB Alnarp	614	1316
TUR001	AARII Izmir	3046	>5000
YUG002	IFVC Novi Sad	1478	3557
YUG040	ATRC Zajecar	26	*26
Total		**131896**	**160311**

* number of accessions = records included in EWDB, total number of accessions in collections is not known

All the data listed above are included in the EWDB. Table 2 shows the rest of the collected records, which could not be included in the database for various reasons (data incomplete or not readily convertible into the EWDB structure). The further cooperation of data contributors with the database manager will be necessary.

Table 2. Other collected data not converted yet into the EWDB structure

INSTCODE	Contributor	No. of records	No. of accessions 2001
FRA040*	INRA Clermont-Ferrand (*T. durum*)	227	1086
ROM007**	GB Suceava	798	3088
UKR001***	PPI Kharkov	5473	5500
Total		**6498**	**11675**

* accessions not available for distribution
** incomplete data in many records
*** data to be transliterated from Cyrillic (used incompatible DOS coding of Cyrillic)

During the first meeting of the WWG in Prague (2001) all participants received records of the data sets which were thought to list unique accessions within EWDB and their task was to evaluate the correctness of the accession names. This was proposed as the first necessary step for the topic "sharing responsibilities", i.e. to specify the list of unique accessions with the correct names. So far only the Spanish data have been returned with corrections. All other Working Group members are once again asked to send their feedback on this point to the database manager.

An overview of EWDB updates during the period 2002-2003 is given in Table 3.

At present practically all the delivered consistent data are included in the EWDB Web application.

Table 3. EWDB updates since 2001

INSTCODE	Update	New data	
	Passport	Passport (no. of records)	Characterization (no. of record sets)
AUT001, AUT005, AUT011, AUT025	corrected accession names	2077	5494
BLR011		19	
CZE122		838*	
DEU001		8737	
ESP004			
GBR011		9461	
HUN020		839	
NLD037		192*	
YUG002,YUG040		1504	
Total		**23667**	**5494**

* data increase since 2001

3. Delivery of missing data

Information from 11 countries has not been delivered yet. Possible reasons may be inadequate data computerization, or an insufficient level of standardization.

For the wheat collections of Ireland, Malta and Moldova neither the collection inventory nor the estimates of accession numbers are available.

Table 4 shows the estimated number of accessions held in non-contributing institutions.

Table 4. Estimated numbers of accessions to be included into EWDB

INSTCODE	Institute	Estimated no. of accessions (1996-2001)
ALB002	ARI Lushnje	9650
BEL001	SAP Gembloux	367
EST001	JPBI Jõgeva	30
HRV015	IPBPP Zagreb	2000
HRV021	AIOS Osijek	1600
HRV045	AF University Zagreb	990
IRL017	DAFF Leixlip	?
ISR002	IGB Volcani Center	4000
ISR005	WIS, Rehovot	2000
ISR004	IE, Haifa University	1000
ISR003	LGB, Tel Aviv University	5000
ITA004	IDG Bari	28000
PRT004	ENMP Elvas	3992
MDA004	IGAS Chisinau	?
MKD001	AU Skopje	465
MLT	Malta	?
YUG009	SGI Kragujevac	1291
YUG	Other institutions	1965
Total		**62345**

Slovenia does not have any PGR wheat collection.

Taking into account the total estimated number of wheat accessions in Europe (Table 5), the proportion of accessions not yet included is relatively high (40.9%). This is caused by the absence of some large data sets of important countries such as Italy and Israel and also perhaps by substantial differences between the estimated and actually available data.

Table 5. Total number of wheat accessions in Europe

EWDB status	No. of accessions/records
Records included	131896
Other collected records	6498
Not included yet	95937
Total	**234331**

The current Web application consists of 131 896 records, which represents about 59.1% of all estimated accessions in Europe. Documentation of 75-80% of all wheat data in EWDB will be considered a very satisfactory result and it is hoped that it will be achieved relatively soon by including the two large collections from Italy and Israel.

4. Inclusion of characterization data

Since the beginning of 2003 the first set of 5494 characterization data, according to the six recommended descriptors (see below) has been included in the EWDB Web page. Up till now, only the data from RICP-Prague have been included. The downloadable set of characterization data from CGN has been tested. These data need to be transformed with the assistance of the collection holder before they can be included in the EWDB, since the data are not fully compatible with the EWDB structure and there are some other problems which require discussion. Other sets of characterization data from former Yugoslavia, Switzerland and Belarus were received, but they are also rather difficult to interpret in some cases.

The characterization data to be presented for descriptors 1 to 6 (1 = awnedness, 2 = grain colour, 3 = glume colour, 4 = glume hairiness, 5 = spike density, 6 = plant height), listed in detail including for scoring on the Web at http://genbank.vurv.cz/ewdb/eval_des.htm or as published in the report of the first meeting of the WWG (p. 134 *in* Maggioni *et al.* 2003) should have the following structure:

Accession number (unique identifier)

Descriptor number

Scoring value

Comment – information on the environment of the scoring (number of experiments, experimental years, conditions).

One data set is expected per accession. To be acceptable, the score should be the mean value from at least three-year experiments.

Browsing of characterization data is enabled by the new advanced search form, where specific criteria can be selected for all descriptors.

5. Established links to Web pages with characterization/evaluation data

The current links on the EWDB Web page are the usual links to important world wheat database Web pages, but individual links at the accession level have not been established yet. Present links were updated recently according to the current URLs of the pages in question.

6. Data download

A script for data extraction from the EWDB into MCPDL format and file zipping has been developed and off-line EWDB data download has been enabled since June 2003 at http://genbank.vurv.cz/ewdb/off_line.htm. Besides the set of standard fields, two non-standard descriptors important for the wheat database can also be found: "EWDB identification number" and "growth class or seasonality". The resulting downloaded file is an ASCII text file, tab-delimited in zip format and its present size is 2.78 MB. All data are available to contributors for verification and validation. Working Group members are requested to load the data and improve their quality by sending feedback to the database manager, who is ready to assist to WG members in case of any problems during data download.

The EWDB Web page also offers downloading of the institution codes used, i.e. FAO INSTCODE enlarged by the EWDB specific codes using non-standard institutions (not included in the FAO list) in the form of a zipped .dbf file at http://genbank.vurv.cz/ewdb/address.zip.

7. Improving procedures for the inclusion of evaluation data

The set of evaluation data should be selected from the existing list of 20 characterization and evaluation descriptors (http://genbank.vurv.cz/ewdb/asp/eval_des.htm). As soon as the list of descriptors and their scoring scales has been validated by the WWG and willingness of participants to supply these data has been confirmed, the database will be ready to include evaluation data. This category of information is the one most wanted by users and will be of crucial value for the future of the EWDB.

Improving the EWDB search possibilities

The advanced search implemented into EWDB in June 2003 enables combined searches on 20 passport descriptors and 6 characterization descriptors. This enlarged searching feature provides greater possibilities for browsing through data according to particular aspects of interest.

Other activities

- **Global Inventory of Wheat Genetic Resources**

The EWDB has been invited to participate in the Global Inventory of Wheat Genetic Resources (GIWGR) developed at the initiative of CIMMYT (Centro Internacional de Mejoramiento de Maíz y Trigo = International Wheat and Maize Improvement Centre, Mexico).

The International Wheat Genetic Resources Network (IWGRN) is conducting a pilot project in cooperation with CGIAR's System-wide Information Network for Genetic Resources (SINGER) under the umbrella of the International Plant Genetic Resources Institute (IPGRI) to develop a Global Inventory of Wheat Genetic Resources. The IWGRN is a network established in 1993 under the auspices of the International Wheat Genetics Symposium. The role of the IWGRN is to coordinate the gathering and collation of primary passport information for wheat (and related species) from national, regional and international organizations holding substantial collections.

A primary objective of the project is to establish collaboration among partners within the wheat information network for the compilation and exchange of standardized passport data that can be linked to SINGER. The structure of MCPDLv2 has been used as the standard.

As well as CIMMYT, AWCC (Australian Winter Cereals Collection) and IPGRI, ICARDA (International Center for Agricultural Research in Dry Areas, Aleppo, Syria) also participates in the GIWGR.

EWDB data were delivered to GIWGR in April 2003 to the CIMMYT address, but there has been no further news about the current GIWGR status since then.

- **EWDB and EURISCO**

The Web application of EURISCO (European Plant Genetic Resources Search Catalogue of passport data on *ex situ* collections maintained in Europe, developed by IPGRI as a result of the EU project EPGRIS), was officially launched in September 2003 (http://eurisco.ecpgr.org/). The development of EURISCO will have a considerable impact on all central crop databases (CCDBs). Up to now, the main objective of the EWDB and other CCDBs has been to complete the inventory of all single-crop collections in Europe. This task will be overtaken by EURISCO, which will contain passport information in extended MCPDL format (EURISCO descriptors).[62] This part of the information will be regularly updated by EURISCO National Focal Points for all crops in national PGR collections and thus the problems of updates or of missing data may be solved. The CCDBs will be able to download their basic passport data directly from the EURISCO application.

The CCDB contributors or managers will be challenged to intensify their efforts to include characterization and evaluation data and to include as much crop-specific information as possible. Stand-alone crop databases without characterization and evaluation data will eventually be useless, because most passport information in updated standardized format will become available from EURISCO.

- **Suggestions for the future of the EWDB**

- To continue the uncompleted tasks formulated by the first WWG meeting: it is expected that missing passport data will be provided via downloads from EURISCO;
- To improve data quality, through coordination between wheat collection curators and WWG members;
- To deliver characterization and evaluation data into the existing EWDB structure;
- To include further characterization/evaluation data including scoring scales;
- To participate in the GIWGR;
- To rationalize collections using the results of EWDB data analysis;
- To develop the role of core collections, by sharing responsibilities.

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[62] Available at http://www.ecpgr.cgiar.org/epgris/Tech_papers/EURISCO_Descriptors.doc

Wheat collections in Austria

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In 2002 the former Federal Office of Agrobiology became part of the Austrian Agency for Health and Food Safety and was renamed "Austrian Agency of Health and Food Safety – AGES Linz". The new agency is a merger of 19 Austrian institutes dealing with human health care, food analysis and agriculture. Responsibility for it belongs to the Ministry of Health and to the Ministry of Agriculture, Environment and Water Management. The reason for the establishment of this agency was to encourage synergy and to reduce costs for the government.

Following this philosophy the genetic resources collection of the institute in Vienna was concentrated at AGES-Linz, since the Austrian collections are quite small.

In Austria there are three wheat collections, maintained by the following institutions:

- AGES Linz
- Genebank Tyrol
- Arche Noah Association.

The collections are well documented, at least as far as the state genebanks are concerned.

The *Index Seminum Austriae/National Inventory* is the survey of plant genetic resources collections in Austria. It follows the FAO/IPGRI *Multi-crop Passport Descriptor* (MCPD) format; it is available on-line on the Internet and has been searchable since 1998 (www.genbank.at/inventory/index.html).

Regarding the distribution of winter wheat and spring wheat in the country, it is clear that in the alpine regions, with long hard winters, and snow cover lasting for more than four months, spring wheat is the more important. Owing to the poor conditions for grain crop growing, agriculture in these areas in the last decades has evolved towards pastures and milk production.

The situation is quite different in the lower parts of Austria, the Pre-Alpine and Pannonical regions, where the grain production level is higher. In these regions snow is not such a problem as it does not cover the arable land for more than a few weeks, and most wheat crops are of winter wheat.

The list of wheat accessions held in the Austrian collections shows that 30% of the accessions are landraces of Austrian origin, while 53% are cultivars, some of which date back to the 1920s (Table 1).

Table 1. Wheat accessions in the Austrian collections by type of sample

Type of sample	No. of accessions	%
Wild	21	1
Weedy	0	0
Landraces	505	30
Breeders' material	258	15
Cultivars	909	53
Unknown	22	1

Most of our wheat accessions originate from Austria or from the neighbouring countries. There are only a few accessions from Africa or Asia.

Except for a few accessions of *Triticum monococcum*, *T. dicoccum*, *T. turgidum* and *T. urartu* which were received from IPK-Gatersleben, the Austrian genebanks maintain only accessions of *Triticum aestivum*.

Sixty-four percent of the wheat collections have been characterized and evaluated. Evaluation is done only on 1000-seed weight, hectolitre weight and protein content.

Characterization follows the recommended descriptors (IBPGR/CEC 1985). All data of the characterized and evaluated accessions are available locally in an Access Database.

The passport data of the available wheat collections were sent to Iva Faberová (RICP Prague) in autumn 2002 and will be updated after screening the recently adopted collections of the Vienna institute, now maintained in Linz (screening to take place in spring 2005).

Characterization data, as far as available, will also be added to the passport data at the same time.

Once all the data of the European collections have been included in the European Wheat Database (EWDB), it will become an important tool for the sustainable use of the European wheat collections.

Reference

IBPGR/CEC. 1985. Revised descriptor list for wheat (*Triticum* spp.). International Board for Plant Genetic Resources, Rome, Italy.

Status of the durum wheat collection in Sadovo, Bulgaria[63]

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Durum wheat is an ancient and traditional crop in Bulgaria. Malkov (1906) made the first botanical studies on wheat accessions found in Bulgaria. The local accessions of durum wheat represent populations of different subspecies.

The base collection is located in the Institute for Plant Genetic Resources (IPGR) in Sadovo. There are other small collections (mostly breeders' lines) in the Institute for Cotton and Durum Wheat in Tchirpan and in the Institute for Wheat and Sunflower in Dobritch.

The total number of accessions in IPGR-Sadovo is 2146. Table 1 shows the origins of the accessions. Among the 1529 accessions for which the origin is identified, 1034 are local. The remaining 617 accessions are of unknown origin (Popova 2001).

Table 1. Origin of the durum wheat accessions maintained by IPGR–Sadovo

Donor country	No. of accessions
USSR	84
USA	46
Turkey	45
Italy	43
Spain	31
Romania	25
Greece	23
France	77
Portugal	20
Mexico	12
Bulgaria	12
Other countries	77
Local accessions	1034
Unknown	617
Total	**2146**

The local accessions of durum wheat have been collected during expeditions in various regions in Bulgaria (Krasteva *et al.* 2003) (Fig. 1).

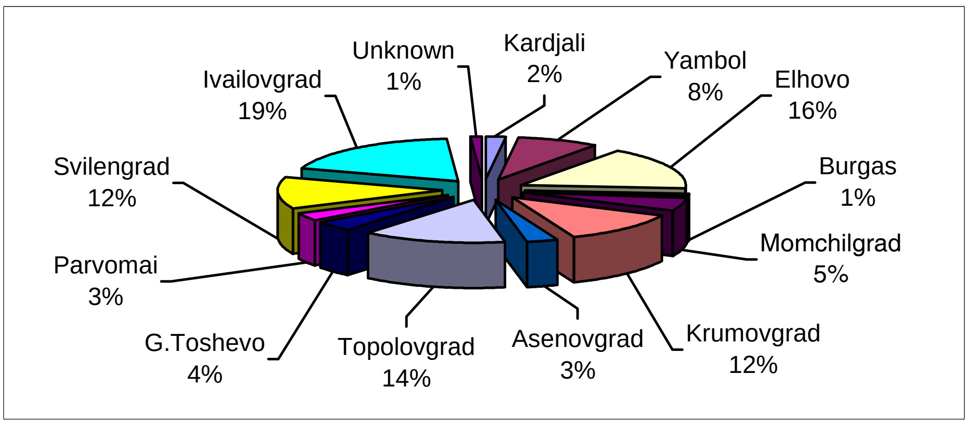

Fig. 1. Distribution of the durum wheat accessions collected in Bulgaria.

[63] See also "Status of the wheat collection in Bulgaria", pp. 252-253.

Most local accessions have been collected in southeastern Bulgaria from the localities of Ivaylovgrad (19%), Elhovo (16%), Topolovgrad (14%), Krumovgrad (12%), etc. Fewer were obtained from northern Bulgaria.

Along with *Triticum durum* Desf. our collection also includes other *Triticum, Aegilops* and triticale species. Their status is shown in Table 2.

Computerized data are available for 1604 accessions.

Table 2. Status of wheat collections in Bulgaria

Species	**No. of accessions**			
	Long-term storage	**Medium-term storage**	**Total**	**Evaluated**
Triticum durum Desf.	1919	227	2146	1859
Triticum spp.	559	184	743	406
Aegilops spp.	307	511	818	303
Triticale	738	15	753	165
Total	**3523**	**937**	**4460**	**2733**

Exchange

The following were sent to different institutes in the country: 27 accessions of durum wheat, 33 of *Aegilops* and 1 of *Triticum*.

IPGR maintains close contacts with the Institute for Cotton and Durum Wheat in Tchirpan who obtain initial material for breeding work from our collections.

References

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Popova, Z. 2001. [Biological and economic traits of introduced durum wheat cultivars. Plant Science (Sofia)] XXXVIII (7-10):313-316. (in Bulgarian).

Preservation and utilization of cereal genetic resources in Estonia [64]

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National Programme for preservation of plant genetic resources for agriculture

The Committee on Plant Genetic Resources for Agriculture coordinates the activities of all institutions involved in the collection and preservation of plant genetic resources for agriculture, merging them into the Estonian national network. Therefore the Committee has prepared and put forward the draft of a National Programme on the preservation and collection of plant genetic resources for agriculture. The government of Estonia approved the National Programme and allocated finances for the activities in 2002.

In accordance with the programme, the Committee is responsible for the development of conservation strategies, development and implementation of the National Programme.

In the plan of action for the period 2002-2006 the following priorities are defined:

- integration of all institutions into the national network for the preservation of plant genetic resources for agriculture;
- finalization of the national survey and inventory of existing collections of cereal crops, potatoes, forage grasses and legumes, vegetables, fruit crops, medicinal and aromatic plants;
- facilitation of the further collection, identification, evaluation and documentation of accessions;
- identification of natural areas with high plant diversity for *on-farm* management conservation;
- organization of collecting expeditions to the natural areas rich in alfalfa, *Koeleria gracilis* and other local forms or landraces;
- continuation of cooperation with the N.I. Vavilov Research Institute of Plant Industry (VIR, St. Petersburg, Russian Federation), the Nordic Gene Bank and the genebanks of other Baltic countries;
- promotion of the integration and collaboration of all relevant institutions of Estonia at international level;
- assurance of safety-duplication of accessions of Estonian origin;
- relevant activities necessary for raising public awareness;
- additional activities for improvement of the legislation to safeguard the preservation of plant genetic resources for agriculture.

Preservation of cereal crops in Estonia

The following institutions are involved in the preservation of cereal genetic resources in the framework of the National Programme:

- the genebank of the Jõgeva Plant Breeding Institute, and
- the Institute of Experimental Biology of the Estonian Agricultural University.

- **Jõgeva Plant Breeding Institute**

The genebank of the Jõgeva Plant Breeding Institute preserves the following species of cereals: spring barley, spring and winter wheat, oats and winter rye.

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[64] See also "The Estonian wheat collection", pp. 256-257.

The Institute is dedicated to collect, preserve and evaluate:

1. accessions of Estonian origin;
2. advanced breeding lines of Estonian origin;
3. accessions of foreign origin adapted to local ecoclimatic conditions.

The genebank of the Jõgeva PBI was established recently and found that little old or historic material was available in Estonia. The first task of the genebank was to collect and repatriate as many accessions of Estonian origin as possible. Therefore the genebank applied to VIR, where plant genetic resources of Estonian origin used to be maintained. In response to these requests, the genebank of the Jõgeva PBI received 8 oat, 1 spring wheat and 2 barley varieties from VIR. None of these varieties appeared to be present in the collection of the Jõgeva genebank.

All accessions as well the plant genetic material of Estonian origin which has been repatriated from different holders of plant genetic resources has been identified according to the recommendations of van Hintum and Knüppfer (1995).

Beside the *ex situ* collection, a large number of breeding lines are maintained by breeders in working collections. The number of accessions of these collections varies periodically, but nearly 8500 accessions are rejuvenated annually by breeders.

To secure *ex situ* material of Estonian origin, the Nordic Gene Bank and the Jõgeva PBI have signed an agreement concerning "black box" arrangements whereby the NGB agrees to maintain safety-duplicates of the most valuable genotypes (Weibull 1999).

Characterization of collections

The genebank is equipped with the appropriate technical facilities to ensure long-term conservation. The seed processing laboratory, drying and storage facilities of the genebank comply with internationally recognized standards.

Barley collection

The *ex situ* spring barley collection is represented by 115 accessions. Advanced cultivars constitute 81% of the collection and breeders' material, 19%. Barley accessions originate from 16 countries, mainly from Russia, Germany and Estonia. The breeders' collection of the Jõgeva Plant Breeding Institute contains 3900 spring barley accessions

Oat collection

The *ex situ* oat collection consists of 130 accessions - 95% advanced cultivars and 5% breeders' material. The collection includes accessions from 18 countries, mostly of Estonian and Russian origin. There are 2020 accessions in the breeders' field collection.

Rye collection

The long-term rye collection consists of 98 accessions: 64% breeding lines and 26% varieties. Most of the breeding lines originate from Estonia.

Wheat collection

The wheat collection consists of 196 *ex situ* accessions (67% spring wheat and 33% winter wheat). Advanced cultivars represent 60% and breeders' material 40% of the collection. Wheat accessions originate from 17 countries, mostly from Estonia, Finland or Germany.

The breeders' field collection consists of 1730 spring wheat and 650 winter wheat accessions.

- **Institute of Experimental Biology of the Estonian Agricultural University**

The Institute participates in the national programme on pre-breeding and immunogenetic, cytogenetic and biochemical research on cereal genetic resources. Particular breeding lines, especially introgressive wheat lines which are of interest to plant breeders, will be further investigated, utilized and maintained by the Jõgeva PBI.

The Institute holds a collection of 50 hybrid wheat lines, which were created by crosses between bread wheat cultivars and wild relatives of wheat used as donors of disease resistance (*Triticum timopheevii*, *T. militinae*, *T. dicoccum* and *Aegilops speltoides).* Methods of monosomic aneuploid analysis and molecular genetics techniques were used for localization and identification of the powdery mildew genes in the introgressive wheat lines. Chromosomes involved in reciprocal translocations were revealed and identified by the cytogenetic analysis of meiosis. Evaluation, description, characterization, documentation and preservation of the 10 most valuable wheat lines were initiated in 2002. The lines created are maintained by the Jõgeva PBI genebank to ensure long-term preservation.

The Institute of Experimental Biology holds a collection of diploid and tetraploid wheat accessions provided by VIR (Peusha *et al.*1995) (see Table 1).

Table 1. Diploid and tetraploid wheat accessions provided by VIR to the Institute of Experimental Biology

Species (ploidy)	No. of accessions
T. monococcum (2n =14, A^b)	5
T. dicoccoides (2n=28, A^uB)	1
T. dicoccum (2n=28, A^uB)	1
T. durum (2n=28, A^uB)	2
T. persicum (2n=28, A^uB)	3
T. timopheevii (2n=28, A^bG)	1
T. militinae (2n=28, A^bG)	1

These accessions are used in wheat breeding for the improvement of disease resistance and protein content (Järve *et al.* 2002).

The collection also includes a set of 21 monosomic aneuploid lines of 'Chinese Spring', which have been used as the recipient tester variety for genetic analysis of common wheat varieties, the sets of near-isogenic lines 'Chancellor' and 'Thatcher' with known genes of resistance to powdery mildew (*Erysiphe graminis* f. sp. *tritici*) and leaf rust (*Puccinia recondita* f. sp. *tritici*), respectively, and the mutant *ph 1b* evidently deficient for the pairing suppressor *Ph1,* "pairing homologous" locus (Enno *et al.* 2002).

Documentation

A database management system is essential for the documentation of accessions and is aimed at increasing the accessibility and usefulness of the collections.

In the database all accessions of Estonian origin will be fully evaluated and characterized; all relevant information is available, though accessions of foreign origin are so far only partially evaluated. Further development of the electronic database, searchable on-line, is foreseen in the framework of the EPGRIS project. The database will be developed in cooperation with the Nordic Gene Bank.

The characterization and evaluation data are obtained by breeders from field experiments. Data are electronically available, though common databases are still under development.

Conclusions

The expected outcomes of the implementation of the national programme on the preservation of cereal crops are:

- assured preservation of plant genetic resources of cereals;
- continuation of collection, preservation, identification, characterization, evaluation and documentation of accessions;
- completion of inventories of existing national *ex situ* and *in situ* collections, including the gathering of passport data;
- assessment of the efficiency of national strategies for the protection of biodiversity;
- identification of the components of biodiversity;
- facilitation of sustainable use of plant genetic resources; and
- extension of national and international cooperation for the exchange of genetic material.

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Aegilops sharonensis: ***a wild relative of wheat endemic to Israel***

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Breeders and geneticists show a growing interest in wild wheats and their close relatives as sources of useful genes for the improvement of cultivated wheats. In parallel with the impoverishment of the primary gene reservoir which exists in the bread and durum wheats grown today, there is also an accumulation of knowledge about the breeding potential inherent in the wild species, based on modern studies.

In addition to providing resources for the improvement of the existing well-studied wheat characters, the genepools of related wild species may also contribute novel traits to this important crop and, as a result, increase its potential economic value.

Eleven species of the genus *Aegilops* grow in Israel. Five are diploid (2n=14), five tetraploid (2n=28), and one species is hexaploid (2n=42). All of the diploid species are members of the section Sitopsis, which is considered the most primitive in the genus. Their genomes are very close to the B genome of the polyploid wheats. This closeness is apparent from the relative ease with which these diploid species can be crossed with the polyploid cultivated wheats. First generation Sitopsis x polyploid-wheat hybrids are sterile; but recurrent backcrosses to their cultivated parents can result in partially fertile progeny. In this way, genes from the Sitopsis genomes can be integrated into the B genome (and also into other genomes) of cultivated wheats. This possibility of gene transfer by conventional methods endows the native diploid *Aegilops* species with a special value as a plant genetic resource.

It is noteworthy that each of the five Sitopsis species has specific ecological requirements. As a result, each species has a limited distribution in a well-defined habitat.

The present paper focuses on one of the Sitopsis species, *Aegilops sharonensis*. This autogamous species is endemic to Israel, with some unproven outposts in southern Lebanon. It is distributed on the sandy soils and stabilized dunes along the Mediterranean seashore. The 150 km stretch of the Israeli seashore is the most densely populated part of Israel. Large-scale urbanization and road-building activities have led to the destruction of many populations of *Ae. sharonensis* (Fig. 1).

Fig. 1. This dense population of *Aegilops sharonensis* has a very doubtful future. It is overshadowed by the chimneys of an electricity power station (Hadera, Israel).

While there is at present no danger of eradication of the species, there is an ongoing loss of genotypes and a very immediate danger to its genetic diversity. Because of the very intensive urbanization and the enormous cost of land in the area, the establishment of *in situ* conservation enclaves for this species, in which populations would be preserved and studied, is not feasible. Instead, the Institute for Cereal Crops Improvement (ICCI) decided on a three-year programme (2003-2005) of *ex situ* conservation.

So far seed collections have been made in 25 populations. In each population, single-plant samples (one spike per sample) were taken along a linear transect. About a thousand collected accessions are stored in the Lieberman Genebank located at the ICCI.

At present each accession is being evaluated with regard to resistance factors to foliar diseases. This study centres on the three wheat rusts and wheat powdery mildew. In many of the accessions we have found resistance to wheat leaf rust, wheat stripe rust and to powdery mildew.

Genetic variation is measured by testing the collections with AFLP markers.

Wheat germplasm collections in the Bari Genebank, Italy

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Introduction

Since 1970, year of its foundation, the former Germplasm Institute of Bari, now part of the Istituto di Genetica Vegetale (IGV), has stored more than 84 000 samples belonging to more than 40 genera and nearly 600 species. Cereals are represented by more than 38 000 accessions, including more than 32 000 accessions of cultivated and wild wheat (Table 1). Out of the total number of samples stored in Bari, more than 13 000 have been acquired through collecting activities in several countries. These include more than 2000 wheat samples (Table 2). Bari is one of the four centres responsible for the conservation of the world wheat collections, together with those in St. Petersburg, Kyoto and Beltsville. Kyoto specializes in wild wheat relatives, while the other two centres store a certain number of duplicated accessions which are also present in the Bari collection.

Table 1. *Ex situ* cereal germplasm collections at the Bari Genebank

Genus	No. of species	No. of samples
Triticum	27	32464
Hordeum	4	1997
Aegilops	31	1599
Zea	2	1356
Secale	12	398
Avena	2	289
Oryza	4	42
Total	**82**	**38145**

Table 2. Number of samples collected since 1971 by the Bari Genebank

Crop	Total
Wheat	2340
Barley	1066
Maize	627
Other cereals	2093
Pea	266
Broad bean	669
French bean	638
Other legumes	1896
Other species	3761
Total	**13356**

Structure and composition of the wheat collection

Most of the Bari wheat collection is represented by populations (samples of different species of *Triticum*: *T. turgidum*, *T. durum*, *T. aestivum*, etc.), which are still just as they were when collected (Table 3). The material collected in the Mediterranean region (Albania, Algeria, Cyprus, Egypt, Greece, Italy, Libya, Morocco, Portugal, Spain, Tunisia) and in Africa (Somalia and Ethiopia) includes 2340 populations of hard wheat, spring wheat and even of other genera, such as *Hordeum*. At least 1158 accessions out of the total number of accessions are nearly pure hard wheat and 1540 are represented by ancient varieties. With respect to those collected in Italy, farmers could provide variety names for only about 150 wheat samples. Details of the names of old varieties and lines of durum wheat are shown in Table 4.

Table 3. Wheat world collection stored in the Bari Genebank

Species, variety, progenies	No. of accessions	No. of countries of origin
Triticum turgidum, durum, aestivum	11736	66
Triticum aestivum	8418	67
Triticum turgidum var. *durum*	5659	58
Triticum dicoccum	371	18
Triticum spelta	310	12
Triticum turgidum var. *turgidum*	237	17
Triticum dicoccoides	173	8
Triticum urartu	139	5
Triticum timopheevii	36	4
Triticum polonicum	24	4
Triticum turgidum, durum	17	1
Triticum persicum	17	2
Triticum sphaerococcum	12	5
Triticum monococcum	7	6
Triticum boeoticum	7	2
Triticum compactum	6	1
Triticum aegilopoides	6	2
Triticum aethiopicum	5	2
Triticum carthlicum	5	2
Triticum araraticum	3	2
Triticum fungicidum	3	2
Triticum macha	3	2
Triticum orientale	3	2
Triticum paleocolchicum	3	2
Triticum vavilovii	3	2
Triticum turanicum	2	1
Triticum turgidum, dicoccum	1	1
Triticum turgidum, compactum	1	1
Triticum militinae	1	1
Triticum timonorum	1	1
Triticum urartu, boeoticum	1	1
Triticum zhukovskyi	1	1
Triticum spp. (varieties and lines of breeders)	3000	different breeders
Triticum turgidum, durum, aestivum (progeny)	11856	active collections
Total	**42067**	

Table 4. Durum wheat varieties held at the Bari Genebank

	Variety name	No. of accessions	Collecting year			MG No. of identification* (= Accession number)		
1	APPULO	3	71	76	77	3721	18276	18340
2	B 132	1	72			5887		
3	B 132 CASTELPORZIANO	1	71			2092		
4	B 144 CASTELNUOVO	2	71	72		5888	2093	
5	B 52	1	77			18341		
6	BIDI	2	71	75		719	17880	
7	C 48 CASTELFUSANO	1	71			2094		
8	CAPEITI	3	71	76	80	3244	18430	27777
9	CAPEITI (LIGURESI)	1	77			22440		
10	CAPEITI 8	1	71			3723		
11	CAPEITI ALTO	1	71			3725		
12	CAPEITI BASSO	1	71			3707		
13	CAPINERA	1	71			3720		
14	CAPPELLI	3	71	77	78	3177	18342	26542
15	CASTEL DEL MONTE	1	71			3712		
16	CASTEL FUSANO	2	72	71		6326	7244	
17	CASTEL PORZIANO	3	71	72	71	3713	6327	7245
18	CASTIGLIONE GLABRO	1	71			731		
19	CASTIGLIONE PUBESCENTE	1	71			735		
20	CRATONE	1	71			732		
21	DAUNO III	1	71			1539		
22	DAUNO STRAMPELLI	1	78			26541		
23	DORO	1	76			18321		
24	DRAGO	2	76	78		18312	26662	
25	DURO CONTI	1	71			3718		
26	DURO LUCANO	1	77			18322		
27	DURO SG 3	1	71			3175		
28	FARRO LUNGO	2	71	71		726	3185	

* MG = Mediterranean Germplasm

Table 4 (cont.). Durum wheat varieties held at the Bari Genebank

Variety name	No. of accessions	Collecting year				MG No. of identification* (= Accession number)			
29 FRANCESONE	1	71				716			
30 GARIGLIANO	3	71	71	78		2711	3714	26543	
31 GERARDO 512 X C. DEL MONTE	1	76				18277			
32 GERARDO 525	1	81				28442			
33 GIGANTE	1	71				717			
34 GIORGIO 331	1	72				4505			
35 GIRGENTENA	1	71				720			
36 GRANATO	1	77				18343			
37 GRANO BIANCO	1	71				3715			
38 GRIFONI	2	71	71			1993	3710	1993	
39 IANCULEDDA	1	71				3704			
40 ICHNUSA	3	71	77	78		3711	18325	26663	
41 INGLESA	2	71	75			721	17874		
42 ISA 1	1	71				3727			
43 ITALIANO RIJO	1	78				26544			
44 MALIANI 11C AWNED	1	72				5978			
45 MALIANI 12D	1	72				5979			
46 MALIANI 16A S 1	1	72				5980			
47 MALIANI 1D	1	72				5973			
48 MALIANI 4B	1	72				5974			
49 MALIANI 5B S 10	1	72				5975			
50 MALIANI 7D	1	72				5976			
51 MALIANI 8D	1	72				5977			
52 MARISTELLA	3	71	77	78		3716	18326	26664	
53 MARTINELLA	1	71				728			
54 MARZUOLO	1	78				26546			
55 MISTO DI DURI A GL. BIANCHE	1	71				3700			
56 MISTO DI DURI A GL. ROSSE	1	71				3724			
57 NARUGUS	2	77	78			18327	26665		
58 OTTAVA	1	77				18328			
59 PATRIZIO	1	76				18303			
60 PATRIZIO 6	1	71				3722			
61 PAVONE	1	71				3178			
62 QUORAM	1	71				2735			
63 RAZZA 181	1	71				1541			
64 RAZZA 208	1	71				2743			
65 REGINA	2	71	75			3183	17881		
66 RICCO	1	71				3726			
67 RINGO	1	76				18290			
68 ROMA	2	71	78			8396	26547		
69 ROSSETTA	1	71				3719			
70 ROSSIA	1	71				3706			
71 RUSCIA	2	71	71			733	3184		
72 RUSSELLO	2	71	78			730	26671		
73 RUSSELLO SG	1	71				3176			
74 S.A.S. 449	1	76				18286			
75 SABAUDIA	2	71	71			709	2723		
76 SARAGOLLA	2	71	71			1950	2156		
77 SAS 38	1	71				3709			
78 SAS 449 DION	1	71				3708			
79 SAS 449 IST	1	71				3701			
80 SCAVUZZA	1	71				723			
81 SCORZONERA	3	71	71	75		736	3182	17875	
82 SEMBEL 2	1	72				6017			
83 SEMENZELLA	1	71				729			
84 SENATORE CAPPELLI	3	71	71	78		710	3703	26548	
85 SINCAPE 9	4	71	77	77	78	3705	18344	18347	26672
86 SORENTINO	1	78				26549			
87 TIMILIA	1	71				3179			
88 TIMILIA SC 1	1	71				1947			
89 TRENTINO	1	71				722			
90 TRIPOLINA	1	71				718			
91 TUNISINA	1	71				724			
92 URRIA	1	71				725			
93 VAL GERARDO	1	81				28443			
94 VALLELUNGA GLABRA	1	71				734			
95 VALNOVA	1	81				28444			
96 VALSACCO	1	77				18345			
97 VALSELVA	2	76	77			18275	18346		

* MG = Mediterranean Germplasm

Distribution and exchange

More than 52 000 wheat samples (populations, single species, varieties, lines and progenies) have been distributed to breeders, researchers, research centres, farmers, etc. of different countries (Table 5). Most of the samples from Bari have been distributed to Europe and Asia, many fewer to North and South America and even fewer to Africa, Australia and New Zealand. This is explained by the fact that wheat samples from Bari have reached Africa, Australia and New Zealand through international organizations (e.g. ICARDA) and other genebanks (e.g. USDA, etc.) Requests for germplasm can be made via email (pietro.perrino@igv.cnr.it) and/or by consulting the genebank database Web site (http://www.igv.cnr.it/bis/bancadati.html). Only small amounts of seeds are available and the requesters have to provide information according to an internal protocol, established on the basis of international agreements.

Table 5. Wheat germplasm distributed by the Bari Genebank throughout the world

Country	No. of accessions distributed
Europe	28672
Asia	17042
North America	4515
South America	1547
Africa	667
Australia and New Zealand	313
Total	**52756**

Multiplication

The wheat germplasm collection has been multiplied several times for different reasons: (i) to increase the size of the collected seed samples, which were often very small; (ii) to duplicate seed samples to the other three centres responsible for the world collection (St. Petersburg, Beltsville and Kyoto); (iii) to meet long-term conservation needs; (iv) to meet breeders' and researchers' requests; and (v) to increase seed viability in cases of fast ageing resulting from adverse weather conditions during growth and ripening (seedborne diseases) or electric power cuts during conservation, etc. Since 1970, the wheat germplasm collection (like all the other Bari collections) has been multiplied from 3 to 5 times to meet the needs mentioned above (Table 6).

Table 6. Germplasm introduced, multiplied, prepared, distributed and studied at the Bari Genebank

Period	Germplasm (no. of samples)				Publications (no. of items)
	Introduced	Multiplied	Prepared for multiplication, conservation and distribution	Distributed	Journals, proceedings, posters, JCR, non-JCR, reports, etc.
1970-1980	38500	119234	189107	31373	101
1981-1990	28919	87040	150779	34820	353
1991-2000	17305	37588	72288	17395	534
Total	**84724**	**243862**	**412174**	**83588**	**988**

Characterization

Most of the collections are identified by passport data. The status of the *Triticum*, *Hordeum* and *Avena* databases is given in Table 7. As far as *Triticum* is concerned, characterization and evaluation have taken place according to specific projects in collaboration with ICARDA and other public and private institutions. Some of this genetic material is ready for distribution and some is still in the process of characterization and is being studied by the researchers of the Bari Genebank (Table 8).

Table 7. Documentation status of cereal databases at the Bari Genebank

Genus	No. of stored accessions	
	Passport data	Characterization data
Triticum	30000	10000
Hordeum	2000	
Avena	300	

Table 8. Databases on selected cereal collections stored at the Bari Genebank

Taxon	Type of descriptors and/or information recorded	Approximate no. of accessions
Triticum	Mediterranean and Ethiopian, biotic stresses*	200
Triticum	selected lines, storage protein quality profiles*	300
Triticum dicoccon	plant, physiology, protein quality*	300
Triticum spelta	plant, physiology, protein quality*	300
Triticum	addition lines	50
Triticum	C and BC lines with wild relatives	100
Dasypyrum	chromosome and DNA description	10

* Characterization carried out within the framework of special projects and with additional and/or external financial contribution from national (Italian Farmers Associations, Basilicata region, CNR-TP (Targeted Projects)) and international organizations (IBPGR/IPGRI, ICARDA, IITA, EU Structural Funds).

Conservation conditions

The whole wheat germplasm collection, including base, active and working collections, is maintained under either short-, medium- or long-term storage conditions, i.e. at 5°C, 0°C and –20°C respectively. In all cases, after seed dehydration down to around 6% moisture, for short- and medium-term needs, seed samples are stored under vacuum in aluminium foil containers and with around 35% RH of air in the storage room, while for long-term needs, seed samples, once properly dried, are stored in aluminium cans, with no control of the air RH.

Discussion

In the last 5-10 years, because of various factors (mainly limited funding), the collecting, multiplication and distribution activities at Bari have been drastically reduced, whereas targeted collecting and characterization work was still carried out within specific agreements or funded projects. On the one hand, maintenance of plant germplasm, including multiplication, characterization and distribution, has become more and more expensive, while on the other hand, funds for these activities have been reduced in favour of research on genetic engineering, based on the assumption that molecular analyses would add value to the germplasm collections and then increase their use and justify the maintenance investment. Experience from genebanks does not seem to confirm this approach. On the contrary, in many cases, the cutting of funds for maintenance and traditional methods of evaluation has resulted in a disastrous loss of germplasm collections and consequently has reduced the possibilities of distribution and utilization of the material.

Conclusions

At least in the case of the Bari Genebank, future maintenance activities will be possible through targeted projects, sponsored by public and private organizations, small and medium enterprises interested in using old varieties, local ecotypes, landraces and GMO-free material, for developing all sorts of eco-compatible and sustainable agriculture. It seems that the decrease in the use of germplasm by breeders is due mainly to competition with genetic engineering. However, one cannot ignore the fact that traditional breeding is being carried out with only limited and sporadic success; many traditional breeders are investing funds and hectares of land for the production and maintenance of huge numbers of lines of wheat, without actually coming up with any new variety suitable to current environmental, cultivation, nutritional, social and economic needs. The past three decades of work on characterization according to standard descriptors, aiming at the rationalization of collections, does not seem to have been successful, since the idea of reducing the size of collections by eliminating "duplicated samples" and concentrating on "core collections" has not proved to be popular.

This short background, together with some scientific and historical background on the Bari Genebank, may be useful to help deciding in which direction the ECP/GR Wheat Working Group (WWG) should move and what kind of recommendations the WWG may provide for enhancing the maintenance and making the optimum use of the wheat germplasm collections, i.e. wheat genetic diversity.

On-farm conservation of hulled wheat in Italy

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Introduction

In Italy, the term "farro" has been used for centuries to cover all of the cultivated hulled wheats, comprising small spelt or einkorn (*Triticum monococcum* L.), emmer wheat (*T. dicoccon* Schrank) and spelt or dinkel (*T. spelta* L.). Cultivation of hulled wheat goes back to 7000 years BC. In early ages they were cultivated in Mesopotamia, Egypt and Palestine, and subsequently, from the VI millennium BC, they spread into the Mediterranean Basin and western Europe. In the third millennium BC they were already being cultivated in Greece. In southern Italy, they arrived through the Greek colonies. Farro constituted the basis of the diet of the ancient Romans, who used its flour for making a kind of "polenta". From the beginning of the twentieth century, this crop became less and less cultivated in Italy as well as in the rest of the world, and particularly in the Mediterranean countries. In fact, with the advent of new varieties of unhulled wheat (*T. aestivum*), farro was unable to remain competitive because of the new wheat superior grain yield, agronomic and technological traits.

However, during the past 20 years, the spreading of the message of organic agriculture throughout the world has attracted the interest of several farmers' cooperatives. This is the result of several factors, the most important of which are the increase in the demand for organic products, and the EU agricultural policies which aim both to promote organic agriculture and to reduce total agricultural production. In this new economic context, the cultivation of farro can find a valid place, especially in the so-called marginal areas, where the exodus of young people toward the big cities, attracted by more profitable activity, is a reality, and where the cultivation of unhulled wheat is not particularly rewarding because of poor yields when compared with those from flatter, fertile lands. Thus, in the past decades, in Italy and other developed countries, agriculture started to face two major problems: the need to reduce overproduction and to preserve the land. Mainly for these reasons, several researchers have devoted themselves to studying the possibility of introducing farro into the crop rotations of marginal areas.

In Italy there are so far no varieties of hulled wheat listed in the National Register. Therefore, studies on farro have been carried out on ancient landraces or populations that some farmers, in various regions of Italy, and in other countries, have preserved for generations. Such landraces do not compete well with the farro from abroad or with unhulled wheat. There is, then, a need to obtain genotypes which will enable a level of production that will make the cultivation of farro economically more attractive and more competitive with hulled wheat coming from abroad.

In the last 25 years, the former Germplasm Institute in Bari (now part of the Istituto di Genetica Vegetale, IGV) has initiated several studies with the aim of reintroducing into Italy, especially in marginal areas, the cultivation of two species of farro (*T. dicoccon* Schrank and *T. spelta* L.), two crops that, in Italy and many other countries of the Mediterranean, were on the edge of extinction. Since then the Germplasm Institute has selected several lines (genotypes) of farro, of which two, 'Farvento' (*T. dicoccon* Schrank) and 'Triventina' (*T. spelta* L.) have been developed within research projects sponsored by the Farmers' Cooperative "Nuova Europa 2000" of Trivento (CB) and two, 'Lucanica' (*T. dicoccon* Schrank) and 'Forenza' (*T. spelta* L.), within projects sponsored by the farmers' "Produttori Cerealicoli Lucani" (APROCEL) of Potenza. In both cases the main objective was to characterize the collection of hulled wheat preserved at the Germplasm Institute with the purpose of selecting genotypes suited for the marginal areas of the Apennine chain of the Molise and Basilicata Regions.

The aim of this article is to summarize the methodology used and the results obtained within these research projects developed in Italy in collaboration with the two enterprises "Nuova Europa 2000", active in the Molise Region, and "APROCEL", active in the Basilicata Region. The first group of projects was carried out for six years, from 1989 to 1995, and the second was carried out from 1991 to 2001, within larger projects denominated "Green Basilicata" and "Program Leader II 1994-99" respectively. In all cases the research was completely financed by the two enterprises, which in turn received financial support from the EU, Molise and Basilicata Regions, and farmers, through specific agreements aiming to reduce production, increase food quality and encourage farming systems with lower inputs of chemicals.

Steps from *ex situ* to on-farm conservation

The Germplasm Institute started the collection of hulled wheats in 1970. The first germplasm was collected in Ethiopia, the later material was collected during expeditions in North Africa, Spain, Greece, Italy, Albania and other Mediterranean countries. In Italy, where collecting activity has been more intensive, the first samples of hulled wheat were collected in 1981 along the Apennine chain, where, at that time, farro was cultivated mainly to feed animals and especially pigs. Only in the Toscana Region were landraces of farro used for human consumption. Apart from the missions in Italy expeditions conducted abroad were made in collaboration with FAO, IBPGR, IPGRI, ICARDA, national institutions and local experts. In all cases, multiplication and conservation activities of the hulled wheat collection was completely funded by CNR and other small public and private Italian enterprises. In particular, the first multiplications of the hulled wheat collection for a preliminary evaluation started at the end of the 1980s, within a research project financed by "Nuova Europa 2000" and at the beginning of the 1990s within a project financed by "APROCEL", in marginal lands of Molise and Basilicata Regions respectively. Thus, it took nearly 20 years to build up the world collection of hulled wheat, preserved in the Gene Bank of Bari, and to carry out characterization and evaluation work aimed at developing and promoting on-farm conservation strategies. From 1994, this activity was greatly stimulated at international level by a project on Underutilized Mediterranean Species (UMS), coordinated by Stefano Padulosi at IPGRI, which also included a Hulled Wheat Genetic Resources Network, chaired by Pietro Perrino, Director of the Germplasm Institute.

Research to promote *on-farm* conservation

In all projects promoted by the Germplasm Institute, research was carried out both in the field and in the laboratory for making agronomic and biochemical evaluations of the hulled wheat world collection comprising 750 accessions collected in different geographical areas.

- **Research work in the Molise Region**

Nearly 500 accessions of *Triticum dicoccon* and 250 of *T. spelta*, of different geographical origins, were grown in small plots, with three replicates and over three years (1989-92) in two locations of Molise Region above 600 m asl. During growth the following agronomic descriptors were recorded: plant height, heading time, lodging, yields of dressed and naked grain, percentage of chaff, seed weight and other plant traits. The results of this first experiment were published in regional or local journals. About 50 out of 750 populations were selected for yield performance, resistance to frost and lodging, and plant habit. In the next cycle of three years (1992-95) of research, the selected 50 populations were grown in two different field trials in the Basilicata Region and also characterized in the laboratory for biochemical traits such as protein content, ash, fat, bran, gluten, test of sedimentation (SDS test) and beta-carotene. The aim was to select within each population the genotypes showing the highest yield and protein content, the best aptitude for bread-, pasta- and soup-making, and the highest stability for these traits over time and localities. Finally, one genotype each of *Triticum dicoccon* and *T. spelta* with these features were chosen and patented, with the names of 'Farvento' and 'Triventina' respectively. Today, these two varieties are cultivated in the marginal lands of southern Italy by farmers associated with the "Nuova Europa 2000" enterprise and marketed directly to make soup, or after processing to make meal, bread, pasta and biscuits.

- **Research work in the Basilicata Region**

The best 100 lines of *Triticum dicoccon* and 100 of *T. spelta*, selected during one of the previous research projects, were grown over three years (1991-94) in a field trial in the Basilicata Region. During the first year, the 100 lines of each species were grown to select the best 50 lines on the base of agronomic traits, such as plant height, heading time, lodging, seed weight and biochemical traits, such as protein content, ash, fat, bran, gluten, test of sedimentation (SDS test) and beta-carotene. Using the same procedures, the 50 selected lines were grown in the second year to select the best 25 lines, which were grown in the third year to select the best line for yield production, protein content, sedimentation test and stability of yield over time and locations. In the end, one genotype of *Triticum dicoccon* and one of *T. spelta* with these features were chosen and patented with the names of 'Lucanica' and 'Forenza' respectively. These two varieties are cultivated in marginal lands of Basilicata and southern Italy by farmers associated with the "APROCEL" enterprise and marketed like 'Farvento' and 'Triventina'.

Comparison of hulled wheats within the Italian network

The research on hulled wheat, started at the Germplasm Institute of Bari in 1970, developed so much that in 1981 it became a constant line of research and at the beginning of the 1990s it started to involve other Italian research centres. It was so successful that in 1996, promoted by the UMS Hulled Wheat Genetic Resources Network, an Italian Farro network was created with the main aim of increasing the cultivation of farro in Italy. In 1996-97, within this network, coordinated by Oriana Porfiri at CERMIS (Centro Ricerche e Sperimentazione per il Miglioramento Vegetale), several lines and varieties of farro, developed in Italy, were compared in several different environments of the peninsula. This gave the opportunity of comparing the two varieties of *Triticum dicoccon* ('Farvento' and 'Lucanica') and the two varieties of *T. spelta* ('Triventina' and 'Forenza') selected by the Germplasm Institute with nine other lines of farro, of which five were *T. dicoccon* and four *T. spelta*. The results showed good possibilities of competition with all the studied lines. The newly selected lines were competitive with the others in national trials. The *Triticum dicoccon* examples showed better performance in marginal and warm-arid environments, while the *T. spelta* were more suitable for marginal and cool but not especially arid environments. It was interesting that the undressed (naked) grain yields of 'Lucanica', 'Farvento', 'Forenza' and 'Triventina' were respectively, on average, of 29, 31, 34 and 30 q/ha, very close to the general mean of 33 q/ha of the national network. These mean values of yields of farro at national level are quite a lot higher than those obtainable in southern Italy, where usually, due to drought, they are considerably lower than 30 q/ha. This may be compensated to some degree by the grain and meal quality.

Influence of environment and nitrogen fertilization on yield and other traits

During the year 1996-97, the four lines of farro 'Lucanica', 'Farvento', 'Forenza' and 'Triventina' were grown in two quite different localities, one in Basilicata (Gaudiano di Lavello), with rich soils, and one in Molise Region (Larino), with poor soils, together with a hard ('Norba') and a bread ('Sprint') wheat variety, using an experimental scheme with three replicates, in order to test all the wheat entries in two environments and at three nitrogen levels (0, 40 and 80 units/ha). The results showed that hulled wheat is not much affected by fertilization, unlike the unhulled wheat. The *T. dicoccon* and the *T. spelta* did not show great differences within the same locality, while significant differences arose between localities. In the field trial in Basilicata, with rich soils, the average yield of undressed grain of all hulled wheat (19 q/ha) was superior to that of the field trial in Molise (16 q/ha), with poor soils. These yields can be considered reasonably good when compared with those of modern varieties of unhulled wheat, such as the hard wheat ('Norba'), with yields of 23 and 19 q/ha, and the bread wheat ('Sprint'), with yields of 18 and 26 q/ha, respectively in Basilicata and Molise. Nitrogen fertilization affected grain yield of hulled wheat negatively in Basilicata (it fell from 21 to 17 q/ha) and positively in Molise (it rose from 13 to 15 q/ha). However, it positively affected grain protein content in both localities: they rose from 17 to 20% in Basilicata and from 13 to 15% in Molise with increased N. Thus, on average, the grain protein content in Basilicata (19%) was higher than that obtained in Molise (14%). For unhulled wheat the protein content was lower than for the hulled wheat, specifically, 16.5% in Basilicata and 10.5% in Molise. In both localities nitrogen supply did not affect protein content. Besides, nitrogen fertilization negatively affected the yellow berry trait in both localities: it fell from 7 to 4% in Basilicata and from 36 to 21% in Molise, which means that the percentage of seeds with yellow berry decreased with an increase of nitrogen in the soil. Therefore, in general yellow berry is a character which is strongly affected by the environment, climatic changes and soil nitrogen content. However, it is worth while pointing out that nowadays yellow berry may be corrected simply by eliminating affected seeds. The quality of the proteins, expressed by the index SDS/proteins, showed that in general the *T. spelta* were superior (4.3) to the *T. dicoccon* (1.4) but similar to unhulled hard (4.2) and bread (3.7) wheat. It seems that this trait is not affected at all by the nitrogen level in the soil, since no entries showed significant variation at 0 to 80 rates of nitrogen units/ha, whereas it was slightly affected by the environment, since on average it was significantly higher in Molise (3.3) than in Basilicata (2.4). In particular, for *T. dicoccon* the mean values were 1.7 and 1.1 and for the *T. spelta* 4.9 and 3.7 respectively in Molise and Basilicata localities. For the unhulled wheat the trend was similar for the hard wheat, changing from 5.7 in Molise to 2.8 in Basilicata, whereas for bread wheat it was respectively 3.4 and 4.0. The higher the value of SDS/proteins index, the higher the suitability for bread- and pasta-making.

New approaches for research

In order to improve research and to further promote on-farm conservation, the Germplasm Institute has strengthened collaboration with the University of Basilicata and that of Molise. As a result new research projects were started and some of them are still in progress. Some students have even written dissertations on these topics for their degrees in Agriculture. In particular, during the years 1995-96 and 1997-98, studies carried out in Basilicata on the influence of nitrogen on yield and qualitative traits confirmed the low or even negative effect of nitrogen supply, especially when there was a concomitant water shortage. The same study showed differences in LAI (Leaf Area Index), in PAI (Plant Area Index) and CGR (Crop Growth Rate) among different entries of hulled and unhulled wheat, fertilized and not fertilized. The influence of fertilization on these growth indexes was different with varieties, though there was no clear correlation with any factor of yield and grain quality. All the experimental data suggested that it would not be worth while to search in hulled wheat for characters or uses similar to those of the unhulled wheat. Instead one should try to identify in hulled wheat factors responsible for very specific characters, such as digestibility, absence of toxicity, tolerance in the case of coeliac disease, the presence of fibres, mineral content, slow absorption of glucides and others.

Future developments

All the past activities, from collecting to *ex situ* conservation and other activities of the Germplasm Institute in collaboration with other international organizations and national research centres, including research projects sponsored by farming enterprises, regions, the Ministry of Agriculture and the European Union, have made it possible to start a big campaign for enhancing the consumption of farro and consequently its cultivation in several regions of Italy. This means that at least part of the genetic diversity collected in the past from traditional farmers and farming systems and maintained *ex situ* for decades in the Gene Bank of Bari has been reintroduced into cultivation and finally come back to the farmers, not only to be maintained on farm but to be used in a sustainable way with new perspectives and new purposes. Due to the success of the farro programme, new research projects have been or are going to be financed by the Ministry of Agriculture and the Chamber of Commerce Industry Craftsmanship and Agriculture of Lecce, in the marginal lands of Salento, the southern part of Apulia region. The aim of these projects is to select adapted genotypes of farro, especially *T. dicoccon*, particularly useful for arid lands. In addition, the two farming enterprises from the Molise and Basilicata regions have made special agreements with the Germplasm Institute for technical assistance during the growth and maintenance of the patented varieties obtained earlier: 'Farvento', 'Lucanica', 'Triventina' and 'Forenza'.

Conclusions

Farro is an ancient wheat crop which, 20 years ago, was considered an underutilized or neglected crop and which it seemed was probably going to be completely abandoned because of its low productivity, and threshing and other agrotechnical problems. In the last 20 years, economic, political and social changes, including those concerning major needs for the conservation of biodiversity and especially of agrobiodiversity, have called the attention of scientists, researchers, politicians, international and national organizations, regional public and private enterprises to the potential of underutilized crops. At the same time there has been an increase of interest in human health as influenced by nutrition, and in environment protection. All these factors suggested investigating the properties of farro and especially of *Triticum dicoccon* and *T. spelta* both from the agricultural and nutritional points of view. Farro, due to its hardy growth habit, is very competitive to weeds, and in marginal areas and poor soils can provide a reasonable yield and be competitive even with modern unhulled wheat. For these reasons, farro, like other minor crops, can be regarded as a crop which is well suited for organic agriculture. It does not need much weed control or nitrogen supply. In the mountainous areas of the Italian peninsula, farro is a valid alternative to modern unhulled wheat varieties. Besides, farro is considered a very important food in respect to the nutritional aspect of the treatment of many illnesses. It is certainly not about to replace all of the other foods in the kitchen or to be used directly as a medicine, but in general it is able to satisfy, better than some other foods, several of the demands of the organism. It is not a miraculous cereal, even if some attribute anticancer effects to it. This matter is very complex and will need further research to investigate the nutritional and therapeutic effects on humans. At the moment, the cultivation of farro in Italy has increased up to more than 3000 ha and this has contributed towards solving problems of agrobiodiversity conservation, environmental protection, utilization of marginal lands, agricultural diversification, human nutrition and health.

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Wheat genetic resources in Lithuania [65]

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Introduction

Systematic scientific work on wheat genetic resources was started in 1922 in Lithuania at the Dotnuva Plant Breeding Station, which in 1956 was incorporated into the Lithuanian Institute of Agriculture (LIA).

Since the first years of wheat work, Dotnuva breeders established good contacts with many breeders and companies in western and eastern Europe and in America. They received the first seed samples from Vilmorin (France) and Petrograd (USSR) in 1925, from the USA in 1927, and from Svalof (Sweden) in 1931. The varieties were tested under Lithuanian conditions and the best ones were included in the crossing programmes. Up until the Second World War Dotnuva breeders collected the local Lithuanian varieties and landraces. Two varieties, 'Akuotuotieji' and 'Dotnuva 458', were developed from the local material.

A special programme on wheat genetic resources was launched in Lithuania in 1994 and is still continuing. The programme involves collecting, evaluation, research and conservation of *Triticum* genetic resources. The scheme is subsidized by the Lithuanian Science and Studies Foundation and coordinated by the Lithuanian Institute of Agriculture.

Status of the Lithuanian *Triticum* collection

The key tasks of those responsible for the present wheat genetic resources collection are to collect wheat germplasm from different geographical regions, test it under local conditions and select valuable genetic material which will be useful for the development of new varieties now and in the future, and to conserve old Lithuanian varieties and the varieties bred in Lithuania which are characterized by some valuable traits.

One part of the wheat collection is kept in long-term *ex situ* storage; the other part is kept in medium-term storage. All accessions included in the long-term storage are duplicated in a working collection.

All accessions are of the winter type and are kept at the Lithuanian Institute of Agriculture only.

The Lithuanian genebank follows IPGRI's recommendations for seed handling in long-term storage (Hong *et al.* 1996); the collections are stored according to IPGRI standards.

The status of the collection is given in Table 1.

Table 1. The Lithuanian wheat collection in 2003

Material	No. of accessions
Old Lithuanian varieties in long-term storage (LTS)	8
Newly developed varieties (LTS)	6
Varieties tested in the State Variety testing (LTS)	7
Advanced breeders' lines (LTS)	18
Active collection	592
Investigation block	49
Introduction block	398
Total	**1078**

[65] See also: "Status of the winter wheat collections in Lithuania", p. 272.

It has been proved that temperature and moisture content are important for long-term storage life of seeds (Vertucci and Roos 1990). Nevertheless the value of critical or optimum relative humidity is still a matter of some debate (Ellis 1998; Walters and Engels 1998).

The seed for long-term storage is prepared in the following way: the seed is dried from the initial water content for three months at 20-25°C in an environment with 10-15% relative air humidity. Long-term seed storage conditions require a seed moisture content of 3-6%. After drying, seeds are checked and packed in foil-laminated bags, then stored at -18°C (Būdvytytė 2002).

Most of the winter wheat accessions are of *Triticum aestivum* (1072 accessions in the active collection and 37 in long-term storage) or *T. turgidum* (37 accessions in the active collection and 1 accession in long-term storage).

The active collection comprises 5 landraces, 360 advanced cultivars and 227 lines of breeders' material. The geographical origin of the cultivars in the active collection is given in Table 2.

Table 2. Origins of the wheat cultivars in the Lithuanian active collection

Origin	No. of accessions	%
1. Local region (Lithuania, Latvia, Estonia, Belarus, Finland)	43	7.2
2. Nearest region (Poland, Germany, Sweden, Denmark)	202	34.1
3. Southwestern Europe (Great Britain, France)	68	11.5
4. Central Europe (Czech Republic, Slovakia, Bulgaria, Romania, Austria)	40	6.8
5. Balkan region, Italy, Hungary	48	8.1
6. Central and South Russia, Ukraine	107	18.1
7. Central and North America	68	11.5
8. Asia	16	2.7
Total	**592**	**100**

Evaluation and documentation

Accessions of Lithuanian origin are thoroughly evaluated and characterized; all relevant information is available. Data on the accessions in long-term storage are available on the home page of the Lithuanian Institute of Agriculture (www.lzi.lt, subsection NAGIKC/Lithuanian PGR, Augalo pasas/passport). Descriptors included in the database are: Accession number; Accession name; Type of accession; Database number; Originator city; Common name; Status of accession; Genus; Species; Subtaxa; Year of release; Donor code.

The old cultivars and some new cultivars are described according to the first set of characterization descriptors for wheat (Maggioni *et al.* 2003).

The most valuable parts of the Lithuanian wheat collection (old local varieties) were described according to the full requirements of the European Wheat Database (EWDB) and were sent to this database.

Varieties and lines currently being included in long-term storage will be described using the first six descriptors.

The EWDB is sometimes used by Lithuanian wheat breeders to check the pedigree of varieties used in the crossing programmes.

Utilization of wheat genetic resources in plant breeding

Lithuania is situated in the southeastern part of the Baltic region between 54° and 56°N. The annual mean temperature of the country is 6.2°C. The air temperature in Dotnuva in January fluctuated between +8.7° and –29.0°C over the period 1990-2003. The soils are not always protected by a snow layer in the winter period. Therefore overwinter survival of the wheat plants is one of the limiting factors.

The humid and mild climate in summer is favourable to disease incidence. The most harmful diseases are powdery mildew and *Septoria*. Nevertheless, plant diseases that are more characteristic of southern countries, e.g. rusts, also cause damage.

The local growing conditions determine the plant genotype and agronomic traits of the varieties created in the wheat breeding programmes. It is important to combine good winter hardiness and resistance to diseases with good agricultural and industrial value of the grain.

To fulfil this task, breeders collect germplasm from western, eastern and southern countries and use it in the breeding programmes. Another reason to include different parent material in the genotype of the varieties under development is the fact that many advanced commercial cultivars have a narrow genetic base.

Between 1922 and 2003 Lithuanian breeders included in the active collections over 2500 varieties from 25 countries. The varieties are included in the working collection after a short screening period of 1-2 years. In total, 4489 lines and varieties were tested in the introduction-screening block at LIA during the period 1990-2003, including 1696 lines and varieties from the FAWWON (Facultative Winter Wheat Observation Nurseries) programme of CIMMYT (Centro Internacional de Mejoramiento de Maíz y Trigo = International Wheat and Maize Improvement Centre, Mexico), 930 from the International Winter x Spring Wheat Screening Nursery of Oregon State University, and 1863 lines and varieties from western European countries.

A significant positive correlation between winter resistance and grain yield as well as between plant height and winter resistance was detected in southern winter wheat (Ruzgas and Liutkevičius 2001a). The results of investigations of the tested germplasm showed that 20-30% of West European varieties and 50-60% of varieties of distant origin demonstrated the same tolerance to Lithuanian winter conditions as local varieties (Ruzgas and Liutkevičius 2001b). The greatest constraint to using southern germplasm of winter wheat is grain yield and susceptibility to the most widespread diseases in humid climates, especially powdery mildew. Therefore screening is obligatory for all foreign genetic material of winter wheat before the lines or varieties are included in the active collection and long-term storage.

An analysis of the hybridization programme of winter wheat breeding in Lithuania in 1991-2002 showed that the material most frequently used in the crosses was varieties from the nearest West European region (male parents 57.2%, female parents 46.1%), Central and South Russia and Ukraine (male 19.3%, female 20%), and local breeding material (male 11.9%, female 20.7%) (Table 3). The varieties from Asia have not been used for crossing due to their high susceptibility to diseases.

All Lithuanian winter wheat varieties are developed on the basis of genetic material originating from different regions (Table 4). The first varieties were created using local varieties collected in Lithuania or regions characterized by similar climatic conditions. The home-bred varieties contain germplasm from West European winter wheat (50%) or from Russia and the Ukraine (24%). The new varieties were developed using Lithuanian varieties or breeding lines (20%) or varieties from Central Europe as well as germplasm obtained from distant geographical regions (3%).

Table 3. Origin of winter wheat varieties included in the crossing programme of the Lithuanian Institute of Agriculture, 1991-2002

Origin of female parent*	Origin of male parent*								
	1	**2**	**3**	**4**	**5**	**6**	**7**	**Total**	**%**
1	53	168	6	12	7	83	21	348	**20.7**
2	72	459	29	18	17	152	27	774	**46.1**
3	1	14	2	3	4	-	-	24	**1.4**
4	18	7	-	1	-	1	-	27	**1.6**
5	3	58	1	-	2	7	-	71	**4.2**
6	45	223	8	9	-	44	7	336	**20.0**
7	10	32	8	1	-	37	13	101	**6.0**
Total	**200**	**961**	**54**	**44**	**30**	**324**	**68**	**1681**	**100**
%	**11.9**	**57.2**	**3.1**	**2.6**	**1.8**	**19.3**	**4.1**	**100**	

* Codes used for regions:
1. Local region (Lithuania, Latvia, Estonia, Belarus, Finland)
2. Nearest region (Poland, Germany, Sweden, Denmark)
3. Southwestern Europe (Great Britain, France)
4. Central Europe(Czech Republic, Slovakia, Bulgaria, Romania, Austria)
5. Balkan region, Italy, Hungary
6. Central and South Russia, Ukraine
7. Central and North America

Table 4. Geographical origin of registered and candidate Lithuanian varieties

Variety	Year of release	Pedigree	Origin of parent material*	
			Female	**Male**
Akuotuotieji	1923	Selected from Kalinovskaja,	Landrace	
Pergalė	1949	Nordost-Zigfrid / Egipetskaja	2	Landrace
Dotnuvos 458	1950	Panser II / Vysokolitewskaja	2	Landrace
Mūras	1958	Kronen / Lesostepka	2	6
Aidas	1961	Carsten Dickopf / Dotnuvos aukštieji (rye)	2	1
Širvinta 1	1989	Miron808 / Miron.jubil50 // Miron808 / Bezost1 / 3 / Omar	6	7
Ada	2001	Širvinta 1 / Lutescens 290	1	6
Seda	2001	Nova / Marabu	2	2
Tauras	2001	B.st.19149-88 / WW27314 (spring)	2	2
Lina	2002	TAW5 / Linija 125	2	6
Milda	2002	Bussard / Viginta	2	4
Alma	2002	Albatross odesskij / Kijanka	6	6
Candidate varieties				
LIA 4514	Pepital / Astron		2	2
LIA 3948	Kijanka / Yacht		6	2
LIA 3937	Astron / Yacht		2	2

* Codes used for regions:
1. Local region (Lithuania, Latvia, Estonia, Belarus, Finland)
2. Nearest region (Poland, Germany, Sweden, Denmark)
4. Central Europe (Czech Republic, Slovakia, Bulgaria, Romania, Austria)
6. Central and South Russia, Ukraine
7. Central and North America

Priorities of work on wheat genetic resources

The future priorities in the field of genetic resources should include further collecting, evaluation and maintenance of accessions in the existing collections.

All domestic collections should make use of identical descriptors proposed by ECP/GR and IPGRI.

Data about the collections should be computerized and accessible through international information systems.

New biotechnology methods, especially molecular markers should be used to describe existing accessions.

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Wheat genetic resources in the Netherlands

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Introduction

Since the last meeting of the ECP/GR Working Group on Wheat held on 8-10 November 2001 in Prague-Ruzyne, Czech Republic, the wheat collection of CGN has been increased by 19 new accessions. Information on the collection was published in the report of the meeting (van Soest and Bas 2003). At present the collection includes 5494 accessions.

This paper provides additional information on the CGN wheat collection relevant to the further development of the European Wheat Database (EWDB).

Wheat collections in the Netherlands

The Netherlands has a centralized genebank system and CGN has the national responsibility for plant genetic resources (PGR) conservation. CGN has optimal facilities for conserving PGR collections. A few private breeding firms in the Netherlands are maintaining their own working collections for breeding purposes. These firms are working closely with CGN, both using the collections and also cooperating in the regeneration and evaluation of the CGN wheat collections. In general these firms do not have the long-term storage conditions for optimal conservation and do not use documentation systems. The wheat collection of CGN includes nearly 5500 accessions and represents the national Dutch wheat collection.

Details of the CGN wheat collection in relation to passport data

- **Percentage of accessions according to growth type (Table 1)**

Table 1. Status of the CGN wheat collection according to growth type

Growth type	%
Spring	51.3
Winter	42.9
Intermediate	1.9
Unknown	3.9

The intermediate types are mainly landraces from Asia (e.g. Pakistan). The group "unknown" includes several wild species and most of this material can be considered spring or intermediate types.

- **Percentage of accessions according to sample status (Table 2)**

Table 2. Status of the CGN wheat collection according to sample status

Ploidy level	Sample status*					Total	% of total
	LR	AC	BL	W	U		
2n	20		5	187	14	226	4.1
4n	148	84	6	214	229	681	12.4
6n	2298	1468	679		142	4587	83.5
Total	**2466**	1552	690	401	385	**5494**	**100.0**
% of total	**44.9**	**28.2**	**12.6**	**7.3**	**7.0**	**100.0**	

* LR = Landraces, AC = advanced cultivars, BL = breeding or research material, W = wild species, U = unknown

Landraces form the majority of the accessions in the wheat collection and most of these accessions are hexaploids belonging to the *T. aestivum* group. The second largest group is the cultivar group including mainly hexaploid wheat species. The 12.6% breeding and research material is mainly of European origin (Austria, Germany, the Netherlands and Russia). The number of wild species is rather limited. Important wild species in the collection are *T. turgidum* var. *dicoccoides* (214), *T. squarrosum* (70), *T. speltoides* (24) and *T. ovatum* (17). Table 2 also shows that the population type of 7.0% of the collection is not known. The EWDB may be useful for finding some missing data on the population types of these accessions. At present, CGN is using the EWDB for updating of the passport data of CGN's wheat collection.

- **Percentage of taxa in the broader sense (Table 3)**

Table 3. Number of accessions in the CGN wheat collections according to ploidy level

Ploidy level	Description of taxa	No. of accessions	% of total collection
2n	Diploid wild species (15)	186	3.4
	T. monococcum	40	0.7
4n	*T. timopheevii*	8	0.2
	T. turgidum group	673	12.2
6n	*T. aestivum* group	4562	83.0
	Synthetic wheats (6n)	22	0.4
?	Unknown	3	0.1
Total		**5494**	**100.0**

CGN follows the classification of Morris and Sears (1967) for the description of the different species in the wheat collection.

The hexaploid group, including a large number of accessions belonging to *T. aestivum* group *aestivum*, forms the largest part of the wheat collection of CGN. The tetraploid group consists of both wild species and cultivated material and with 12.4% forms a relatively small group. The diploid group includes material of some 15 different wild species but also some cultivated accessions of *T. monococum*. It forms the smallest group (4.1%) of the collection.

- **Percentage of cultivars and landraces according to geographical origin (Table 4)**

Table 4. Distribution of cultivars and landraces of the CGN collection according to their origin

Continent	Cultivars (AC)	% of total no. of cultivars	Landraces (LR)	% of total no of landraces
Europe	1023	65.9	652	26.5
Asia	80	5.2	1394	56.5
North America	185	11.9	10	0.4
South America	79	5.1	10	0.4
Africa	46	3.0	380	15.4
Australia	81	5.2	0	0.0
Unknown	58	3.7	20	0.8
Total	**1552**	**100.0**	**2466**	**100.0**
% of total collection		**28.3**		**44.9**

Most of the cultivars in the collection are from Europe and particularly from France (171), the Netherlands (130), Germany (132), Russia (94), Italy (69), United Kingdom (51) and Sweden (50). The large group of landraces from Asia was mainly collected in the period

1953-1981 in and near the centres of diversity in the Middle East (van Soest and Bas 2003). Dutch researchers participated in some of these expeditions (Hashmi *et al.* 1981; van Soest and Boukema 1995).

Details of the characterization and evaluation data of the CGN wheat collection

Information on the available characterization and evaluation data of the CGN wheat collection is presented in Table 5. Approximately 50% of the material of the *T. aestivum* group has been characterized for 12 different descriptors. The characterization of cultivated material is conducted with a minimal list of descriptors developed by CGN (van Loosdrecht 1985). Thirty-nine accessions of different wild species have been characterized for a set of 13 specific descriptors. Occasionally material has been characterized for additional descriptors (see Table 5).

Table 5. Details of the available characterization and evaluation data of the CGN wheat collection

Character	No. of accessions characterized
A. Characterization data on cultivated *Triticum* material	
Spike density	992
Lodging susceptibility	1967
Growth height	2067
Seed colour	1708
Seed shape	1723
Glume colour	697
Seed size	1204
Awnedness	2071
Spike emergence time	1202
Spike length	1973
Awn length	1148
Threshability	186
Stem brittleness	550
Seed shattering tendency	195
Annuality	1375
Winter susceptibility	336
Sprouting tendency	254
Glume hairiness	671
Awn attitude	24
Rachis brittleness	101
Heading time	66
B. Characterization data of wild species	
Rachis hairiness	39
Stem pith presence	39
Spike width	39
Glume length	39
Spikelet width	39
Seed number per spikelet	35
Endosperm structure	39
Palea splitting tendency	39
Glume keel shape	39
Growth habit	39
Flag leaf width	39
Spikelet number per spike	39
Spike breaking susceptibility	39
C. Evaluation data of cultivated material	
Puccinia recondita	81
Puccinia striiformis	273
Fusarium culmorum	163
Erysiphe graminis	1680

Evaluation data are only available for disease susceptibility to four wheat diseases, *Erysiphe graminis, Puccinia recondita, P. striiformis* and *Fusarium culmorum*.

In the framework of a cooperative evaluation programme with breeding firms from the Netherlands, more than 1200 accessions have been evaluated for field resistance to a number of diseases. The data from these screenings still need to be included in the database of CGN.

Information as well as passport and evaluation data on the CGN wheat collection can be found on the Web site of CGN (http://www.cgn.wur.nl/pgr/). The evaluation data can be downloaded per trait in zipped Excel format.

Information related to the EWDB

The passport data of the CGN wheat collection have been submitted to the EWDB; probably only a very few recently included accessions have not been included yet. As a consequence more than 99% of the CGN wheat accessions should be recorded in the EWDB. At present no characterization data of the CGN are included in the EWDB.

CGN staff uses the EWDB Web application for the following purposes:

- to locate specific wheat material upon request by Dutch users, and
- to use passport data included in the EWDB for updating of information on accessions included in the CGN wheat collection.

Furthermore users requesting wheat accessions not available in the CGN collection are informed about the existence of the EWDB.

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Wheat genetic resources in Romania [66]

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Introduction

Wheat is grown in Romania on an area of 1 866 000 ha, representing 33% of the area occupied by cereals and 22% of the total cultivated area. The total wheat production in 2000 was 4 720 000 tonnes, with an average yield of 2.5 t/ha. As regards wheat utilization, 71% of the crop is destined for human consumption, at an average per capita of 223 kg/yr, while 11% goes to animal feed.

The Suceava Genebank and six breeding institutions maintain the genetic resources of wheat, the second most important crop in Romania in terms of cropped area after maize.

The Genebank is responsible for long-term conservation; the other collections are working collections for breeding and research purposes.

The last survey of the status of wheat collections was made in 2000 and the results were included in the Romanian catalogue of plant genetic resources prepared and edited by the Suceava Genebank with financial support from IPGRI (Strãjeru *et al.* 2000).

The composition of the Romanian wheat collection

The present national wheat collection consists of 3200 accessions held by seven state-funded institutions as listed in Table 1.

The major part of the collection is represented by winter forms (2400 accessions = 75%), whereas intermediate and spring types are present in smaller numbers: 640 (20%), and 160 accessions (5%) respectively.

Table 1. Institutions holding wheat collections in Romania

Institution	No. of accessions
Genebank of Suceava	1285
Agricultural Research and Development Institute Fundulea	97
Agricultural Research and Development Station Turda	684
Agricultural Research and Development Station Suceava	371
Agricultural Research and Development Station Simnic	488
Agricultural Research and Development Station Podu Iloaie	243
Agricultural University Timisoara	32
Total	**3200**

Most of the accessions included in the wheat collection belong to *Triticum aestivum* L. (3034), followed by *T. monococcum* L. (83), *T. turgidum* L. (20), *T. dicoccoides* Koern ex Schweinf. (16), *T. dicoccum* (Schrank) Schübl. and *T. timopheevii* Zhuk. (13 entries each), *T. spelta* L. and *T. durum* Desf. (6 entries each) and *T. polonicum* L. (3). Six other species are represented by only one accession each (*T. aethiopicum* Jakubz., *T. carthlicum* Nevski, *T. ispahanicum* Heslot, *T. persicum* L., *T. urartu* Thum. ex Gandilyan and *T. vavilovii* (Thum.) Jakubz.).

Given this taxon representation, 95.2% of the material is made up of hexaploid forms, while diploid or tetraploid varieties are represented by almost equal proportions (2.6% and 2.2% respectively).

[66] See also: "Wheat genetic resources in Romania", p. 278.

The geographical origin of the wheat germplasm by continent is shown in Fig. 1 and the structure of the collection in terms of sample status is illustrated in Fig. 2.

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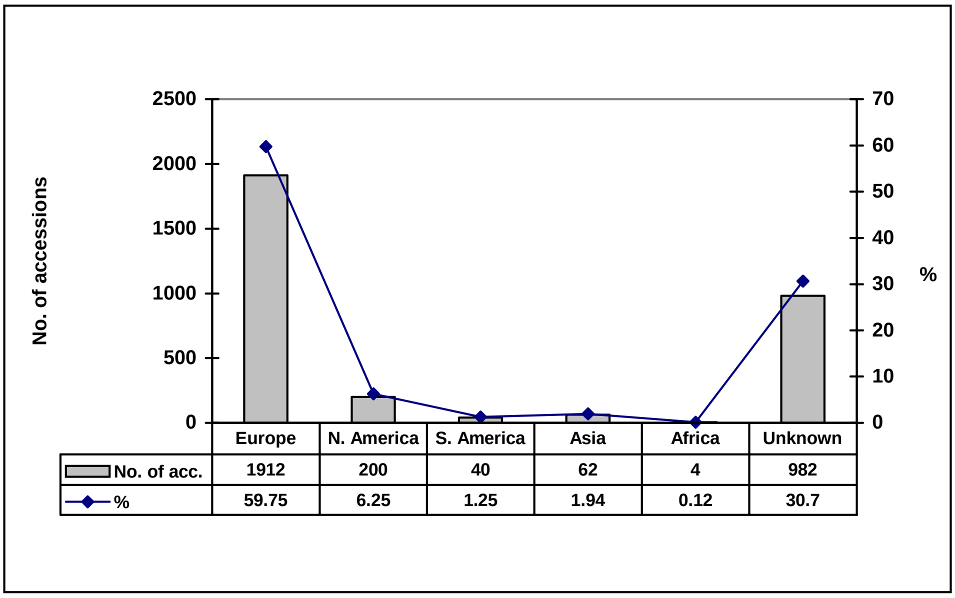

Fig. 1. Geographical origin of the Romanian national wheat collection.

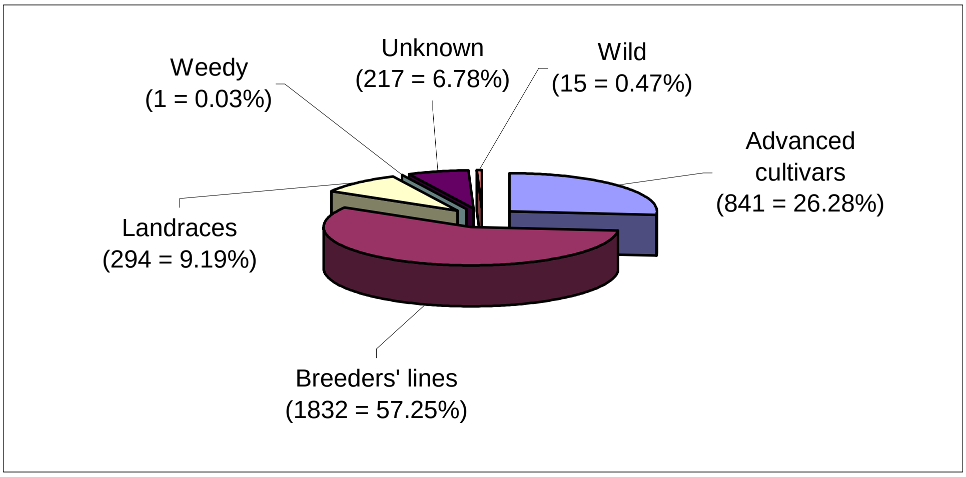

Fig. 2. Status of samples in the Romanian wheat collection.

Collecting

In the last two years three collecting missions of one month each were conducted in the northern part of Romania and the Apuseni Mountains area. The expeditions were multicrop collecting missions and focused on gathering local landraces, old varieties and related information. As some villages were sampled three times in the previous years (1991, 1994 and 1995), the progress of genetic erosion was monitored. By visiting 228 localities a number of 1544 samples belonging to 58 plant species were collected.

Of these, 46 local populations of *Triticum aestivum* L. and 2 samples belonging to *Triticum monococcum* L. were found in 39 collecting sites.

Comparing the current situation with the results obtained from the previous collecting missions it was noted that the land cultivated with *Triticum aestivum* L. in the remote mountainous areas has decreased as grain fields have been converted into grassland.

An even worse situation was recorded for *Triticum monococcum* L. where the distribution area was drastically reduced. If in the early years it was identified in six or four localities of Hunedoara and Alba counties respectively, in our recent trip cultivated einkorn was only collected from one village of the Alba district, where it is still cultivated on small-scale farms.

Characterization and evaluation of Suceava Genebank's wheat collection

Until now, 364 accessions (28%) of the Suceava Genebank collection were described during the period 1997-1999 (Table 2), using IBPGR's descriptors (IBPGR/CEC 1985) adapted to breeders' needs as listed below. The tested material includes 9 Romanian landraces, 259 breeders' lines and 96 advanced cultivars.

Table 2. Characterization and evaluation of the Suceava Genebank's collection

Taxon	No. of accessions characterized/evaluated		
	1997	1998	1999
Triticum aestivum L. (winter type)	30	130	201
Triticum monococcum L. (winter type)	3		

List of descriptors used for the characterization of the wheat collection

1. Sowing date	9. Number of tillers per plant	17. Winter susceptibility
2. Emergence date	10. Number of fertile tillers per plant	18. Cold susceptibility
3. Spike emergence date	11. Spike length	19. Disease susceptibility
4. Flowering date	12. Number of spikelets per spike	19.1 *Septoria tritici*
5. Tillering capacity	13. Number of seeds per spike	19.2 *Erysiphe graminis*
6. Growth habit	14. Number of seeds per plant	19.3 *Puccinia* sp.
7. Growing rate	15. Seed weight per spike	19.4 *Fusarium* sp.
8. Plant height	16. Seed weight per plant	

Biochemical studies to assess protein, tryptophane and lysine content were conducted on 224 accessions (17%) of the Suceava Genebank collection of the following *Triticum* species: *T. aestivum* (210 accessions), *T. dicoccum* (2), *T. monococcum* (11) and *T. turgidum* (1).

Conservation

Suceava Genebank's wheat collection is preserved under long-term and medium-term storage conditions, at –20°C and +4°C. Before entering the cold store the caryopses are dried in order to reach 5% moisture content and then packed in aluminium foil bags or glass jars according to collection type.

Documentation

The documentation system BioGen, designed by Suceava Genebank in Visual Fox Pro, records passport data, characterization and evaluation data and collection management data. In particular, all local landraces and traditional varieties are documented with 20 "on-farm" descriptors developed by the Genebank staff. The Genebank stores passport data for the National Wheat Collection.

Future activities

- To continue collecting activities, particularly in the areas where no collecting has been done previously;
- To continue evaluation and characterization, giving special attention to abiotic and biotic stress studies;
- To introduce molecular techniques for genetic diversity assessment;
- To provide passport data to the European Wheat Database (EWDB);
- To duplicate the most valuable breeders' wheat accessions under long-term conditions at Suceava Genebank; and
- To promote utilization of the Genebank's collection by exchange with other genebanks, breeding or research centres.

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Activities and current status of the national wheat collection in the Slovak Republic [67]

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Wheat is the most important crop grown in the Slovak Republic and on a worldwide scale it is one of the three major crops providing food for more than half of mankind on Earth. *Triticum aestivum,* owing to its suitability to intensive cultivation, high production and good digestibility overtook all other wheat species (*T. dicoccon*) and other arable crop species.

The Research Institute of Plant Production (RIPP) in Piešťany received a mandate to coordinate the conservation of cultivated plant germplasm (Table 1). The RIPP Genebank, which started operating in 1996, is responsible for medium- and long-term conservation of genetic resources in the Slovak Republic.

In 2002 the list of registered varieties of winter wheat included a total of 37 varieties of winter wheat and 8 varieties of spring wheat. Six varieties of durum wheat were included (2 spring and 4 winter).

Table 1. Status of institutions holding wheat collections in Slovakia

Institution and location	Status
Research Institute of Plant Production, Piešťany	Centralized collection/Genebank
Research and Breeding Station, Maly Šariš	Breeder's collection
Research and Breeding Station, Pstruša	Breeder's collection
Istropol, JSC Solary	Breeder's collection
Hordeum Ltd., Sladkovičovo	Breeder's collection
WOOD Breeding station s.r.o., Radošina	Breeder's collection

Taxonomic composition of the Slovak wheat collection

The classification of the wheat collection follows the system of Marhold and Hindák (1998). The genus *Triticum* is represented by eight species:

- winter wheat (*Triticum aestivum* L.)
- club wheat (*Triticum compactum* Host.)
- two-grained spelt (*Triticum dicoccon* Schrank, syn. *Triticum turgidum* subsp. *dicoccum* Schrank
- durum wheat (*Triticum durum* Desf., syn. *Triticum turgidum* subsp. *durum* (Desf.) Husn.
- one-grained wheat (*Triticum monococcum* L.)
- Spanish wheat (*Triticum polonicum* L., syn. *Triticum turgidum* subsp. *polonicum* (L.), Á. Löve et D. Löve)
- spelt wheat (*Triticum spelta* L., syn. *Triticum aestivum* subsp. *spelta* (L.) Thell.), and
- English wheat (*Triticum turgidum* L.).

An overview of the Slovak wheat collection is given in Table 2. Most cultivated accessions in the collection belong to the *T. aestivum* group. This group includes 3276 accessions of winter wheat and 299 spring types.

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67 See also: "The wheat genetic resource collection in the Slovak Republic", pp. 280-281.

Table 2. Taxonomic distribution of wheat accessions in the Slovak wheat collection

Species	Winter	Spring
Triticum aestivum L. (incl. *T. compactum, T. spelta, T. sphaerococcum, T. petropavlovskyi, T. vavilovii)*	3276	299
Triticum monococcum L. (incl. *T. boeoticum*)	7	10
Triticum timopheevii Zhuk. (incl. *T. araraticum, T. militinae*)	-	5
Triticum turgidum L. (incl. *T. durum, T. dicoccoides, T. dicoccon, T. carthlicum, T. polonicum, T. ispahanicum, T. aethiopicum, T. karamyschevii)*	78	56
Triticum dimococcum	-	1
Total	**3361**	**371**

Historical background

The first data on collection and conservation of plant genetic resources date back to the 16th and 17th centuries. The collections were mostly those of botanical gardens and arboreta. The first indirect data regarding landrace gathering are connected with the beginning of plant breeding in Slovakia (wheat breeding in Sládkovičovo, 1870). In several regions of Slovakia, landraces were gathered for breeding purposes ('Šurany', 'Bučany', 'Slovenský Meder', 'Lučenec', 'Trnava', 'Radošina', 'Vígľaš' and others).

Klinovský (1970) distinguishes the following periods in the history of breeding:

1. Till 1920: period of landraces and selections of landraces ('Diosecká 777');
2. Till 1930: period of crossbreds of various imported accessions and domestic varieties;
3. Till 1955: period of combination with qualitatively excellent, mainly 'Bankuti' wheat varieties ('Slovenská intenzívna', 'Viglľašská tvrdá');
4. Till 1966: period of the so-called "promising wheat varieties" ('Kaštická ostnatá', 'Pavlovická 198', 'Košútska' and 'Diana I');
5. Since 1966: period of penetration of the "Soviet" wheat varieties into our production ('Mironovská 808', 'Bezostnatá 1', 'Belocerkevskaja 198').

Storage of genetic resources in the Genebank of the Slovak Republic

- **Base collection**

This collection contains all the original domestic varieties, landraces and other important genetic resources. The base collection is duplicated in the active collection. From the base collection the samples are not usually distributed. The seed is taken from the base collection only for regular testing of the germinating capacity (first test after 10 years) and not for research purposes. The samples are stored at -17°C with the assumption that their viability will last for up to 50 years. All accessions of which the countries of origin are Slovakia or former Czechoslovakia are stored in a safety-duplication collection in the Research Institute of Crop Production in Prague (RICP).

- **Active collection**

The active collection includes all genetic resources included in the collections currently being studied. The samples from the active collection are freely distributed to breeders and scientists and exchanged. They are stored at 2–5°C for 10-15 years according to the size of the seed reserves.

- **Working collection**

This collection is intended as an active collection for the needs of breeders and scientists; there are not enough seeds for storing, and multiplication is needeed.

The RIPP wheat collection currently contains 3732 accessions (Table 3). This includes 3361 accessions of winter wheat and 371 of spring wheat. Their distribution, according to status of sample and origin, is shown in Figs. 1-3.

Table 3. *Triticum* accessions maintained at the Genebank of the Slovak Republic

Type of collection	No. of samples
Base	451
Active	2631
Working	650
Total	**3732**

Fig. 1. Percentage of *Triticum* accessions according to status of sample.

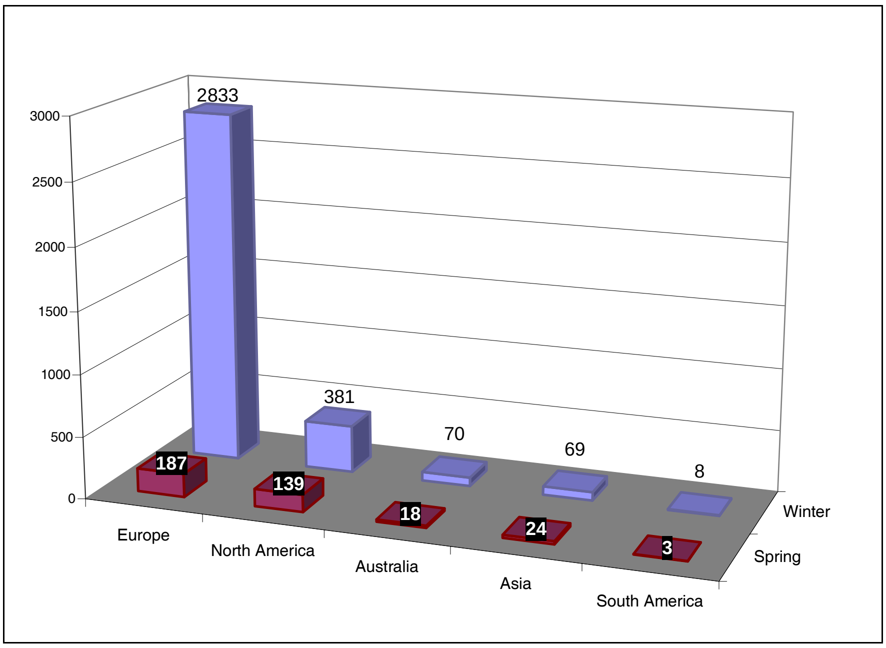

Fig. 2. Number of genotypes according to geographical origin.

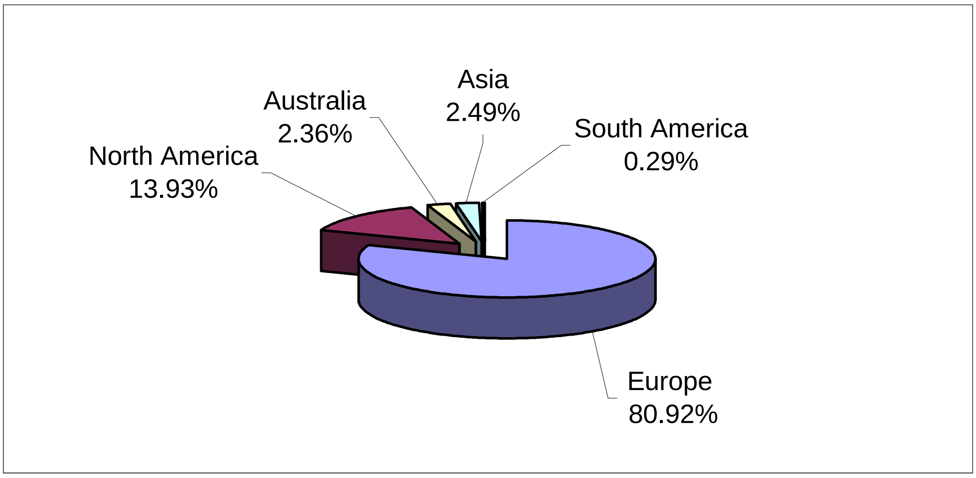

Fig. 3. Percentage of genotypes according to geographical origin.

Study and utilization of wheat genetic resources

The wheat accessions are evaluated under field conditions on the RIPP experimental station. The aims are:

- collecting and conservation (varieties, old historical material, landraces, breeding material, wild species, etc.);
- characterization and evaluation according to the standard descriptors (morphological characteristics, phenological stages, evaluation of yield characters, disease resistance and postharvest quality analyses);
- selection of suitable genotypes for breeding programmes.

At present about 45 morphological characters and economic traits are being studied.

Future and priorities

In recent years the RIPP has played an important role in genetic and breeding research on winter wheat.

Research deals with cultivation technology, evaluation of the collected genepool for morphological and yield characters, and analyses of DNA markers.

The main task in future will be the development of new wheat genotypes with introduced resistance genes *Lr19* and *Lr24* to wheat rust (*Puccinia recondita* f. sp. *tritici*) and the development of genotypes with resistance gene *Lr19* and alleles of the *Glu-1* locus controlling good breadmaking quality.

Molecular breeding approaches will be used for the introduction of new alleles. The selection process includes electrophoretic analyses of these proteins and detection of the uniformity of newly bred lines.

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Current status of the wheat collection maintained at the CRF-INIA (Spain) and research activities [68]

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Current status of the wheat collection maintained at the CRF-INIA

The Centre for Plant Genetic Resources (Centro de Recursos Fitogenéticos, CRF), located in Alcalá de Henares (Madrid), is under the responsibility of the National Institute of Food and Agrarian Research and Technology (Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, INIA) of the Spanish Ministry of Science and Technology. The aims of the CRF-INIA are the conservation of the base collection (-18°C, seed moisture <7%) of the Network of the National Plant Genetic Resources Programme, and the management and computerization of the Permanent Inventory of the Network. The aims of the CRF also include the conservation and regeneration of the active wheat collection (-4ºC, seed moisture <7%). The wheat collection at CRF consists of 2906 accessions.

The distribution of accessions according to sample status is given in Table 1 and shown according to their origin in Table 2.

Table 1. Composition of the CRF wheat collection according to sample status

Species	Sample status	Percentage	
		per type of sample	per taxon
T. monococcum L.	wild relatives	0.07	0.65
	local varieties	0.59	
T. turgidum L.	unknown	0.59	38.09
	wild relatives	0.10	
	local varieties	31.98	
	breeding material	3.20	
	commercial varieties	2.24	
T. timopheevi Zhuk.	local varieties	0.14	0.21
	breeding material	0.07	
T. aestivum (L.) Thell.	unknown	4.34	61.05
	local varieties	42.20	
	breeding material	2.44	
	commercial varieties	12.05	

Table 2. Composition of the CRF wheat collection according to country of origin

Country	%	Country	%	Country	%
Unknown	27.08	Great Britain	0.07	Romania	0.24
Argentina	1.00	Greece	0.17	Former Soviet Union	0.07
Australia	0.83	Hungary	0.14	Spain	53.96
Canada	0.31	India	0.28	Sweden	0.14
Czech Republic	0.03	Italy	3.27	Tunisia	0.10
Switzerland	0.17	Japan	0.34	Turkey	0.69
Algeria	0.31	Morocco	0.07	Uruguay	0.10
Egypt	0.10	Mexico	0.89	USA	3.72
Ethiopia	0.03	Portugal	4.75	South Africa	0.03
France	1.10				

[68] See also: "Status of the *ex situ* wheat collection at the CRF-INIA (Spain)", p. 282.

The status of the collection as regards characterization and evaluation is given in Table 3. All these data are computerized in an Access database.

Table 3. Characterization and evaluation status of the CRF wheat collection

Species	%	% of Spanish accessions	No. of descriptors used*
T. monococcum L.	0.45	0.83	16
T. turgidum L.	11.46	21.24	13
T. timopheevi Zhuk.	0.10	0.19	13
T. aestivum (L.) Thell.	14.22	26.34	13
Total	**26.23**	**48.60**	-

* (IBPGR/CEC 1985)

Inclusion of the Spanish collection in the EWDB

The CRF-INIA sent about 2800 passport records to the European Wheat Database (EWDB) in 1996. In March 2002 we checked those of our data loaded into the EWDB and sent our revised data to Iva Faberová. We also identified most foreign accessions with their country of origin in our collection. However, we have some accessions of unknown origin. We have not yet started using the six characterization descriptors recommended by the last meeting of the Wheat Working Group in 2001 (p. 134 *in* Maggioni *et al.* 2003), but we hope to achieve this soon. As regards the utilization of the EWDB Web application, we have used it sometimes to check some variety names.

Research activities: Identification of common duplicates in durum wheat with different types of characterization data

The main objective of our study was to assess the value of agromorphological (qualitative and quantitative) traits and gliadins for identification of duplicates in the durum wheat collection maintained at the CRF-INIA.

The search for duplicates focused on accessions with known identifiers and was limited to landraces and cultivars. Potential duplicates were identified initially based on similar accession names for the cultivars and similar local names and geographical origins for the landraces (van Hintum and Visser 1995). As a result of this search 106 cases of potential duplicates (92 landraces and 14 cultivars) were identified. The number of accessions involved in a duplicate varied from 2 to 12. The total number of accessions studied was 277, so approximately 28% of the collection consisted of accessions with duplicate names. These accessions were sown in the field in an augmented design (Petersen 1985).

- **Agromorphological and biochemical characterization**

All accessions were evaluated for 25 qualitative agromorphological characters (Table 4) and five quantitative agromorphological traits (Table 5).

For each accession, gliadins were extracted from flour milled from the same five plants used for the morphological characterization. The extracted proteins were fractionated by A-PAGE (lactic acid-polyacrylamide gel electrophoresis) following the method described by Lafiandra and Kasarda (1985).

Qualitative and quantitative agromorphological data were subjected to multivariate statistical analysis (Multiple Correspondence Analysis (MCA) and Principal Component Analysis (PCA) respectively) to detect the most useful discriminating characters. Genetic similarity between accessions was estimated by cluster analysis (UPGMA (unpaired group-mean analysis) aggregation method). The first 15 factorial axes scores from the MCA plus the first five factorial axes scores from the PCA (100% of the variance explained) were used as variables for the clustering analysis of qualitative plus quantitative data. It was expected that two potential duplicate accessions should present an aggregation level of zero or at least be lower than the maximum one found between two known distinct entries (Ortiz *et al.* 1998). Thus the first level of aggregation was selected to identify the agromorphological duplicates.

Table 4. Class partition and frequencies of each qualitative agromorphological character for 277 Spanish durum wheat varieties

VEGETATIVE

Qualitative character	Frequency
Growth habit (young)	
Prostrate	93.1
Upright	6.9
Auricle hairiness	
Absence	82.3
Presence	17.7
Auricle anthocyanin pigment	
Absence	1.8
Low	11.6
High	86.6
Flag leaf habit	
Erect	9.0
Recurved	65.0
Deflexed	26.0

SEED

Qualitative character	Frequency
Grain colour	
White	79.7
Red	20.3
Grain shape	
Oval	28.6
Long	71.4
Apical rachis hairiness	
Weak	98.2
Medium	1.8

INFLORESCENCE

Qualitative character	Frequency
Anther anthocyanin pigment	
Absence	20.9
Presence	79.1
Spike waxiness	
Absence	6.5
Presence	93.5
Mature spike habit	
Erect	22.4
Semierect	76.9
Deflexed	0.7
Spike neck shape	
Straight	79.3
Flexuous	20.7
Spike shape	
Pyramidal	80.1
Tapering	19.9
Lemna awn barbs	
Rough	98.9
Smooth	1.1
Awn colour	
White	20.0
Black at the base	69.5
Red to brown	10.5
Awnedness	
Awnless	4.7
Awned (3 to 8 cm)	1.5
Long awned (>8 cm)	93.8
Spike density	
Lax	2.2
Intermediate	67.4
Dense	30.4

Qualitative character	Frequency
Glume hairiness	
Absence	70.7
Presence	29.3
Glume colour	
White	54.3
Red to brown	35.2
Purple to black	10.5
Glume shape	
Circular	0.4
Oval	46.3
Long	53.3
Glume length	
Medium	31.9
Long	68.1
Glume internal hairs	
Weak	99.6
Strong	0.4
Glume-shoulder shape	
Sloping	6.9
Square	15.6
Elevated	64.1
Indented	13.4
Glume-shoulder length	
Narrow	88.4
Wide	11.6
Glume-beak curvature	
None	87.0
Medium	13.0
Glume-beak length	
Very short (<1 mm)	12.0
Short (1-2 mm)	59.8
Medium (2-5 mm)	27.2
Long (5-10 mm)	0.7
Very long (>10 mm)	0.3

Table 5. Mean and standard deviation of each quantitative agromorphological character for 277 Spanish durum wheat varieties

Quantitative character	Mean	Standard deviation
Days to flowering	164.52	4.06
Days to maturity	206.64	4.51
Plant height (cm)	117.21	16.67
Spike length (cm)	89.58	12.33
Spikelets per spike	21.49	5.52

- **Relationships between agromorphological and gliadin data**

The qualitative characters that contributed more strongly to the variance explained by the first three factors of the MCA were those related to the inflorescence and to the auricles of the leaf. The rest of the vegetative traits and seed characters showed low contributions. With respect to the quantitative characters they showed a high discriminating power, particularly plant height, days to flowering and days to maturity.

Sixty potential duplicates were established with the qualitative plus quantitative data, some of them showing slight agromorphological differences. The duplication was verified at the gliadin level in 54 cases (90%). In one out of the six cases of disparity (morphological similarity but differences in gliadin patterns) the accessions were different in one morphological character and in an α-gliadin block coded by one allele (Kudryavtsev *et al.* 1996). These two accessions can be considered as biotypes. In the rest of disparate cases, the accessions were different in no more than three agromorphological descriptors (mature spike habit and/or some inflorescence characters). In these cases, gliadin characterization permitted differentiation of similar material with greater refinement than agromorphological data. In contrast, 14 cases of potential duplicates showing similarity in gliadin patterns were not verified in the quantitative plus qualitative dendrogram. They differed in a maximum of five agromorphological characters, the most frequent being glume beak length, days to flowering, glume length, mature spike habit and/or flag leaf habit. This result revealed that accessions with similar biochemical data may differ in just a few important agromorphological characters, e.g. two accessions derived from the 'Alaga' landrace had the same gliadin pattern and different values for seed colour and days to flowering. In the present work the probability that identical gliadin pattern was a result of chance is extremely low given the number of loci screened. Probably, these accessions had been split into sub-samples in the past, each containing one morphotype, and this could be the cause of the discrepancy between gliadin and agromorphological similarity. In fact, all the cases which were identical in gliadin and qualitative traits appeared as duplicates in the qualitative plus quantitative data dendrogram.

Our results show that genetic similarity measured on the basis of gliadins generally agreed with that obtained from the agromorphological characters, demonstrating the usefulness of gliadins to verify duplicates in wheat. Furthermore, to diminish redundancy in our durum wheat collection we should consider as duplicate accessions only those that are agromorphologically similar and possess the same electrophoretic banding pattern.

- **Present and future lines of work**

Currently, our objectives are to carry out a more intense genetic study of gliadin proteins by identification of the alleles at the main loci *Gli-A1*, *Gli-B1*, *Gli-A2*, *Gli-B2* and *Gli-B5*. These studies will allow us to measure genetic variability more adequately. Moreover we have initiated the analysis of durum wheat accessions by means of microsatellites in order to examine their usefulness in variety identification and their relationships with agromorphological and gliadin data.

Acknowledgements

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Wheat genetic resources in Switzerland[69]

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Conservation of plant genetic resources in Switzerland had already started more than 100 years ago. The oldest indication of wheat collecting dates back to 1900 and the very landrace collected then is still available from the genebank of the Federal Research Station for Plant Production of Changins (RAC). In Switzerland, wheat genetic resources conservation is carried out by three organizations. RAC holds an *ex situ* collection of 7258 accessions, while the foundation "Pro Specie Rara" and the "Sortengarten Erschmatt" conserve and maintain 25 and 96 accessions respectively in on-farm schemes. The accessions conserved on-farm are also included in the genebank at the RAC.

Not all these accessions are included in the European Wheat Database (EWDB). From the genebank RAC 4362 accessions are included, 4 from "Sortengarten Erschmatt", and none from "Pro Specie Rara". An update will be carried out when the EURISCO database becomes available.

Safety-duplication of the RAC accessions is ensured by IPK-Gatersleben, Germany.

The origin, growth type and sample status of the accessions are indicated in Tables 1, 2 and 3 respectively.

Table 1. Accessions in the Swiss wheat collection according to geographic origin

Region	No. of accessions
Europe	6175
North America	344
Africa	61
Asia	72
South America	300
N.W. Pacific	64
Near East	37
Unknown	324

Table 2. Accessions in the Swiss wheat collection according to growth type

Growth type	No. of accessions
Winter	5228
Spring	2030
Unknown	121

Table 3. Accessions in the Swiss wheat collection according to sample status

Sample status	No. of accessions
Wild	37
Landrace	2490
Breeding line	1902
Cultivar	1435
Mutant	69
Unknown	1446

[69] See also "Wheat genetic resources in Switzerland – Update 2005", p. 283.

During the first meeting of the ECP/GR Working Group on Wheat (2001) six characterization descriptors were added to the EWDB (p. 134 *in* Maggioni *et al.* 2003). For plant height, data are available. For awnedness, grain colour, glume colour and glume hairiness only an indication of presence or absence is available. To include the grades of difference requested, all the accessions need to be analyzed. The Swiss Government has prepared a National Plan of Action for the conservation and sustainable use of plant genetic resources. For the second phase of this programme (2003-2006), CHF 2.5 million are available for projects dealing with plant genetic resources. For this period 62 projects were submitted and 50 were accepted or partially accepted. Two projects deal with wheat. These two projects concern on-farm conservation in two different parts of Switzerland as well as characterization, evaluation and documentation. Another project financed by the Federal Office for Agriculture is the creation of the National Database for Plant Genetic Resources. This database is being developed by the Swiss Commission for the Conservation of Cultivated Plants (CPC) in close collaboration with the RAC. The first phase of the creation of this database is finished and it is available on the Internet at http://www.cpc-skek.ch/.

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Wheat and triticale genetic resources in Ukraine [70]

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Introduction

The National Plant Genebank in Ukraine was established from a beginning in 1992 when it was based on the collections of leading institutes and experimental stations of the Ukrainian Academy of Agricultural Sciences, the Ministry of Agrarian Policy of Ukraine and the National Academy of Sciences of Ukraine, dealing with breeding and genetics. The National Centre for Plant Genetic Resources of Ukraine (NCPGRU) was established at the Yurjev Institute of Plant Production in Kharkiv. The National Centre coordinates the research work on plant genetic resources of 40 institutions. The plant genebank of Ukraine contains 125 000 accessions of 310 crop species and 500 wild species which are of practical significance for the Ukrainian people.

The collections of wheat (16 386 accessions) and triticale (2751 accessions) were mainly based on the collections of the Yurjev Institute of Plant Production in Kharkiv (IR), the Breeding and Genetics Institute in Odessa (BGI), the Myronivskiy Wheat Institute V.M. Remeslo (MWI) and the Ustymivska Experimental Station of Plant Production (UES), which in the past had been included in the system of the All-Union Institute of Plant Industry N.I. Vavilov.

Contents of the National Wheat and Triticale Collections in Ukraine

At present, the National Wheat Collection contains 16 386 accessions (Table 1). It includes 23 accessions of diploid species, 2778 of tetraploid species, 13 849 of hexaploid species, 6 synthetic octoploid forms, 83 tetra- and hexaploid synthetic forms and 55 wild wheat relatives (*Aegilops* and *Dasypyrum*).

The predominant species in the collection are *Triticum aestivum* (13 818 accessions) and *T. durum* (2139 accessions) (Table 2).

Table 1. Composition of the National Wheat Collection of Ukraine by taxonomic group

Taxonomic group	No. of accessions	%
Diploid (2n=2x=14) species	23	0.14
Tetraploid (2n=4x=28) species of *T. timopheevii* group	8	0.06
Tetraploid (2n=4x=28) species of *T. turgidum* group	2370	14.4
including *T. durum*	2139	13.1
Hexaploid (2n=6x=42) species	13849	84.5
including *T. aestivum*	13818	84.3
Octoploid (2n=8x=56) synthetic forms	6	0.04
Other synthetic forms (2n=28, 42)	83	0.52
Wild wheat relatives	55	0.34
Total	**16386**	**100.0**

[70] See also "The Ukrainian collections of wheat and triticale genetic resources", pp. 286-288.

Table 2. Composition of the National Wheat Collection of Ukraine by taxon

Ploidy level	Taxon	No. of accessions
2n=2x=14	*T. urartu* Thum. ex Gandilyan	2
	T. monococcum L.	16
	T. boeoticum Boiss.	4
	T. sinskayae A.Filat. et Kurk.	1
		Total = 23
2n=4x=28	*T. timopheevii* Zhuk.	5
	T. araraticum Jakubz.	2
	T. militinae Zhuk. et E.Migusch.	1
	T. durum Desf.	2139
	T. turgidum L.	12
	T. dicoccoides Koern. ex Schweinf.	3
	T. dicoccum (Schrank) Schübl.	173
	T. carthlicum Nevski.	15
	T. polonicum L.	6
	T. turanicum Jakubz.	3
	T. ispahanicum Heslot	1
	T. aethiopicum Jakubz.	9
	T. karamyschevii Nevski	1
		Total = 2370
2n=6x=42	*T. aestivum* L. em. Fiori et Paol.	13818
	T. compactum Host.	7
	T. spelta L.	14
	T. macha Dekapr. et Menabde	1
	T. sphaerococcum Perciv.	6
	T. petropavlovskyi Udacz. et E.Migusch.	1
	T. vavilovii Jakubz.	1
	T. kiharae Dorof. et E.Migusch.	1
		Total = 13849
2n=8x=56 (synthetic species)	*T.* x *timococcum* Zhuk.	1
	T. x *fungicidum* Zhuk.	1
	T. timonovum Heslot et Ferrary	1
	Amphidiploid *(Ae. ventricosa* x *T. dicoccum)*	1
	Amphidiploid *(T. dicoccum* x *Ae. triuncialis)*	1
	Aegilotricum x *cylindroaestivum*	1
		Total = 6
Other synthetic forms (amphydiploids) 2n=28, 42	Wheat interspecific Wheat x *Aegilops* Wheat x *Dasypyrum* Wheat x *Elymus*	**83**
Wild wheat relatives	*Aegilops, Dasypyrum*	**55**
Grand total		**16386**

The collections of **bread wheat** are concentrated in five holding institutions located in different zones of the Ukraine (Table 3). The largest collection of spring and winter forms is held at the Yurjev Institute in the eastern forest-steppe zone of Ukraine; other collections include winter forms in BGI (southwestern steppe) and UES (northern steppe); winter and spring forms in MWI (central forest-steppe); and winter accessions under irrigated conditions at the South Region Agricultural Research Institute (southern steppe).

Table 3. The Ukrainian *Triticum aestivum* collection and holding institutions

Holding institute	No. of accessions				
	Total	Winter	Spring	Documented for passport data	In medium-term storage
Yurjev Plant Production Institute	7915	4965	2950	5876	4536
Ustimivska Experimental Station	2364	2364	-	1394	1249
Breeding and Genetics Institute	4303	4303	-	1679	105
Myronivskiy Wheat Institute	2580	1557	1023	738	20
South Region Agricultural Research Institute	363	363	-	16	3
Total	**13818 (3707)***	**13552**	**3973**	**5996 (3707)***	**5913**

* duplicated accessions

Some of the *T. boeoticum, Aegilops cylindrica, Ae. triuncialis, Ae. biuncialis, Ae. geniculata, Ae. triaristata, Ae. tauschii* and *Dasypyrum villosum* accessions were collected by expeditions of the NCPGRU in the steppe near the Black Sea, the Crimea and the Caucasus. One of the expeditions was carried out with financial assistance of the USDA-ARS and the participation of two American scientists (Dr Harold E. Bockelman, National Small Grains Germplasm Research Facility and Dr Richard C. Johnson, Washington State University, Regional Plant Introduction Station). The other accessions of wild relatives and amphidiploid forms were obtained from VIR, ICARDA, the Czech genebank, the Armenian Agricultural University, the Institute of Breeding and Genetics of Azerbaijan, the Breeding and Genetics Institute of the Ukrainian Academy of Agricultural Sciences (UAAS, Odessa); we are very grateful to the donors.

The predominant part of the material includes lines possessing valuable agrobiological traits (51.9%) and advanced cultivars (44.8%) (Fig. 1). The Ukrainian cultivars are represented by highly winter-hardy and drought-tolerant cultivars ('Kooperatorka', 'Odeska 16', 'Ferrugineum 1239', 'Lutescens 329', 'Myronivska 808', 'Kharkivska 63', etc.).

Spring forms make up 22.7% of the collection and winter forms 77.3%.

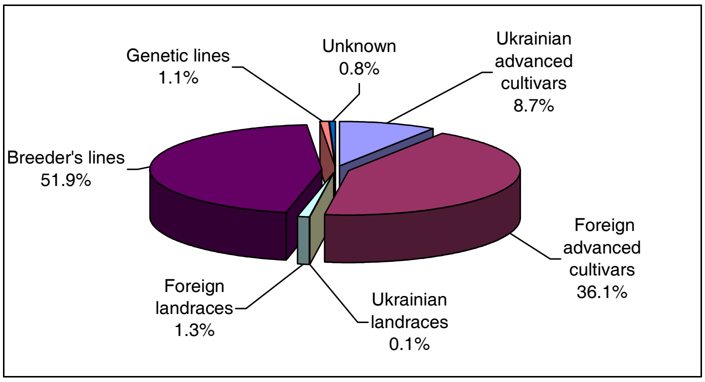

Fig. 1. Status of samples belonging to the Ukrainian *Triticum aestivum* collection.

The collections of **durum wheat** are held in the Yurjev Institute, BGI and MIW (Table 4).

Table 4. The Ukrainian *Triticum durum* collection and holding institutions

Holding institute	No. of accessions				
	Total	Winter	Spring	Documented for passport data	In medium-term storage
Yurjev Plant Production Institute	1554	107	1426	1554	883
Breeding and Genetics Institute	475	475	-	193	95
Myronivskiy Wheat Institute	300	-	300	100	2
Total	**2418 (90)***	**582**	**1726**	**1657 (190)***	**980**

* duplicated accessions

The cultivars from Ukraine and other countries make up 47.8% of the collection, breeding lines 47.1% and landraces 2% (Fig. 2). Spring forms prevail in the collection (74.8%).

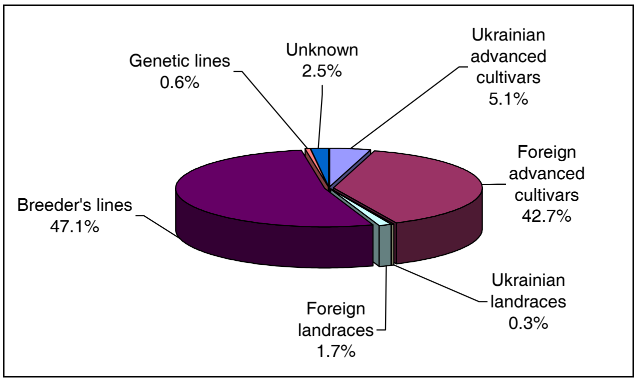

Fig. 2. Status of samples belonging to the Ukrainian *Triticum durum* collection.

The Ukrainian **triticale** collection includes 2751 accessions (Table 5). The collection of winter and spring forms was established at the Yurjev Institute. A duplicate collection of some of the winter and spring forms is maintained in the UES. Breeding lines prevail in the collection (81.7%) (Fig. 3). The genetic diversity of triticale was initially represented by primary forms created mainly on the basis of tetra- and hexaploid wheats and diploid rye. During the past two decades, the diversity has been significantly broadened with the creation of secondary forms using interline hybridization, hybridization of triticale with wheat, and hybridization between octo- and hexaploid forms.

Table 5. The Ukrainian triticale collection and holding institutions

Holding institute	No. of accessions				
	Total	Winter	Spring	Documented for passport data	In medium-term storage
Yurjev Plant Production Institute	2375	1495	880	2427	487
Ustimivska Experimental Station	522	240	282	146	146
Total	**2751 (146)***	**1735**	**1162**	**2427 (146)***	**633**

* duplicated accessions

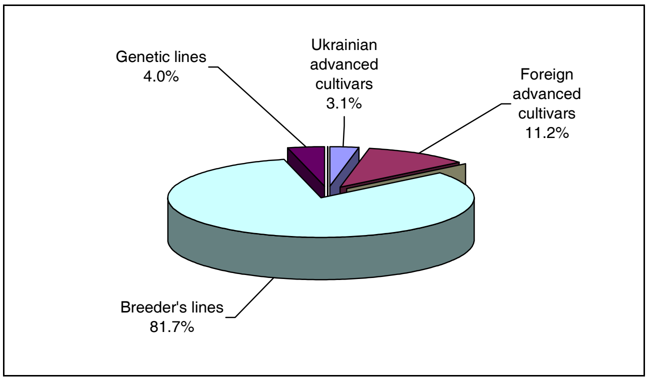

Fig. 3. Status of samples belonging to the Ukrainian triticale collection.

Hexaploid forms predominate in the collection (97.5%). Octoploids and tetraploids are represented by several original forms. Winter triticale makes up 59.9% of the collection and spring, 40.1%.

In the collections of bread and durum wheat and triticale, most accessions (66.3%) were acquired from European countries (Table 6). Among the 24.2% of accessions obtained from North America, most are spring forms from CIMMYT.

Table 6. Continents of origin of the wheat and triticale accessions in the Ukrainian collections

Continent	No. of accessions		
	Triticum aestivum	*Triticum durum*	Triticale
Europe	9305	994	2102
Asia	1056	193	17
North America	2818	817	616
South America	331	53	10
Australia	101	7	3
Africa	207	75	3
Total	**13818**	**2140**	**2751**

Characterization and evaluation

In order to identify the accessions, their botanical varieties were determined and characters described according to UPOV guidelines.

The accessions in the collection are being studied for the major phenotypic characters of economic value using the methodological guidelines of VIR (Merezhko *et al.* 1999) and the COMECON descriptors (Anonymous 1974).

In the first stage all accessions are sown according to the standard method (Merezkho *et al.* 1999). Data are recorded on phenology, plant height, hardiness to unfavourable factors (winter and drought), resistance to diseases and pests, yield from 1 m^2, 1000-seed weight and grain filling.

The initial trial is repeated for 3 years. The accessions selected for high values of the individual or combined traits are then studied for 2-3 years in replicated trials. In addition, some of the accessions are studied for plant structure, disease resistance in an infective environment, grain quality and winter hardiness. For winter accessions, this is achieved by keeping them in a freezing chamber (Table 7).

Table 7. Evaluation and characterization of the Ukrainian wheat and triticale germplasm collections

Crop	No. of accessions / no. of traits				
	Main agronomic traits	Additional traits			
		Winter hardiness	Disease resistance	Plant structure	Quality test
Bread wheat					
Winter	10920 / 21	545 / 5	3460 / 2	1128 / 9	956 / 16
Spring	3108 / 17	-	825 / 3	565 / 8	310 / 16
Durum wheat					
Winter	492 / 21	90 / 5	-	476 / 8	80 / 1
Spring	1526 / 17	-	290 / 3	350 / 8	196 / 1
Triticale					
Winter	1495 / 12	120 / 5	-	633 / 8	200 / 1
Spring	1162 / 12	-	420 / 2	110 / 8	315 / 16

Some accessions are subject to more thorough genetic research (molecular markers).

Based on the research results, the following collections are built: base, core, trait, genetic, special, working, educational and duplicate collections.

The trait collections are in high demand by users. They contain accessions which show in their phenotypes a certain level of individual or combined traits. The key elements of a trait collection are standard samples which have a stable manifestation level of a trait at a higher productivity level (Ryabchoun and Boguslavskiy 2002).

Documentation

The Information System "Plant Genepool" is maintained at NCPGRU. It includes databases, references, programs for database development and analysis.

New accessions introduced into the National Genebank are registered in the "Introduction database" which contains three sections: breeding material, landraces and wild forms.

The accessions included in the collections are documented for passport data. At present, passport data are available for 7938 wheat accessions (5996 bread wheat, 1652 durum wheat, 290 neglected species, wild relatives and synthetic forms) and 2427 triticale accessions. The wheat and triticale passport data have been prepared for inclusion in the European catalogue EURISCO.

Characterization databases were developed using Visual FoxPro. Databases were created to record the evaluation data on accessions (agronomic traits); in the case of bread wheat, there is a special database for the electrophoretic patterns of storage proteins.

A database of wheat and triticale varieties' pedigrees is under development.

The development of these computerized databases is enhancing considerably the access by users to the germplasm held in the collections and the effectiveness of the further formation of different types of collections.

Storage

Suitable conditions for medium- and long-term storage of seed are available at NCPGRU. The seed of the wheat and triticale national collection grown in the holding institutes is deposited for medium-term storage into the National Depository. The seed is dried to a moisture content of 6-7%, placed in hermetically sealed glass containers or multilayer bags and stored at low temperatures (+4°C) in a chamber, or at medium temperature (+7°C) in the depository. Medium-term storage facilities contain 5913 accessions of bread wheat, 980 of durum wheat and 633 of triticale.

In the UES the duplicate collection is stored in similar conditions.

Active collections are stored in non-regulated conditions and are regenerated after every 5 to 6 years.

Availability of material to users

The material of the main collection is freely accessible to users as small seed amounts upon signing of a Material Transfer Agreement. Transfer of trait collections, accompanied by their evaluation results, is subject to a special agreement. Valuable registered accessions are transferred according to the conditions agreed with the author or owner, most often by exchange.

In 2002 the following numbers of package samples were distributed to users:

- bread wheat: 3204 winter, 217 spring;
- durum wheat: 174 winter, 66 spring;
- triticale: 55 winter, 59 spring.

The educational collections are sent to agricultural universities. Requests for samples from breeders, researchers and private persons are responded to appropriately.

Information about the collections has been published in the journals "*Plant Genetic Resources*", "*Breeding and Seed Production*" edited by the Yurjev Institute of Plant Production, and other publications (Kirjan and Kolotilov 2001; Ryabchoun 2001).

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Other cereals

The European Triticale Database (ETDB)

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Introduction

The creation of a European Triticale Database (ETDB) was discussed during a workshop on wheat genetic resources held in Paris, France, on the 21-23 March 1996. A first contact with the European genebanks showed that 12 323 triticale accessions were conserved in 14 different countries and that the genebank managers were very interested in participating in the ETDB.

ETDB status 2003

The current ETDB is based on MS Access and records 5203 accessions from nine European genebanks (Table 1). The database uses the FAO/IPGRI *Multi-crop Passport Descriptors*. No characterization descriptors are included yet. Analysis of the available data shows serious gaps in the descriptors of the accessions. For instance, 2165 accessions are winter type, 846 spring and 46 intermediate. The seasonal growth class of the remaining 2146 accessions is unknown. Triticales may have different ploidy levels: 119 accessions of the ETDB are tetraploids, 2136 are hexaploids and 310 are octoploids. The ploidy level of the other 2638 accessions is unknown. The "sample status" descriptor shows that most (3278) of the accessions are breeders' lines, 5 are mutants or genetic stock and 553 are advanced cultivars.

Table 1. Contributions of European genebanks to the ETDB

INSTCODE	Genebank	No. of records
AUT001	Federal Office for Agrobiology, Linz, Austria	17
CHE001	Federal Station for Plant Production, Changins, Switzerland	784
DEU001	Institute for Crop Science (FAL), Braunschweig, Germany	498
DEU416	Institut für Pflanzengenetik (IPK), Gatersleben, Germany	1090
CZE122	Research Institute of Crop Production (RICP), Prague, Czech Republic	333
ESP004	Centro de Recursos Fitogenéticos, Alcalá de Henares, Spain	511
LVA006	Priekuli State Plant Breeding Station, Priekuli, Latvia	179
RUS001	N.I. Vavilov Institute, St. Petersburg, Russian Federation	1255
SVK001	Plant Breeding Station, Piešťany, Slovakia	536
Total		**5203**

Triticale is a new species and therefore has some peculiarities. The recent creation of this crop is illustrated by the fact that 63% of the accessions are breeders' lines, and by the absence of landraces.

Some of the accessions lack genetic stability. Chromosome counts of octoploid triticales of the genebank of Changins showed the difficulty in finding euploid plants for several accessions, and in most of the accessions aneuploids were observed. This can lead to a decrease in fertility and increases the risk of outcrosses.

Future activities

- To make the ETDB accessible on the Internet (to be carried out before the end of 2003);
- To complete the ETDB (only 42% of all European triticale accessions have been included so far);
- To fill the gaps in the list of passport data by contacting the genebank managers or by downloading from EURISCO;
- To study the possibility of including characterization and evaluation data. This will increase the value of the ETDB by offering more information about the accessions to the users.

Minor cereals and pseudocereals

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Introduction

The Network Coordinating Group on Minor Crops met for the first time in Turku (Finland) in 1999.[71] The initial objectives were the selection of species that are to be considered as minor, the identification of priority species, and the starting of data collecting and evaluation.

Minor cereal crops/species

An open list of minor species was compiled by minor cereals and pseudocereals experts contacted by the author (Table 1).

Table 1. Open list of minor cereal crops/species

Crop		Botanical name
Cereals		
Hulled wheats	1. Einkorn	*Triticum monococcum* L.
	2. Emmer	*Triticum dicoccon* Schrank (Schuebl.)
	3. Spelt wheat	*Triticum spelta* L.
Other wheat species	4. Polish wheat	*Triticum polonicum* L.
	5. Club wheat	*Triticum compactum* Host.
	6. Turgidum wheat	*Triticum turgidum* L.
	7. Carthlicum wheat	*Triticum carthlicum* Nevski
	8. Macha wheat	*Triticum macha* Dekapr. et Menabde
Rye	9. Semi-perennial rye	*Secale cereale* L. var. *multicaule* Metzg.
Barley	10. Naked barley	*Hordeum vulgare* L. subsp. *distichon* (L.) Koern. var. *nudum* L.
Oat	11. Naked oat	*Avena nuda* L.
Sorghum and millets	12. Sorghum	*Sorghum bicolor* (L.) Moench
	13. Common millet	*Panicum miliaceum* L.
	14. Foxtail millet	*Setaria italica* (L.) P. Beauv.
	15. Barnyard millet	*Echinochloa frumentacea* (Roxb.) Link.
	16. Crabgrass	*Digitaria sanguinalis* (L.) Scop.
Pseudocereals		
Buckwheat	17. Common buckwheat	*Fagopyrum esculentum* Moench
	18. Tartary buckwheat	*Fagopyrum tataricum* (L.) Gaertn.

Selection of priority crops

On the basis of the initial information, buckwheat and millet should be considered as priority minor cereals. Both of these crops meet the "criteria for minor crops" referred by the Network Coordinating Group on Minor Crops (risk of genetic erosion, economic importance, regional or sub-regional distribution, traditional crops in Europe, indigenous origin, use of the crops, present use of the genetic resources for plant breeding or other research, level of available genetic diversity).

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[71] Note from the ECP/GR Secretariat: the Minor Crops Network was partially merged with the Vegetables Network at the end of 2003, giving rise to the Vegetables, Medicinal and Aromatic Plants Network (see Report of the Ninth Meeting of the ECP/GR Steering Committee, 22-25 October 2003, Menemen, Izmir, Turkey – http://www.ecpgr.cgiar.org/SteeringCommittee/Outcome_SC9/SC9Report_nocover.pdf). Activities on non-vegetable minor crops can still be initiated within the context of the other existing networks, i.e. the Cereals Network in the case of minor cereals.

Within Europe, some relatively large national collections of buckwheat and millet exist but up to now no international databases have been created. The situation is relatively better for other cereals (hulled wheats, naked forms of barley and oat and also semi-perennial rye), which are traditionally included in the collections of major cereals and have also been included within the scope of existing ECP/GR Cereal Working Groups.

Collecting information

In order to make progress on the open list of minor cereals crops/species inventory, forms were prepared and sent by email to most European countries and Israel. The tables were designed in such a way that the contacted person or another person nominated for every country could easily fill them in and return them to us. The main purpose of collecting such data was to find out whether the listed crops are represented in national collections or not. Contact persons were asked to state the number of accessions, status and availability and also their use, if known.

Results

From the 33 countries contacted only 12 responded. Data about minor cereals and pseudocereals were provided by Austria, Czech Republic, Hungary, Israel, the Nordic countries (responses from Finland and Sweden for the Nordic Gene Bank), Slovakia and Switzerland; Estonia, Macedonia FYR and Malta reported that such information was not available but Estonia expressed the wish to participate in our activities. The national inventory of minor crops is in progress in Ireland.

- **Minor wheat species**

According to the data received, a large part of the national collections is composed of minor *Triticum* species (Table 2). The biggest collections of *Triticum* species are in Switzerland, where a large number of spelt wheats has been collected, and in Israel with significant collections of einkorn, spelt wheat and turgidum wheat.

Table 2. Minor wheat (*Triticum*) species

Crop / species	Country							
	Austria	Czech Republic	Hungary	Israel	Nordic countries (NGB)*	Slovakia	Switzerland	Total
Einkorn *T. monococcum*	3	56	109	481	66	15	22	**752**
Emmer *T. dicoccon*	11	102	39	64	21	7	84	**328**
Spelt wheat *T. spelta*	14	81	53	336	20	18	2263	**2785**
Polish wheat *T. polonicum*	2	19	1	6	4	13	5	**50**
Club wheat *T. compactum*	0	49	0	3	11	5	32	**100**
Turgidum wheat *T. turgidum*	2	55	22	596	14	20	37	**746**
Carthlicum wheat *T. carthlicum*	1	16	11	11	3	4	4	**50**
Macha wheat *T. macha*	1	6	4	3	2	0	6	**22**
Total	**34**	**384**	**239**	**1500**	**141**	**82**	**2453**	**4833**

* data includes all NGB accessions (Sweden, Finland, Norway, Denmark, Iceland)

- **Minor rye, barley, oat and sorghum species**

These collections are listed in Table 3. Semi-perennial rye is maintained in Switzerland, Czech Republic and also in Slovakia (1 accession). The biggest collections of naked barley are held in the Czech Republic and at the Nordic Gene Bank, while Slovakia has the widest collection of naked oat. Sorghum has been collected mainly in the warmer parts of Europe, and Hungary has the biggest collection of this species.

Table 3. Minor species of rye, barley, oat and sorghum

Crop / species	Country							
	Austria	Czech Republic	Hungary	Israel	Nordic countries (NGB)*	Slovakia	Switzerland	Total
Semi-perennial rye *Secale cereale* var. *multicaule*	0	2	0	0	0	1	21	**24**
Naked barley *Hordeum vulgare* subsp. *distichon* var. *nudum*	5	36	0	0	0	0	10	**51**
Naked oat *Avena nuda*	0	8	6	0	3	18	1	**36**
Sorghum *Sorghum bicolor*	2	1	539	61	0	0	1	**604**
Total	**7**	**47**	**545**	**61**	**3**	**19**	**33**	**715**

* data includes all NGB accessions (Sweden, Finland, Norway, Denmark, Iceland)

- **Millet and small millets**

Regarding common millet and "small millets" there are important collections in Hungary and the Czech Republic (Table 4). The group of "small millets" is represented mostly by foxtail millet (*Setaria italica*). There are few accessions of barnyard millet (*Echinochloa frumentacea*) and crabgrass (*Digitaria sanguinalis*) in the national collections of the represented countries.

Table 4. Minor species in the group of millet and "small millets"

Crop / species	Country							
	Austria	Czech Republic	Hungary	Israel	Nordic countries (NGB)*	Slovakia	Switzerland	Total
Common millet *Panicum miliaceum*	10	162	210	1	0	53	6	**442**
Foxtail millet *Setaria italica*	0	21	109	0	0	1	3	**134**
Barnyard millet *Echinochloa frumentacea*	0	1	5	0	0	0	0	**6**
Crabgrass *Digitaria sanguinalis*	1	3	0	0	0	0	0	**4**
Total	**11**	**187**	**324**	**1**	**0**	**54**	**9**	**586**

* data includes all NGB accessions (Sweden, Finland, Norway, Denmark, Iceland)

- **Buckwheat**

Significant collections of common buckwheat and tartary buckwheat are found in the Czech Republic and Hungary. Some buckwheat accessions are kept also in Austria (Table 5).

Table 5. Minor buckwheat species

Crop / species	Country							
	Austria	Czech Republic	Hungary	Israel	Nordic countries (NGB)*	Slovakia	Switzerland	Total
Common buckwheat *Fagopyrum esculentum*	30	121	100	8	10	0	9	**278**
Tartary buckwheat *Fagopyrum tataricum*	4	16	40	0	0	0	0	**60**
Total	**34**	**137**	**140**	**8**	**10**	**0**	**9**	**338**

* data includes all NGB accessions (Sweden, Finland, Norway, Denmark, Iceland)

The results presented above do not yet seem to us to be very valuable, mainly as the data on the collections which are probably the biggest and the most important (Ukraine, Russia) are missing. So we would like to appeal to all participants in the ECP/GR Cereal Network Meeting to collect and deliver the above data on minor cereals and pseudocereals.

Ongoing and further activities

The original aim of our activity was to gather as much information as possible and prepare all data for the development of a database. But at present the European project EPGRIS is already dealing with the collection of passport data for all crops, so the purpose of the activity was adjusted to be: "acquire essential characterization and evaluation data about minor cereals and pseudocereals once passport data are gathered by EPGRIS". Further assessment of data concerning minor cereals and pseudocereals obtained from the database remains to be accomplished. There is also a need to identify duplicates within the same species and eliminate them. Further national contact persons should be nominated to participate in the activity, as well as the curators of national collections, to receive important information for the identification of forms of certain minor species, which cannot be achieved from the databases alone. This problem has been observed in the barley and oat databases where it is impossible to identify unhulled forms.

Further aims which remain are to distribute collected data within different research areas and projects, and to disseminate them to the public and among those who are in need of such information throughout the European region and worldwide.

The identification of registered buckwheat varieties (genotypes) using electrophoresis is an activity that could be carried out in the Czech Republic. The project was originally focused on European registered buckwheat varieties, but since most countries do not have their own registered varieties it was decided to explore registered buckwheats worldwide, identify them electrophoretically and organize the acquired data in a catalogue of buckwheat electrophoretic spectra.

Further activities will include cooperation with other organizations and institutes working on this group of minor cereals and pseudocereals (ICUC (International Centre for Underutilized Crops), GFU (Global Facilitation Unit for Underutilized Species), NGOs, etc.) and organizing scientific events on minor crops (9th International Symposium on Buckwheat in Prague, August 2004 – http://www.vurv.cz/buckwheat).

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Reports on activities on cereal genetic resources

Building a Small Grains Genetic Resources Centre at the INRA Clermont-Ferrand Research Unit

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Introduction

The "Biological Resource Centre" (BRC) concept was developed during wide-ranging discussions at the OECD (Organisation for Economic Co-operation and Development). France leads the Task Force on BRCs. *"Biological Resource Centres are an essential part of the infrastructure underpinning life sciences and biotechnology. They consist of service providers and repositories of the living cells, genomes of organisms, and information relating to heredity and the functions of biological systems. BRCs contain collections of cultivable organisms (e.g. micro-organisms, plant, animal and human cells), replicable parts of these (e.g. genomes, plasmids, viruses, cDNAs), viable but not yet cultivable organisms, cells and tissues, as well as databases containing molecular, physiological and structural information relevant to these collections and related bioinformatics."* (definition based on the one adopted at the 1999 Tokyo Workshop on Biological Resource Centres).

Since 2002, INRA has received funds to develop projects linked to the BRC concept. All cereal genetic resources accessions previously originating from different INRA locations have now been grouped together at Clermont-Ferrand. New facilities have been built to store all accessions in one location.

Contents and description of collections

The INRA Clermont-Ferrand Centre currently comprises more than 10 000 hexaploid wheats (mainly *T. aestivum*) and 2000 accessions of wild relatives (tetraploid and diploid wheat). Other cereal crop species are also conserved at this Centre: barley (6500 accessions), triticale (1000 accessions), oats (700 accessions) and rice (50 accessions). A great effort has been made to eliminate all duplicates within several INRA locations (Rennes, Montpellier, Estrées-Mons, Dijon, Le Moulon) in order to keep in the Central Genebank only one stock for each accession). New accessions are introduced every year, originating from institutes or organizations in different countries through the exchange of germplasm, or from international nurseries: they consist of registered cultivars, breeding lines and also landraces. A preliminary evaluation is carried out in the field nursery and in the laboratory for agronomic and technological traits, respectively. The main agronomic traits evaluated are heading date, height, response to diseases (powdery mildew and rusts), cold tolerance and 1000-kernel weight. Technological traits are mainly the NIRS spectra obtained from whole grains. Equations are used to calculate protein content and hardness after calibration. Other quality tests such as the Zeleny or SDS sedimentation test, and the Pelshenke or Chopin alveograph are carried out on newly introduced accessions. The data obtained and the degree of novelty allow us to select which accessions will be included in the collection.

Recently, about a third of the bread wheat collections (about 3500 accessions) have also been evaluated for molecular diversity, using a set of 42 microsatellites markers (one per chromosome arm). Diversity calculated from all the evaluation data may eventually allow us to distinguish groups of diversity which will assist in building a core collection.

The French evaluation network involving INRA research stations and private breeders was established in 1988 to share the work of evaluation and regeneration of wheat genetic resources. It allows breeders to obtain new potential breeding material in order to increase the genetic diversity of breeding parents.

Management of collections

Accessions are first regenerated when the stock quantity falls under a defined level, or otherwise, regularly every 15 years. A means of automating the sowing list is being developed.

After harvest, the seeds are dried in a drying chamber under 30% relative air humidity to less than 10% moisture content, and packaged in Minigrip plastic bags.

Seed stocks are stored long term in a cold chamber at +4°C and 30% relative air humidity. Two types of stocks are conserved: a regeneration stock, in which a part originates from self-pollinated ears and a part from free-pollinated ears, and a distribution stock. Each stock is kept in plastic containers. A module in the French National Cereal Genetic Resources database (ERGE), maintained by GEVES, allows us to automate the weighing of samples: a barcode reader registers the database code and after that the weight of sample, and either puts it in the right table within the database for a new sample or updates the weight in the database after sample distribution.

A safety-duplicate sample in an aluminium foil sealed bag is kept in a deep freeze unit at a temperature lower than –20°C.

A set of two reference ears is kept in the cold chamber at 4°C for comparison with field samples.

Germination will be monitored after harvest and then every 5 years, in order to provide information for deciding upon seed lot regeneration. All will be done to ensure the best seed quality.

Data registration and sample distribution

Information is recorded in a database in Access: passport data (accession code, name, country of origin, donor, pedigree, etc.), evaluation data (agronomic traits such as disease tolerance, heading date, height, and morphological traits such as ear and seed colour, awnedness and spike compactness) and seed stocks (weight of regeneration and distribution stocks).

In the software the addresses of recipients of seed samples are entered in a table so that we can track statistics about distribution. Labels can be printed upon request. For each order, a dispatch form is set up, including a print-out of a label for each sample. The dispatch form mentions the code and location of each sample in the cold chamber.

An information form including passport data is also established and joined to the sample.

Future developments

Efforts will be made to develop software programs to allow on-line consultation of data and the ordering of accessions and to increase the available information by introducing indications on genes of interest and storage protein alleles. This will probably require the use of new database management software.

The main task of a Biological Resource Centre is to facilitate better utilization of accessions by breeders and other users. This requires the highest level of information for each accession, which we are endeavouring to fulfil now.

Further scientific information resources such as mapping populations, cytogenetic material (monosomic, substitution and aneuploid lines) will be progressively introduced in the Centre.

A quality assurance process for research will be developed in the coming years: the establishment of a Material Transfer Agreement for genetic resources distribution, the definition of repeatable germination tests and the preparation of management protocols in order to increase the traceability of different steps. A Laboratory Information Management System (LIMS) is being developed to integrate the processes of evaluation, follow-up of accessions and seed stocks.

These steps will allow us to obtain accreditation for the organization as a Biological Resource Centre.

Acknowledgements

The authors wish to thank Roland Nely, Christophe Serre and Armelle Boude for their technical assistance. The development of the Centre was supported by the French Board for Genetic Resources (BRG) and the French Auvergne Region.

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German Network for the evaluation and use of disease resistance in cereals (EVA II)

Annette Kusterer[1], Hilke Riemer[1], Siegfried Harrer[2], Edgar Schliephake[1] and Volker Lind[1]

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Introduction

To improve a crop or enhance its resistance to stresses and diseases, plant breeders have relied on the genetic diversity in their working collections, on collections of genetic resources stored in genebanks, and on those varieties maintained and selected by farmers. Today, biotechnology and genetic engineering promise to break the biological barriers imposed on conventional plant breeding by incorporating desirable genes and gene complexes from wild relatives across species (Smale *et al.* 1998).

Public concern has focused on the potential for plant disease epidemics caused by uniformity in the genetic base of resistance (Smale and Singh 1998). Many virulence genes in pathogens correlate to the corresponding resistance genes in the host populations. Specific resistances in such diseases as the cereal rusts contribute to a "boom-bust" cycle of resistance and vulnerability, because the pathogen is able to mutate rapidly and form new races (Vanderplank 1963). The average duration of a resistance based on major resistance genes appeared to be only a few years (Beek 1988). One can distinguish between vertical, i.e. race-specific, often only temporary resistance, which is mostly monogenic, and horizontal or partial resistance, which is race-non-specific, more durable, and with a polygenic base. Recently, efforts have been concentrated on enhancing the horizontal resistance in crops (Walther *et al.* 1996). To assess this, repeated scorings are necessary.

In the past, huge amounts of evaluation data have been collected for various species, but often data from varying sources or test conditions cannot be compared. EVA II aims to provide plant breeders with accelerated access to resistant genotypes, thereby supporting the sustainability of agriculture by increasing the genetic diversity present in cultivars. The overall goal is a better transfer and dissemination of new resistance genes into commercial breeding programmes. For this purpose, secondary evaluations of wheat and barley are being carried out and a network information system for data acquisition, overview, and provision has been developed. EVA II also pursues the refinement of standardized systems for resistance evaluation.

Material and methods

- **Material**

For wheat and barley (both spring and winter forms) sets of a maximum of 100 genotypes are chosen for testing. The material is chosen by reference to earlier disease evaluations. Databases from genebanks and institutes are used as well as variety lists and relevant publications. The sets consist of actual pre-breeding material, mainly from Institutes of the Federal Centre for Breeding Research (BAZ), as well as foreign varieties and genebank material. Furthermore, the contributing partners may supply the network with their own breeding material. All tested genotypes should carry new or unknown resistance genes or combinations. At least two standards (susceptible and resistant) for each fungal pathogen are included in order to characterize the infestation conditions of all sites. Resistance to most important fungal pathogens in wheat (Table 1) is evaluated. Additionally, virus resistance is screened at several sites.

Table 1. Fungal pathogens screened and standards for evaluation

Pathogen		Standards	
Common name	**Latin name**	**resistant**	**susceptible**
Winter wheat			
Powdery mildew	*Blumeria graminis* f. sp. *tritici*	Cortez	Monopol
Tan spot	*Drechslera tritici-repentis*	Dream	Bussard
Scab	*Fusarium* spp.	Romanus	Darwin
Leaf rust	*Puccinia triticina*	Travix	Dekan
Stripe rust	*Puccinia striiformis*	Cortez	Flair, Mikon
Leaf blotch	*Septoria tritici*	Dream	Renan
Glume blotch	*Stagonospora nodorum*	Petrus	Monopol
Spring barley			
Powdery mildew	*Blumeria graminis* f. sp. *hordei*	Alexis	Prisma,
Net blotch	*Drechslera teres*	Annabell	Barke, Pasadena,
Leaf rust	*Puccinia hordei*	Barke, Hanka	Alexis, Prisma,
Scald	*Rhynchosporium secalis*	Sissy	Pasadena
Winter barley			
Powdery mildew	*Blumeria graminis* f. sp. *hordei*	Verena	Regina, HJ171
Net blotch	*Drechslera teres*	Camera	Krimhild
Leaf rust	*Puccinia hordei*	Carola	Cornelia, Vogelsanger Gold
Scald	*Rhynchosporium secalis*	Leonie	Intro, MS Scald

Twenty-two private German cereal breeders, mostly organized in the "German Federation of Private Plant Breeders (GFP)", Bonn, and several research institutes conduct the evaluation trials, score the material, and collect data.

- **Methods**

The sets are evaluated for field resistance in multi-site field trials. Usually, micro-plots of $1m^2$ are used; the trials may use one or several replications. Each partner screens the whole set for all the relevant diseases. Artificial infestation with a pathogen race mixture is recommended according to local infestation conditions and the capabilities of the partners. Replicated scoring over more than one year is planned only for the standards, for the most promising candidates, and in the case of missing information, e.g. due to insufficient infestation conditions in certain seasons. Prepared Excel files to assist with filling in the scores, and relevant pedigree and resistance information are sent to all partners together with the seed.

Evaluation scoring should be made by % infected leaf area. Scores (1-9) are transformed by a logarithmic scale to % (Walther *et al.* 1996). The methods should be simultaneously applicable to several cereal diseases. In contrast to vertical resistance, for a rating of partial resistance, the extent and the development of the infection need to be quantified. For these purposes, the area under the disease progress curve and the mean disease severity is determined. A reliable estimate of the partial resistance of a given genotype requires several scoring dates (Walther *et al.* 1996). Therefore, the partners are asked to conduct three scorings for every disease which occurs, starting when the infestation becomes apparent and then scoring every 7 to 14 days.

Comparison is made between the scores of the test candidates and the standards. If no standards are available (as in the case of winter wheat 2000-01), conclusions can be drawn from comparisons with the minimum and maximum values of the specific location. Besides this, genotypes with interesting resistance reaction are evaluated for the presence of known resistance genes using molecular markers. The results are summarized and soon after harvest shared among the project partners for direct use in their own breeding programmes. This network information system for data acquisition, overview, and provision was developed by the German Centre for Documentation and Information in Agriculture (ZADI/IBV, Bonn).

Contracts officially regulate the rights and duties of all partners; the most important detail is the right of the breeders to use all of the screened material for their own breeding programmes and the obligation to score a defined minimum of the cereal sets. Thus, the network information system acts for the mutual benefit of all participants.

Results and discussion

Interesting material was observed in wheat over the last three growing seasons. The sets contained the numbers of genotypes with origins listed in Table 2.

Table 2. Overview of evaluated winter wheat genotypes

Growing season	BAZ-lines	Genebank material	Foreign varieties	Breeding material	Standards (resistant and susceptible)	Total
2000/2001	54	-	-	50	52	**156**
2001/2002	42	-	35	24	15	**116**
2002/2003	-	13	26	2	15	**56**

The material from the Institutes of the Federal Centre for Breeding Research was pre-selected for scab resistance. The genebank material was selected for powdery mildew and/or rust resistance.

Summarized results over all genotypes and locations for the growing period 2001-2002 are presented in Fig. 1. For leaf rust (*Puccinia triticina*), resistance scores ranged from 1.1 to 6.2. The resistant standard had the score of 1.9 and the susceptible was evaluated at 4.5. For resistance to septoria (*Septoria tritici*) the scores ranged between 2.7 and 5.7 with 3.9 and 4.7 for the resistant and susceptible standards. For powdery mildew (*Blumeria graminis* f. sp. *tritici*) the scores ranged from 1.3 to 5.8 with 1.3 for the resistant and 5.3 for the susceptible standard. Scab (*Fusarium* spp.) was scored over all locations from 1.0 up to 6.5 and the resistant and susceptible standards were scored with 3.7 and 5.8.

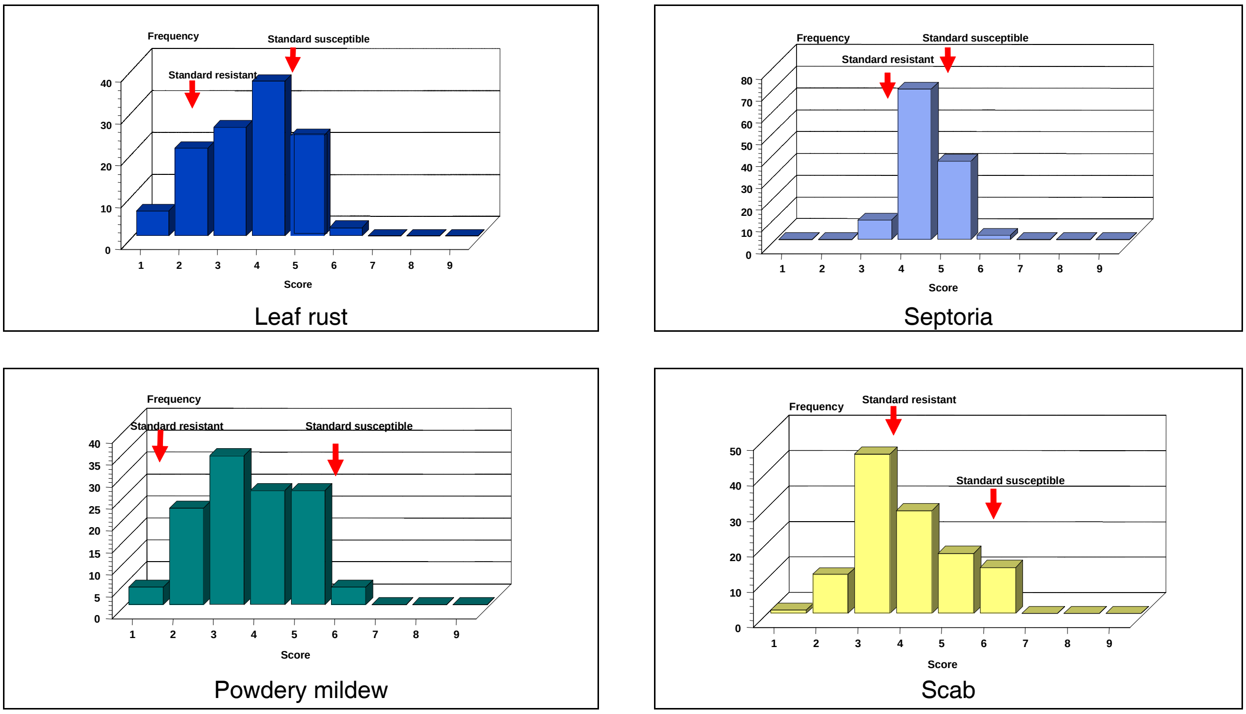

Fig. 1. Frequencies for the disease scores for the evaluated diseases.

Looking in detail at the results concerning scab, out of 58 lines derived from the BAZ, 43 turned out to be better than the resistant standard 'Romanus', 14 genotypes were better than the susceptible standard (though below the resistant standard) and one genotype was even more susceptible than 'Darwin'(Fig. 2).

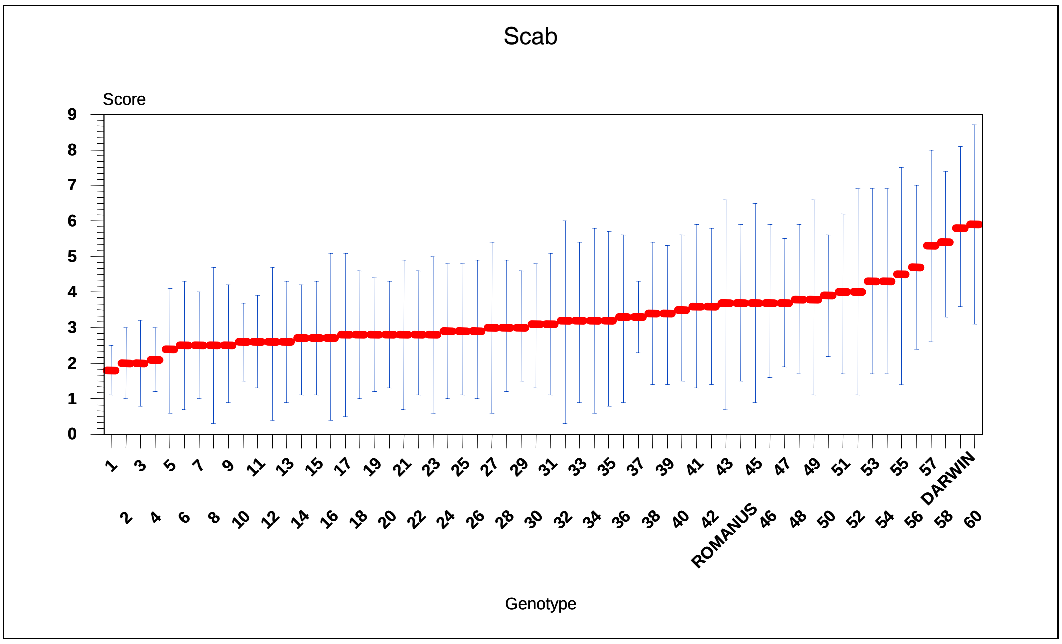

Fig. 2. Scab (*Fusarium* spp.) disease scores in the field 2002 for the accessions described as resistant to scab (resistant cultivar: 'Romanus', susceptible cultivar: 'Darwin').

For five genotypes selected for leaf rust resistance, three genotypes turned out to be more resistant than the resistant standard, one genotype was scored between the resistant and susceptible standard and one genotype showed a worse disease score than the susceptible standard (Fig. 3).

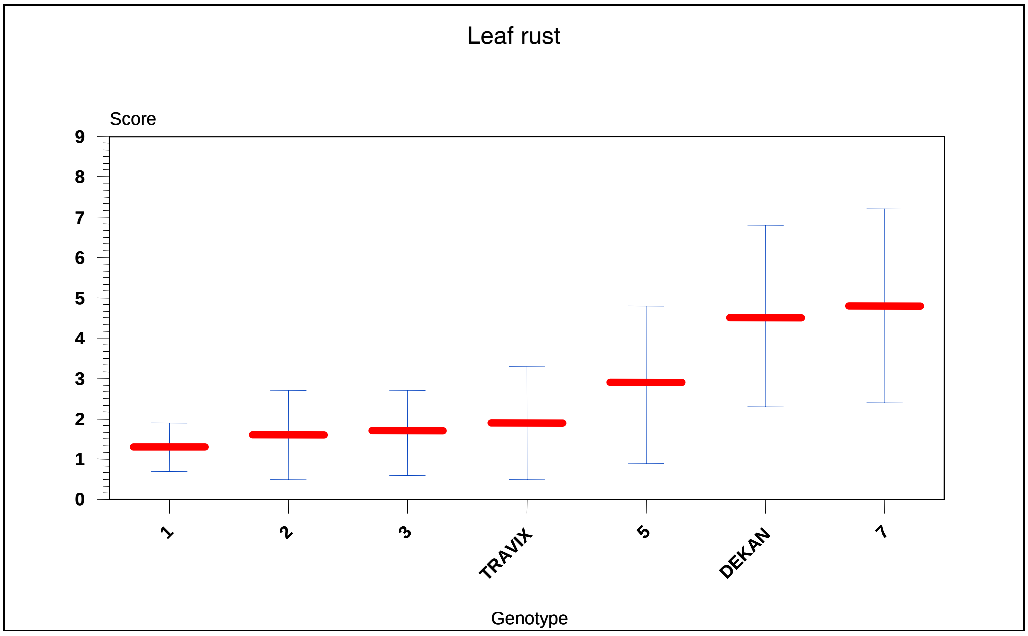

Fig. 3. Leaf rust (*Puccinia triticina*) disease scores in the field 2002 for the accessions described as resistant to leaf rust (resistant cultivar: 'Travix', susceptible cultivar: 'Dekan').

For powdery mildew, the set contained 13 genotypes with defined resistance. The evaluation showed that none of these genotypes showed a higher level of resistance than the resistant standard. They all ranged between 'Cortez' and 'Monopol' (Fig. 4).

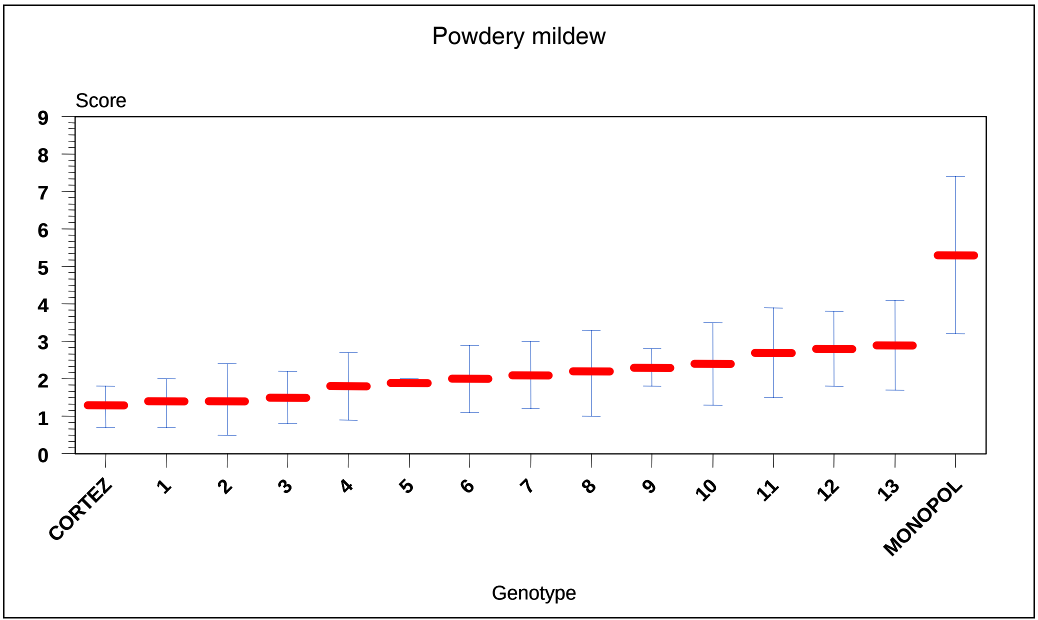

Fig. 4. Powdery mildew (*Blumeria graminis* f. sp. *tritici*) disease scores in the field 2002 for the accessions described as resistant to powdery mildew (resistant cultivar: 'Cortez', susceptible cultivar: 'Monopol').

To investigate wheat leaf rust resistance genes present in the tested genotypes, tests with known PCR markers were carried out (Schachermayr *et al.* 1994, 1995; Prins *et al.* 2001). Up to now, no genotype carrying the highly effective genes *Lr 9, Lr10, Lr19,* or *Lr24* has been detected.

The results of the evaluations are available on the Internet. Participants have access to the data at http://www.genres.de/eva/eva_2/index.htm. Partners of EVA II can search the results by year, culture and disease or by location. A combined search is also possible. The first access and use of the results are limited to the participants. After a 3-year period the data are made available to the public.

In general, the participating partners found the system efficient and were motivated to continue with the project after the initial 3-year period because interesting material was being found.

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APPENDICES

Appendix I. Minutes of an *ad hoc* meeting of the ECP/GR Barley Working Group, 20 June 2004, Brno, Czech Republic

Helmut Knüpffer
Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

Agenda

Time	Topic	Speaker
12:00	Welcome, introduction, adoption of agenda, reporting	H. Knüpffer
12:05	Brief report on the Session on Barley held during the Cereals Network Meeting, July 2003, Yerevan, Armenia	H. Knüpffer
12:20	Cereals Network matters (Coordinating committee, agreement on Barley WG representatives, confirmation of Chairpersons, budget)	H. Knüpffer
12:30	Finalizing priorities and recommendations of the Barley WG for EPC/GR Phase VII	H. Knüpffer
12:50	Utilization of characterization and evaluation data at the national and European level	D. Murariu (intro)
13:10	Other matters	
13:30	End of meeting	

Introduction

The *ad hoc* meeting was organized in conjunction with the 9th International Barley Genetics Symposium (IBGS) in Brno, Czech Republic (20-26 June 2004), on Sunday 20 June. Financial support from ECP/GR allowed a few more members to participate in addition to those registered for the IBGS. H. Knüpffer, Chairman of the ECP/GR Barley Working Group (BWG), had organized the meeting on request of the Group in cooperation with the IBGS Secretariat. BWG matters of interest for the wider audience were discussed in the following Workshop on Barley genetic resources:

- Barley Core Collection
- International information system on barley genetic resources
- Pre-breeding and base-broadening.

The agenda was adopted by the participants. It was agreed that no formal report would be produced, since the main results of the meeting would be reflected in the Priorities and Recommendations of the report of the Cereals Network meeting. The informal minutes would be uploaded on the ECP/GR Barley WG home page and included as an appendix in the report of the Cereals Network meeting.

Brief report on the Session on Barley held during the Cereals Network Meeting, July 2003, Yerevan

The participants were briefly informed about the previous meeting held during the first meeting of the Cereals Network, based on the available draft report.

Cereals Network matters[72]

The composition of the Cereals Network Coordinating Group (CNCG) and the budget of the Network were briefly presented by H. Knüpffer. The CNCG consists of seven members representing the Working Groups on *Avena*, Barley and Wheat, as well as the *ad hoc* initiatives on triticale and rye. The Barley WG is represented by H. Knüpffer (co-chairing the CNCG together with A. Le Blanc) and M. Jalli (Vice-Chair of the Barley WG). The composition of the CNCG and the budget were agreed upon during spring 2004, mainly via email and telephone contacts. The budget was finalized in June 2004.[73] It was agreed that the Barley WG would be considered as having lower priority during the present Phase VII of ECP/GR, compared to *Avena* and Wheat. Thus, activities on barley can be financed by a separate ECP/GR budget line, which provides limited funds for lower priority WGs. An *ad hoc* meeting of the database managers of the European Barley Database (EBDB) and of NGB with EURISCO and SINGER developers at IPGRI or ICARDA is planned to discuss linking of the respective databases into a worldwide information network on barley genetic resources. The WGs on Barley and *Avena* were able to hold small meetings in conjunction with international symposia in June and July 2004 respectively, at relatively low cost for ECP/GR. The second full meeting of the Cereals Network will be held for five working days, including three full-day meetings of the *Avena*, Barley and Wheat WGs on successive days, followed by a two-day plenary meeting, during which parallel brainstorming sessions on various crosscutting issues can be held. The information on the CNCG composition and the Network budget was circulated among the BWG. The members present at the meeting agreed on the CNCG composition and the budget.

Priorities and recommendations of the Barley WG during ECP/GR Phase VII

The group was requested to finalize the priorities and recommendations for Phase VII as drafted in Yerevan in July 2003. With respect to the priority areas for Phase VII defined by the ECP/GR Steering Committee in October 2003, the Working Group recommended the following:

1. Characterization and evaluation (including use of modern technologies)

- Complete the International Barley Core Collection with an Ethiopian/Eritrean subset and a subset on genetic stocks; further develop BCC documentation; study the BCC using molecular markers.
  Research is being carried out to create the Ethiopian/Eritrean BCC subset (Ethiopian PhD student under supervision of A. Björnstad, Norway), and the candidate accessions for the Genetic Stocks subset were selected and initially multiplied by J. Franckowiak (Fargo, ND, USA) and U. Lundqvist (Svalöv, Sweden) (reported at the Barley Genetic Resources Workshop in Brno, 20 June 2004).
- Set up an ECP/GR task force of barley breeders and scientists with an interest in pre-breeding and base-broadening, and develop regional cooperation on this issue in collaboration with FAO.
  This group of scientists and breeders was formed under the coordination of Marja Jalli (Finland) during the Barley Genetic Resources Workshop in Brno, 20 June 2004. The group will prepare a background paper together with FAO as a basis for possible funding of pre-breeding activities.

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[72] For full information see: *ECP/GR Phase VII (2004-2008). Proposal for Networks' budget allocation. Submitted by the EPC/GR Secretariat to the Steering Committee. 27 September 2004* (http://www.ecpgr.cgiar.org/Introduction/Budget_PhaseVII.pdf).

[73] Some additions were made in September 2004.

- Continue the ring test on barley net blotch (under the coordination of Marja Jalli, Finland) that started as an activity of the Barley WG at its meeting in Salsomaggiore in 2000. The main objective is to test the behaviour of net blotch resistant breeding material under different environments.

2. Task sharing
- Identification of duplicates and designation of "primary collection holders", as a concerted action in harmony with other groups of the Cereals Network. Methodology and database-supported procedures will be developed in a pilot study of the Documentation and Information Network (AEGIS project approved by the ECP/GR Steering Committee in October 2003 and started mid-2004). The Barley WG will adopt and implement the results from AEGIS.
- Set up a system for safety-duplication. To be developed for all cereals within the Cereals Network, in cooperation with the ECP/GR Documentation and Information Network.

3. *In situ* and on-farm conservation
- The Barley Working Group stressed the importance of facilitating the conservation of wild relatives and encourages an on-farm task force. Prepare a list of wild *Hordeum* spp. occurring in the ECP/GR mandate region, identify species and areas in need of protection, in cooperation with the EU project PGR Forum and the ECP/GR *In situ* Task Force.

4. Documentation and information
- Further develop the European Barley Database at IPK, transfer it to Oracle, and develop new and user-friendly search interfaces. The Barley Working Group is very keen to ensure that the development of the EBDB is guaranteed in the future.
- Develop updating mechanisms based on retrieving barley data from EURISCO instead of, or in addition to, requesting new updates from data providers (the contributing genebanks). The mutual access procedures between EURISCO and central crop databases need to be clarified.
- Seek cooperation and integration between the EBDB and other international databases and information networks on barley genetic resources (such as SINGER, Global Barley Genetic Resources Inventory, GRIN) and the Database on Barley Genes and Genetic Stocks (BGS).
  A short technical workshop is planned.

Utilization of characterization and evaluation data at the national and European levels

The topic was introduced with a presentation by Danela Murariu (Romania). The Suceava Genebank has participated in the GENRES barley project since 1999. Besides evaluation for biotic stresses, the barley samples studied were completely analyzed using the following steps:
- Establishment of a minimal descriptor list in cooperation with Romanian breeders from agricultural research institutions.
- Development of the characterization and evaluation database with the aim of best serving the users' needs. A minimal statistical analysis programme was linked to the database to assist genebank staff and users to select desired material easily.

- Establishment of a genetic collection of barley samples very resistant to the diseases studied, complemented with complete morphological, agronomic, physiological and biochemical descriptions.

The following priorities related to characterization and evaluation data were proposed:

1. Establish a ranked list of the 10-15 most important traits by a survey among European breeders;
2. Improve molecular characterization, and the conditions for such analysis, especially in countries lacking financial resources and equipment;
3. Develop new and user-friendly search interfaces to the international database to improve its accessibility;
4. Integrate the characterization/evaluation data from any study or evaluation carried out by researchers worldwide, with Web-based access to the evaluated barley germplasm.

These topics were briefly discussed. H. Knüpffer noted that a European survey of priority characterization/evaluation descriptors was already carried out 20 years ago[74], which could serve as the basis for a new survey.

Closing

All participants also joined the following Workshop on Barley Genetic Resources.

Participants

1. Croatia: Darko Babic (representing D. Novoselovic), darko.babic@poljinos.hr
2. Czech Republic: Jarmila Milotová, milotova@vukrom.cz
3. Finland: Marja Jalli (Vice-Chair), marja.jalli@boreal.fi
4. Germany: Helmut Knüpffer (Chairman), knupffer@ipk-gatersleben.de
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7. Lithuania: Algė Leistrumaitė, alge@lzi.lt
8. Nordic Countries: Louise Bondo, louise@ngb.se
9. Romania: Danela Murariu, dmurariu@suceava.astral.ro
10. Spain: José Luis Molina Cano, joseluis.molina@irta.es

Unable to attend

Some members had planned to attend the meeting, but were unable to get there in time because of travel problems. BWG members who did not respond to the invitation are not included.

1. Bulgaria: Zapryanka Popova
2. Cyprus: Andreas G. Kari
3. ECP/GR: Lorenzo Maggioni
4. Estonia: Hans Küüts, Ülle Tamm (representing Vahur Kukk)
5. FAO (observer): Elcio Guimarâes
6. France: Louis Jestin

[74] See Appendix VI. List of characterization/evaluation data to be registered in the EBDB (pp. 21-22) and Appendix VII. Results of a survey on breeding information needs (pp. 23-30) *in* UNDP/IBPGR. 1986. Report of a Barley Workshop. European Cooperative Programme for the Conservation and Exchange of Crop Genetic Resources. IBPGR, Rome.

7. IPGRI/Global Crop Diversity Trust (observer): Brigitte Laliberté
8. Israel: Abraham Korol, Tzion Fahima
9. Netherlands: Noor Bas
10. Russian Federation (observer): Olga Kovaleva, Irina Terentyeva
11. Serbia and Montenegro: Novo Pržulj
12. Slovakia: Michaela Benková

Appendix II. Minutes of an *ad hoc* meeting of the ECP/GR *Avena* Working Group, 23 July 2004, Helsinki, Finland

J. Mike Leggett

IGER, Plas Gogerddan, Aberystwyth, Ceredigion, United Kingdom

Draft agenda

1. Welcoming address
2. Introduction of the participants
3. Approval/amendments of the agenda
4. Election/appointment of Chairperson of the *Avena* Working Group (AWG)
5. Election of two AWG representatives to the Cereals Network Coordinating Group (CNCG)
6. Plan of action for Phase VII (2004-2008)
7. Council Regulation 870/2004 (1467/94) New GENRES project
8. Budget proposals
9. Drafting of the report
10. Conclusion

The Chairman welcomed the participants to the working group meeting, and stated that he intended to chair the meeting throughout even though it was hoped a new Chairperson would be elected. It was explained that both the present meeting and the previous meeting in Yerevan during 2003 were going to be considered to be *ad hoc* meetings as ECP/GR had thought that on both occasions it had not been feasible to ensure that every member had the opportunity to attend either meeting. The next *Avena* Working Group meeting would thus be the VIth, which is currently scheduled to meet during 2007 in conjunction with the Cereals Network meeting.

The Chairman welcomed frank and open discussion from all present regardless of their status in terms of full member or observer, though if any agenda item came to a vote, only full members would be able to cast a vote.

The participants introduced themselves and gave a brief description of their work.

The agenda was approved as it stood.

Some discussion was held regarding who might best represent the *Avena* Working Group (AWG) as Chairperson and a couple of suggestions were made. Ultimately it was thought that the new representative from Greece, Andreas Katsiotis might be best suited to the position as he has already had experience in coordinating the EU/GENRES project and was familiar with genetic resources and molecular biology (of oat and olive). All present agreed to this and Andreas accepted the position.

With regard to selection of two AWG representatives to the Cereals Network Coordinating Group (CNCG), the Chairman suggested that it would be sensible to elect the new Chairman as the CNCG representative for the AWG, and to retain the European *Avena* database (EADB) manager (Christoph Germeier) as the second representative. This was accepted by all present.

The Plan of action for Phase VII (2004-2008) was discussed and the following were the main conclusions.

In situ *conservation*

The Chairman has already alerted the Spanish AWG representative (Pedro García) to an ongoing PGR Forum. He may be able to incorporate *A. murphyi* into their project. Pedro has already made contact with José Iriondo (Spanish partner in the EU project PGR Forum) and we await any progress.

Regarding the *in situ* conservation of *A. insularis*, the Italian AWG representative (Fulvia Rizza) thought that there may be a possibility of conserving some sites in Sicily and would pursue the matter further.

Regarding the *in situ* conservation of *A. maroccana* and *A. murphyi* in Morocco, Chaouki Al Faiz and Nezha Saidi thought that there may be some avenues which could be explored in order to conserve at least some areas in Morocco.

Some further discussion around the subject of *in situ* conservation followed and it was agreed that it might be feasible to have *A. maroccana, A. murphyi, A. insularis* and possibly *A. prostrata* included as red list species, which should prompt the respective governments to act to preserve these endangered *Avena* species.

Further collection of endangered species

The Chairman pointed out that there was a budget allocation (Euro 10 000) for 2005 for two collectors over a three-week period to further collect the species mentioned above. A request was made for suggestions as to who might make the collections. The Chairman anticipated that the country representative would be involved, possibly with one other. After some discussion, it was suggested that the Chairman (Mike Leggett) who had considerable experience in the collection of *Avena* might undertake the task. The Chairman replied that his future next year (2005) was very uncertain and he could make no formal commitment to undertake such a task.

Council Regulation 870/2004 (1467/94) New GENRES Project

The Chairman pointed out that there was still little detail of the new call and that it was anticipated that further detail would be published in September and certainly by the end of the year. The present GENRES project (Evaluation and enhancement of *Avena* landrace collections for extensification of the genetic basis of *Avena* for quality and resistance breeding) was to hold its final project meeting the following day (24/07/04) and had invited Mr Fred Steenhoff from the EU Commission who, it was hoped, might be able to give a better indication as to what angle the group should take with regard to the submission of a further proposal.

Various suggestions for topics were raised including: quality, drought, salt and cold tolerance, resistance to pests and diseases, grazing season duration, plant height and percentage husk (i.e. genetic variation for reduced husk, rather than having a completely naked grain).

It was thought that this round might require bigger projects and that it might be prudent to include at least one of the 'new' EU member states. A bigger project might also need to involve the other cereal crops, especially barley, though it was thought that if wheat were to be included this might dominate an application.

Bioinformatics seems to be one of the 'hot topics' and it was thought that there should be a bioinformatics input to whatever project was finally decided on. Likewise, it was thought that there should be some emphasis on molecular biological technologies in relation to the project.

The suggestion that the new project might involve the genetic variation for organic farming practices was also made, which might involve organic bakers.

It was also thought that the genetic variation for the various quality issues such as the small but valuable 'micro ingredients' (e.g. ß glucan and Avenathramides, etc.,) might be a suitable topic for a new proposal. It might indeed be advantageous to build on the present landrace project data to give 'added value' to the previous submission.

It was also suggested that pre-breeding might be incorporated into a project as this had been identified as desirable during the Cereals Network Meeting in Yerevan in 2003.

The Chairman reported that the sum of Euro 3000 for the participation of 3-5 participants to attend a one-day meeting to formally prepare a GENRES project proposal was available. This was earmarked for 2004 and would need to take place shortly after the final text appears.

Any other business

The system which has been adopted by the steering committee for the selection of attendees at the various working group meetings was discussed. There was concern that in essence, country coordinators choose which working groups will be supported at any time during the current phase. This has a clear possibility of the 'stronger' groups taking precedence over smaller working groups. The AWG requests that ECP/GR monitors this situation to avoid any possible bias.

The Chairman said that it had become evident during the International Oat Conference (IOC) that there was a lot of oat genetic resources work going on throughout the Nordic countries, and that input to the group from the individual scientists would be highly beneficial, improving the genetic resources communication and collaboration within the Group and the EU.

List of participants

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Lenka Nedomova	Czech Republic
Ilmar Tamm	Estonia
Jean Koenig	France
Christoph Germeier	Germany
Andreas Katsiotis	Greece
Fulvia Rizza	Italy
Rita Redaelli	Italy
Nezha Saidi	Morocco
Chaouki Al Faiz	Morocco
Louise Bondo	NGB
Igor Luskutov	Russian Federation
Rickard Jonsson	Nordic Countries
Mike Leggett	United Kingdom

Appendix III. Agenda

First Meeting of the ECP/GR Cereals Network
3-5 July 2003, Yerevan, Armenia

Wednesday 2 July

Arrival of participants

Network Coordinating Group: 17:00–20:00, closed session for meeting preparations

Other participants: dinner at the hotel

Thursday 3 July

09:00 – 10:15	**Introduction** • Opening of the meeting, welcome address and opening remarks (*David Lokyan, Minister of Agriculture of Armenia; Levon Rukhkyan, Deputy Minister of Agriculture and National Coordinator for plant genetic resources in Armenia; Lorenzo Maggioni, IPGRI, 15 min)* • Short presentation of the national PGR activities of Armenia (*Alvina Avagyan, Agricultural Support Republican Center, Yerevan, 15 min*) • Information on ECP/GR and current international PGR events (*L. Maggioni, 20 min.*) *Discussion* • Introduction to the structure/main topics of parallel meetings, e.g. Databases, Characterization, Evaluation, Regeneration, Safety-duplication, Conservation and management of wild relatives, Pre-breeding (*Network Coordinating Group, 10 min.*)
10:15 – 10:45	*Coffee break*
10:45 – 12:30	**Parallel meetings of the *Avena*, Barley and Wheat WGs in separate rooms** Review of workplan progress and discussion on Working Group priorities for the future. Chairs/rapporteurs ensure that relevant items for plenary discussion are summarized in written form and/or as PowerPoint presentation, and reported to the plenary on the following day - *Avena*: Chair (*J. M. Leggett*), Rapporteur (*to be nominated*) - Barley: Chair (*R. Ellis*), Rapporteur (*to be nominated*) - Wheat: Chair (*G. Kleijer, on behalf of A. Le Blanc*), Rapporteur (*to be nominated*)
12:30 – 14:00	*Lunch*
14:00 – 15:30	**Parallel meetings – continuation**
15:30 – 16:00	*Coffee break*
16:00 – 17:30	**Parallel meetings – continuation**
	End of the first day

Friday 4 July

09:00 – 10:15	**Plenary session – Reporting** Rapporteurs present results of the first day discussion on issues of Network-wide interest: brief report of the WG achievements, such as on databases, characterization, evaluation, regeneration, safety-duplication, conservation and management of wild relatives, pre-breeding, etc. - *Avena* WG *(Rapporteur, 25 min.)* - Barley *WG (Rapporteur, 25 min.)* - Wheat WG *(Rapporteur, 25 min.)*
10:15 – 10:45	*Coffee break*
10:45 – 11:50	**Reporting - continuation** - *Secale* activities and Database *(W. Podyma, 15 min.)* - Triticale activities and Database *(G. Kleijer, 15 min.)* - The European Maize Database *(D. Jelovać, 15 min.)* - Initiatives on Minor Cereals (*A. Michalová, 15 min.*) *Discussion of reports*
11:50 – 12:30	**Thematic issues** • Documentation - Progress of the EPGRIS project and the EURISCO catalogue (*L. Maggioni, 15 min.*) - Computer-assisted duplicate search in a medium-size cereal central crop database – The case of *Avena* (EADB) (*C. Germeier, 15-20 min.*) *Discussion*
12:30 – 14:00	*Lunch*
14:00 – 15:30	**Thematic issues - continuation** • On-farm conservation - On-farm conservation of hulled wheat in southern Italy (*P. Perrino, 15-20 min.*) *Discussion* • Other thematic issues of Network interest: Possible themes: Sharing of responsibilities, evaluation and use of the collections, core collections, pre-breeding, public awareness, etc.
15:30 – 16:00	*Coffee break*
16:00 – 17:00	**Identification of priorities for the future at Network and Working Group level (ECP/GR end of Phase VI – Phase VII)** **Any other business**
18:00 - 20:00	Drafting of the report *(only Network Coordinating Group is involved in the drafting)*
	End of the second day

Saturday 5 July

8:00 – 10:00	Drafting of the report *(only Network Coordinating Group is involved in the drafting)*
10:30 – 17:30	*Excursion to Erebuni State Reserve*
20:00	*Social dinner*

Sunday 6 July or Monday 7 July

Departure of participants

Appendix IV. List of participants

First Meeting of the ECP/GR Cereals Network
3-5 July 2003, Yerevan, Armenia

N.B. This list includes only participants having attended the meeting. The composition of the Working Groups is subject to changes and the latest update can be found on the ECP/GR Contacts Web page (http://www.ecpgr.cgiar.org/Contacts/ecpgr_contact.htm).

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REPORT OF A WORKING GROUP ON WHEAT

Second Meeting, 22-24 September 2005, La Rochelle, France

CONTENTS

PART I. SUMMARY OF THE MEETING

Introduction

Opening of the meeting

Annick Le Blanc welcomed all the participants to this second meeting of the ECP/GR Working Group on Wheat and wished them a pleasant stay in La Rochelle. She presented the agenda which was adopted by the participants.

The participants then briefly introduced themselves. Several new members were present, some of them attending an ECP/GR meeting for the first time.

Lorenzo Maggioni, ECP/GR Coordinator, also welcomed the participants on behalf of IPGRI. He pointed out that this Working Group was one of the largest of all ECP/GR Working Groups, which illustrates the significant interest in wheat genetic resources that exists in all European countries. He particularly welcomed the new members, whose active participation will be most appreciated. Observers from Ukraine and the Russian Federation also attended the meeting.

Briefing on ECP/GR Phase VII

L. Maggioni gave an introductory briefing on the status of the ECP/GR programme. He explained that ECP/GR entered its VIIth Phase (2004–2008) with some modifications made to its structure and mode of operation by the Steering Committee (SC) in its last meeting in Izmir, Turkey, October 2003.[80] The Cereals Network remained unaltered with three Working Groups (*Avena*, Barley and Wheat). The function and composition of the Network Coordinating Groups (NCGs) was revised and it was decided that NCGs will formulate proposals, in consultation with Working Groups (WGs), for the attention of the Steering Committee (SC), on WG priorities and activities, following the planning and prioritizing mechanism established by the Steering Committee. They will also define which of the WGs will remain prioritized during the 5-year Phase, according to the planning and prioritizing mechanism established by the SC. The Steering Committee requested the Cereals Network Coordinating Group to define two priority groups out of the three within the Network, and to make proposals, in consultation with the WGs, for actions on the basis of a budget of about 90 000 euro allocated to the Network for Phase VII. As a result of this exercise, which went on during 2004, the Wheat WG was included among the priority WGs for Phase VII, together with the *Avena* Working Group. The following proposed actions to be funded, with relevance for the Wheat WG, were approved by the SC:

- September 2005: 2nd meeting of the Wheat WG
- March 2006: All Network Coordinating Groups meeting
- 2007: Cereals Network meeting (all 3 WGs meeting together)
- Rescue collections and *ex situ* preservation of *Aegilops* from endangered wild locations in Israel.

Further information on ECP/GR can be obtained by checking the ECP/GR Web site (www.ecpgr.cgiar.org), where several reference documents are available, including the Network's budget and the Terms of Reference for the ECP/GR operational bodies. A specific

[80] See Report of the Ninth Steering Committee Meeting, also available on Internet at http://www.ecpgr.cgiar.org/SteeringCommittee/SC9.htm

Web page is also dedicated to the Wheat Working Group and this can be improved with the help of, and according to the needs, of the WG.

The foreseeable development of the EURISCO catalogue and the overall mechanism of data flow in Europe will be relevant for this WG as well. Although for the moment it is recommended that the specific Central Crop Databases, such as the European Wheat Database (EWDB), continue to be developed in the traditional way (i.e. gathering all the available data from any available source), in the medium-term, it should become possible to obtain all the European wheat accessions' passport data from EURISCO and to focus the attention of the EWDB on characterization and evaluation data and on the analysis of the database in order to offer other services to the users of wheat genetic resources.

Improvement of the download facilities was acknowledged to be an essential requirement of the EURISCO catalogue and this is planned to be implemented by IPGRI not later than October 2005.

Briefing on international events

EC regulation 870/2004

A briefing was then given about the recently launched first call for submission of project proposals under EC regulation 870/2004, with a deadline of 30 September 2005. Several groups are preparing proposals, ranging from the further development of the European plant genetic resource information system (*ex situ* and *in situ* data) to the characterization of several specific crops (Cucurbits, Leafy vegetables, Maize, Oats, Umbellifers, *Vitis*, etc.).

Some considerations for submission of a proposal from the Wheat Working Group to the EU RESGEN call

J. Koenig considered it very important for the Wheat Working Group to make a proposal for the second call of the EU RESGEN programme in 2006. Each Working Group member in the EU countries should be concerned and involved in this initiative.

Some general considerations:

- Not too many participants: max.12?
- Objectives of the project: contributing to the objectives of the EU agricultural policy
- Breeding genotypes for sustainable agriculture
- Helping to obtain genotypes that may carry useful traits for food quality and health
- Helping to conserve relevant accessions of the main European collections.

Which accessions?

Landraces, hardy cultivars (i.e. those with good response to low-input systems of production), some accessions from existing local core collections, a few relevant wild ancestors.

Which traits to evaluate?

- **Disease resistance** is very important: mainly characterization of resistance genes to the main diseases to avoid fungicide treatments
- **Quality of wheats**
  - Food safety: presence of mycotoxins
  - Quality for human consumption: protein content, micronutrient composition and amount
  - Hardiness and suitability for organic farming

Final aims
- Complete the coverage of the EWDB
- Promote pre-breeding and the use of some accessions by breeders and researchers
- Help to build a European wheat core collection.

Networking activity on wheat and EWDB: stocktaking

Country reports
Annick Le Blanc presented a summary of the information contained in the country reports submitted prior to the meeting (Armenia, Azerbaijan, Bulgaria, Czech Republic, Estonia, France, Germany, Hungary, Ireland, Israel, Italy, Lithuania, Macedonia FYR, Nordic Gene Bank, Poland, Romania, Russian Federation, Spain, Switzerland, Ukraine) (*full reports are included in Part II).*

The Working Group on Wheat is very numerous and the 28 partner countries attending this meeting agreed not to present their respective country reports individually in order not to spend all the available time on these presentations. The Chair, Annick Le Blanc, received the papers before the meeting and had prepared a comprehensive presentation on the status of the different collections and on the progress made since the last meeting in 2001 in Prague, Czech Republic.

As no special recommendations were made for report writing, information retrieved from them was very heterogeneous. Nevertheless, it was possible to compile information on the following subjects:
- Organizations
- Facilities and methods used
- Description, characterization and evaluation of the collections
- Documentation – Computerization
- Use of the collections
- Specific activities, needs and projects

From these different topics, A. Le Blanc drew some conclusions in order to help the establishment of a new workplan for the Wheat Working Group (WWG).

1. Organizations
In most cases, wheat genetic resources are managed by one or several institutions/institutes that are not genebanks; the cases of CGN, the Netherlands or the Nordic Gene Bank, where activities are only focused on plant genetic resource management, are not general in most other countries. Usually, a department or laboratory is entrusted with genetic resource management within a research, breeding or experimental station. The advantage of hosting genetic resources within such institutes is the tight link to the users. By responding to requests for parents to be included in breeding crosses, material for research purposes or for experimental trials, the genetic resources centres/genebanks can satisfy the users and their needs directly.

All the WWG members hold and manage genetic resources under the control of a National Programme and National Collections have been set up. This general pattern represents significant progress for the WWG, which can now rely on a stronger basic framework.

2. Facilities and methods used

All countries with a few exceptions conserve their germplasm in cold rooms. This allows a longer time between two regeneration cycles, especially when freezers are used. But generally, seeds are stored both in cold rooms (active collections) and in freezers (base collections). In such cases, the active collection is essentially used for seed distribution and other direct uses, and the base collection is for sample regeneration. The temperature of most of the cold rooms is between 0°C and 4°C, and freezers are kept at -18/-20°C.

No detailed information was given concerning the packaging but we know that different systems are used, according to the history, financial means and established habits of the collection holders: paper or plastic bags, heat sealed bags, glass bottles, cardboard boxes, metal tins and glass jars are used.

3. Description, characterization and evaluation of the collections

- **Description**

The country reports were not equally detailed on the number of accessions held in the respective collections, especially as seeds are sometimes conserved in different places in the same country, according to specific plans for responsibility sharing within the country. The following list must then be considered as a brief overview of the European Collection description (to be compared with data included in the EWDB – see below, presentation by I. Faberová) *(numbers of accessions between brackets):*

Albania, Armenia (2740), Austria, Azerbaijan (5054), Belgium, Bulgaria, Croatia, Cyprus, Czech Republic (10 018), Estonia (284), France (11 965), Georgia, Germany (22 172), Greece, Hungary (8290), Ireland (30), Israel (8723), Italy (9771), Latvia, Lithuania (690), Macedonia (FYR), Malta, Netherlands, Nordic Gene Bank (1677), Poland (10 327), Portugal, Romania (3234), Russian Federation (37 000), Serbia and Montenegro, Slovakia, (4 154), Slovenia, Spain (2912), Switzerland (7445), Turkey (5763), Ukraine (20 626) and United Kingdom.

The Group was pleased to learn about the new Irish collection and extended its congratulations for the efforts made to set up this new collection and to collect original landraces and varieties. It was noted that Ireland holds a set of interesting Ethiopian accessions.

The case of France was also highlighted, due to the increased number of accessions included in the European collection since the last data transfer to the EWDB; it was specified that the former inventory concerned only material of French origin for which the French cereal genetic resource management network gave priority in terms of official conservation. From now on, foreign material maintained in France will also be included in the European inventory, while respecting upcoming international agreements on the exchange and use of plant genetic resources.

It was also noted that the larger collections were maintained in countries where breeding and domestication activities have long-standing traditions. Countries which are also well known for their collecting missions in the diversity centres of cereals are holding interesting collections of wild species or wild relatives/progenitors of wheat.

- **Characterization/evaluation**

Concerning the six characterization descriptors recommended at the last meeting, no relevant information could be obtained from the country reports but investigations made on EWDB can reveal the progress made.

Characterization and evaluation were performed during regeneration of seed samples. Data were also collected from research programmes on reactions to pests and diseases and from molecular analysis. These data are often scattered across different laboratories and centralization of these data into national inventories is ongoing. Many different descriptors are used in the genebank databases (passport, characterization and evaluation descriptors). The following list includes the most frequently used descriptors relating to morphology, biology, disease resistance and productivity:

- Plant height, number of spikelets per ear, 1000-kernel weight, number of kernels per ear, heading date, winter hardiness, awnedness, plant height, resistance to lodging
- Protein content
- Technology (bread making quality)
- Identification tests (gliadins, glutenins, molecular markers).

4. Documentation – Computerization

In most cases, countries have developed centralized documentation systems but data are often kept in different institutes taking part in the national programmes. It seems also that many data, essentially the characterization data, are not yet computerized, only recorded on paper. All the participant countries however declared that computerization is in progress, and future improvement of the European central database is expected.

5. Use of the collections

As genebanks are often hosted by research or breeding institutes, their first task is to provide the breeders with accessions that can be used as parents in crosses and the related descriptive data.

Well documented information systems could provide tools to analyze the diversity, and to help to define core collections.

New molecular techniques may allow the localization and identification of major genes which are very important to breeders.

As the use of not very well adapted material such as old varieties, landraces or wheat progenitors in breeding programmes generally takes many years to achieve good results, genebanks could be encouraged to carry out pre-breeding activities.

6. Specific activities, needs and projects

Some genebanks have collected accessions from centres of diversification, thereby enlarging the available diversity in the European wheat collections. This material is freely available.

WG members and other stakeholders would benefit from transparent information on the activities and expertise of the European institutions involved in PGR national programmes, since exchange of material, data and expertise would be facilitated.

Activities concern proteomic research, use of isogenic lines, phytogenetic studies, gene identification, definition of a core collection, etc. A list of available Web sites is given in Appendix I.

Urgent regeneration is needed in a few cases but good improvements have been made in long-term storage for a large part of the European collection. The storage capacity or availability of qualified staff are sometimes limited so that rationalization of the storage through bilateral or multilateral collaborations may be necessary. The specific needs must be identified in order to involve the WWG in a global conservation approach.

7. Establishment of a new workplan

The Chair suggested the participants should think about:

- what they could actually expect from European cooperation;
- what commitments each partner can reasonably undertake in a given timeframe;
- what are their respective interests in cooperating with the ECP/GR WWG.

The Group could also improve transfer of expertise and use. It should also better identify needs and available means in each partner country in a spirit of solidarity and cooperation.

While defining the new recommendations, the Group must keep in mind what is reasonable to undertake and well-defined deadlines must imperatively be set in order to be more efficient than in the past.

The European Wheat Database (EWDB) – Overview 2005

Iva Faberová presented the progress made since the Cereals Network meeting in Yerevan (July 2003). A summary is given below; related tables and figures are given in Appendix II.

Passport data

The EWDB currently holds data from 55 contributing institutions from 31 countries, with a total of 152 524 records representing 63.6% of the estimated total of 240 000 wheat accessions held in European countries.

Considering the total number of records in the EWDB, 98% were provided by 18 countries (out of 31) and 95% by 19 institutions (out of 55). However the value of each contribution does not correspond to the size of the contribution, but to its quality. Many small collections may be unique and very valuable.

Increase of records 1998-2005

The coverage of the passport information in the database has increased, both through downloading of data from EURISCO and by the inclusion of data sets received from contributing countries, to give a total of 20 358 new records.

Data analysis

Details on the taxonomic composition of the EWDB are given in Appendix II.

In terms of completeness of the data, the global data analysis shows that improvements are still needed:

- there are important gaps in the **completeness of passport and collecting data**. It should be noted that the European database contains mainly European accessions.
- the proportion of **safety-duplication and characterization data** included is very low:
  - safety-duplication: 8680 records = 6%
  - characterization data received for the six descriptors agreed upon in 2001 (awnedness, grain colour, glume colour, glume hairiness, spike density, plant height): 10 524 records = 6.9% (update since 2003: 5030 record sets)

I. Faberová mentioned some problems encountered with some of the available “raw data sets” (NLD, CHE, YUG) which are difficult to interpret (use of different descriptors, unknown abbreviations, etc.).

She insisted that the information value of the database was fundamentally linked to the presence of information on characterization/evaluation and on the seed sample location. The passport information in standard format will be available in EURISCO, and crop databases without characterization and evaluation data will be useless. The motivation and actions of the WWG members for supplying characterization and evaluation data are therefore essential to reach the level of quality expected from the EWDB.

Assessment of WWG activities

Considering the priorities which were formulated at the Cereals Network meeting in Yerevan 2003 for the activities of the WWG relating to documentation, to be carried out in Phase VII, the achievements can be summarized as follows:

- **Fill the gaps in EWDB**
- downloading from EURISCO was completed for ARM, AZE, GEO, IRL, ISR, PRT, ROU and UKR, bringing the total number of contributing countries to 31 (note: data from ROU and UKR were delivered in the past, but there were some inconsistencies)
- ITA delivered data in 2005
- data from the following countries are still missing: ALB, BEL, BiH, HRV, MDA, MKD, MLT

- **Data quality improvement**

Updates represent a continuous task, dependent on the WWG members' activity.

- **Characterization and evaluation data delivery**

Very limited progress was made owing to the inactivity of the majority of the WWG members. The proportion of records with characterization data is only 6.9% (AUT, CZE, ESP, EST, LTU, RUS).

- **Safety duplicates**

Documented for only 6% of EWDB (8680 records).

I. Faberová concluded with the recommendation that the WG should follow the accepted priorities for Phase VII:

- Sustained improvement of data quality (WWG members + DB manager)
- Delivery of characterization and evaluation data (WWG members)
- Inclusion of further characterization/evaluation descriptors?
- Development of the new List of Unique Accessions (DB manager)
- List of MOS and (probably) unique accessions, which will be the responsibility of the genebank (country?) (WWG members)
- Push ahead EWDB participation in GWIS (ECP/GR) (see below)
- *Aegilops* database?

Other wheat information systems

In addition to her report on the EWDB, I. Faberová reviewed briefly the major information systems relevant to the WWG:

- EURISCO (European Plant Genetic Resources Search Catalogue), a multicrop information system containing only passport data (926 463 accessions; wheat is represented by 127 113 accessions) (http://eurisco.ecpgr.org/)
- SINGER (System-wide Information Network for Genetic Resources of the CGIAR), a multicrop information system for passport, characterization and evaluation data (672 997 accessions; wheat = 112 170 wheat accessions, including 70% from CIMMYT and 30% from ICARDA (http://www.singer.grinfo.net/)
- ICIS (International Crop Information System), a comprehensive crop-oriented documentation system (http://www.icis.cgiar.org:8080/)

  ICIS systems implemented include the Global Wheat Information System (GWIS) and the International Rice Information System (IRIS). Systems for other crops are under development.

  GWIS includes germplasm pedigrees, field evaluations, structural and functional genomic data (including links to external plant databases) and environmental (GIS) data.

  GWIS participants are GRDC (Grains Research and Development Corporation, Australia), Queensland University; CIMMYT (Centro Internacional de Mejoramiento de Maíz y Trigo = International Wheat and Maize Improvement Centre, Mexico; Agriculture and Agri-Food Canada.

I. Faberová pointed out that EWDB data were delivered to GWIS in April 2003 but are not included yet.

- Global Database of Wheat Wild Relatives (ICARDA - Jan Konopka)
  An off-line version is available (CD) (12 476 *Aegilops* accessions).
- Pedigrees and identified alleles of wheat – collected from literature sources by Dr S. Martynov and T. Dobrotvorskaya from VIR, St. Petersburg (http://genbank.vurv.cz/wheat/pedigree/). This currently contains 69 632 records: an update in progress will bring the total to 73 043.

Presentation and discussion on AEGIS

A short account was also given of the ECP/GR-funded project AEGIS (A European Genetic Resources Integration System), which is aiming, through a feasibility study, to promote the creation of a European rational PGR genebank system of genetically unique and important accessions, in order to conserve them safely in the long-term, at the same time ensuring their genetic integrity, viability and availability to users.

The creation of the AEGIS system is planned to offer a technical and political framework within which the theoretical proposals developed by the ECP/GR Working Groups in recent years for the sharing of responsibilities for conservation in Europe can be converted into reality.

More information on AEGIS is available from www.ecpgr.cgiar.org/AEGIS/AEGIS.htm.

Presentation of GEVES Le Magneraud

The second day of the meeting was held at Le Magneraud, the local station of GEVES (Groupe d'Etude et de contrôle des Variétés et des Semences).

Bruno Richard, Head of the Variety Testing Unit, welcomed the participants. He described the structure and organization of GEVES in France and the activities carried out in the station at Le Magneraud.

The GEVES head office is in La Minière, near Versailles. The Group's technical activities are carried out at the National Seed Testing Unit (Station Nationale d'Essais des Semences, SNES) located in Angers and in the 11 experimental stations of the Variety Testing Unit (Secteur d'Etude des Variétés, SEV) distributed all over the country.

Variety testing includes testing for DUS (Distinctness, Uniformity and Stability) according to the CPVO protocol if available or to UPOV recommendations, and for VCU (value for cultivation and use) for agricultural crops. One reference sample is stored for each variety. There are about 1400 applications per year; about 25% are accepted for the French national list.

The autonomous unit in Le Magneraud, located on the site of INRA Poitou-Charentes, consists of an experimental unit and of the Biogeves laboratory.

The experimental unit carries out DUS and VCU trials and the management of the VCU networks. Crops under study include cereals (except rye), rapeseed, maize, sunflower, sorghum, vetch and field beans. VCU trials are carried out on maize, sorghum, beans and vetch. The seed management department has two cold rooms and one seed treatment unit. It manages all the reference samples for the agricultural crops (35 000) and genetic resources. It also organizes the treatment and dispatching of the samples for all the VCU trials in France.

Activities of the Biogeves laboratory include biochemical analyses of varieties proposed for registration (molecular analysis is planned in the future); variety identity checking;

research on suitable markers for variety identification; GMO detection in seeds; training; ring testing with other laboratories (UPOV).

Presentation and discussion on COST 860 – SUSVAR (sustainable low input cereal production)

Gert Kleijer presented COST, "an intergovernmental framework for European Co-operation in the field of Scientific and Technical Research", which may be of interest to the Working Group.

Founded in 1971, COST allows the coordination of nationally funded research on a European level. COST Actions cover basic and pre-competitive research as well as activities of public utility.

The goal of COST is to ensure that Europe holds a strong position in the field of scientific and technical research for peaceful purposes, by increasing European cooperation and interaction in this field.

Its major characteristics are:

- networking and coordination
- pan-European
- non-competitive
- involves national financing of researchers and therefore national responsibility
- bottom-up approach and built-in flexibilitiy
- "à la carte" participation
- multidisciplinary (wide range of disciplines covered)
- open to wider cooperation.

COST has a geographical scope beyond the EU and most of the Central and Eastern European countries are members. COST also welcomes the participation of interested institutions from non-COST member states without any geographical restriction.

COST has developed into one of the largest frameworks for research cooperation in Europe and is a valuable mechanism coordinating national research activities in Europe. Today it has almost 200 Actions and involves nearly 30 000 scientists.

COST countries include 34 member states (25 EU countries, EFTA member states (Iceland, Norway, Switzerland), candidate countries to the EU (Bulgaria, Romania, Turkey) and other countries (Serbia and Montenegro, Croatia, Macedonia FYR)) and one cooperating state (Israel). Institutions from non-COST countries and non-governmental organizations (NGOs) may join COST Actions.

COST managing bodies include a Committee of Senior Officials (2 representatives per COST country), Technical Committees (up to 2 representatives per country), a Management Committee and Working Groups.

In terms of funding , COST represents an estimated volume of national funding of more than 2.0 billion euro per year. An average of 80 000 euro per Action is available for coordination depending on the size and activities of the Action. This funding is basically used to cover coordination costs such as contributions to workshops/conferences, travel costs for meetings, contributions to publications and short-term scientific missions of researchers to visit other laboratories.

As an example of what can be achieved within the framework of a COST Action, G. Kleijer reported on the activities of one of the Actions in which he participates: "COST 860 - SUSVAR: sustainable low input cereal production - required varietal characteristics and crop diversity". Full details can be found on the Action's Web site (www.cost860.dk).

The steps to follow for the development of a COST action are summarized below (more details can be found on the COST Web page (http://www.cost.esf.org/):

- Find a subject
- Contact institutions all over Europe (5 COST countries)
- Prepare a project outline
  - objectives
  - benefits
  - scientific programme
- Evaluation in Brussels
- If accepted, development of the project, preparation of a Memorandum of Understanding
- Evaluation in Brussels
- Signature by individual COST countries

G. Kleijer said that he thought there might be good opportunities for the Wheat Working Group in this framework and encouraged the members to consider whether they would be interested in developing a COST proposal in a relevant domain of activity of the WWG. The participation would not have to be restricted to the institutes currently represented in the Wheat Working Group.

The Group expressed interest but no decisions were taken.

Establishment of a new workplan for the Wheat Working Group

Discussion and recommendations

Descriptors

Inclusion in EWDB of the six characterization descriptors agreed in 2001

- *It was agreed that it was important and urgent to complete the EWDB with characterization data for the six descriptors adopted at the first meeting in Prague, 2001.*
- *It was agreed that descriptors 1, 2 and 3 could be scored on alternative scales, reduced to three values. This point will be defined by Jean Koenig and Iva Faberová* ***by the end of October 2005.*** *The use of the reduced scale should be mentioned in the REMARK field (e.g.: "used reduced score for descriptor no. 3"). If the REMARK field is empty, it will be assumed that the full scale was used for scoring.*
- *It was agreed that each country should make precise commitments regarding data delivery. To facilitate implementation and monitoring, it was agreed to collate all individual commitments in a table containing the following information: current status (% of collection already documented for these six descriptors); expected deadlines for the transmission of data to EWDB manager, and % of the collection that is expected to be documented by the agreed country deadline.*

  This table was prepared and circulated immediately to the participants in the meeting, and some preliminary information was gathered. It will be circulated by email to the whole Group including the non-attending members for completion (deadline ***end October 2005).***

  When completed, the table will be loaded on the Wheat Web page (http://www.ecpgr.cgiar.org/Workgroups/Wheat) and eventually published in the report of this meeting (Appendix III).

Considering that the scoring of the six characterization descriptors would be facilitated by the use of common standards, it was agreed that J. Koenig will propose a set of standard varieties to be used for this purpose and will seek feedback from the Group on their suitability. The seeds will also be provided.

Evaluation descriptors

The 14 additional evaluation descriptors originally defined were reconsidered for use in the EWDB and they were all reconfirmed. It was agreed that:

- *the descriptors would be corrected to show the accepted names of pathogens,*
- *a new descriptor would be added: General disease susceptibility, based on field scores using a simplified scale (1 = very low susceptibility, 5 = variable susceptibility, 9 = very high susceptibility).*

The Group agreed that the data already available for the agreed evaluation descriptors will be sent to the database manager ***by the end of 2005*** *using the requested format.*

Additional scoring value for all descriptors

It was agreed that in all appropriate cases, an additional scoring value "X" would be provided, to be used for cases where scoring is variable (different values received, or unstable expression of the character).

Documentation of gene data

Identified genes should be entered into separate tables devoted to genes, containing the accession identifier, name of identified gene, and corresponding allele identified.

Safety-duplication

The Group agreed on the importance to safety-duplicate all the unique accessions in a different location, possibly a different country, as black boxes.[81]

The WG members will inform the WG Chair about progress achieved in safety-duplication ***by the end of 2006.***

The availability to host black boxes in their storage facilities was expressed by the WG members, as follows:

- Alcalá de Henares, Spain: yes
- Gatersleben, Germany: yes, to a limited extent
- Clermont Ferrand, France: on the basis of reciprocal exchange
- Nyon, Switzerland: yes, depending on quantity.
- CGN, the Netherlands: yes, depending on quantity
- Suceava Genebank, Romania: yes, depending on quantity

For the NGB, it will not be possible to take in safety-duplicates.

81 A sample of bilateral agreement for safety-duplication established between the Nordic Gene Bank and the Institute of Biology in Salaspils, Latvia, is available as Annex I, Pp. 101-102 *in* Maggioni, L. and T. Gass. 1998. Safety-duplication of germplasm collections in Europe. Pp. 96-102 *in* Report of a Working Group on Forages. Sixth meeting, 6-8 March 1997, Beitostølen, Norway (L. Maggioni, P. Marum, R. Sackville Hamilton, I. Thomas, T. Gass and E. Lipman, compilers). International Plant Genetic Resources Institute, Rome, Italy.

Repatriation of accessions

As an opportunity to rationalize the conservation of accessions on a European level, repatriation of germplasm to the country of origin was recommended.

The initiative to repatriate can be taken by a particular genebank, by informing other genebanks of the existence of accessions originating from their country, or genebanks can consult the EWDB or the curator in order to monitor the existence of national material in other countries' collections.

Repatriation can be accompanied by transfer of responsibility for conservation to the country of origin, while each genebank can decide to continue or terminate the maintenance of the repatriated samples, as preferred.

In order to facilitate the consultation of the EWDB, the DB manager will split the file in three parts and make the download easier. In specific cases (very urgent requests) the database manager will assist in extracting the desired listings of accessions.

Aegilops

The Group agreed that data on Aegilops *material should be included in the EWDB. Passport data should be sent to the database manager by the genebanks hosting* Aegilops *(France, Hungary, Israel, Switzerland, Turkey, and others)* ***by the end of 2005****.*

The taxonomic table can be changed allowing new taxa to be included in the EWDB, in order to have a list of accepted names. Eitan Millet will send the key for the taxonomy of Aegilops *to the database manager.*

The question of artificial species (amphiploid lines) was raised and the Group thought that this is to be considered scientific material and that it would not be included in the EWDB. For Triticale *a separate Central Crop Database exists.*

The EU project "Bioexploit"

Noor Bas informed the Group about the project "Bioexploit: Exploitation of natural plant biodiversity for the pesticide-free production of food", which was submitted in the sixth EU framework programme. This project will start on 1 October 2005 with a duration of 60 months and involves 42 partners from 14 countries.

It concerns two important staple crops: potato and wheat, for which pesticides are indispensable at the moment. The diseases taken into consideration for wheat are the following: *Septoria tritici; Blumeria graminis*, *Puccinia* spp. and *Fusarium* spp. The four strategic objectives of the project are the following: 1) to understand molecular components involved in durable resistance; 2) to explore and exploit natural biodiversity in disease resistance; 3) to accelerate the introduction of marker-assisted breeding and genetic engineering in the plant breeding industry; and 4) to coordinate and integrate resistance-breeding research. One of the subtasks is to analyze available taxonomic, passport and characterization data from EU genebanks to establish preliminary core collections for marker development and testing. Therefore, a collaboration between the project and the WWG can be expected to bring reciprocal advantages.

The Global Crop Diversity Trust and the ECP/GR Wheat Working Group

On behalf of the Global Crop Diversity Trust (http://www.croptrust.org), L. Maggioni described this joint FAO/CGIAR initiative, consisting of the establishment of an independent fund (under international law as of 2004), with a mission to support the conservation of the world's most important collections. At its centre is an endowment fund with an initial target of US$260 million, generating approx US$12 million per year for conservation, in perpetuity.

The eligibility principles and criteria for allocation of funds to the most important crop collections in the world were described (PGR must be included in the International Treaty Annex I crops, must be accessible under internationally agreed terms of access and benefit sharing; the holder needs to be committed to their long term conservation; the recipient of funds from the Trust will have to work in partnership with the aim of developing an efficient and effective regional and global conservation system).

The Trust approach of developing regional and crop conservation strategies was also described, and an invitation was extended to the Wheat WG to join the process of developing the wheat/rye/triticale global strategy, by identifying 1-2 persons who could join the specific Strategy Advisory Group, as representatives of the European region.

The timeframe for the preparation of the wheat/rye/triticale strategy is from 1 September 2005 through to 28 February 2006. The main event of this consultative process will consist in a stakeholders' workshop, possibly organized together with the 7th International Wheat Conference (27 November-2 December 2005, Mar del Plata, Argentina).

Feedback would be welcome from the ECP/GR WWG on the following issues:

- Feedback on the proposed process
- Representation of WWG in the process - suggestions
- Proposal for Advisory Group (1-2 persons from the WG)
- Existing information on collections, content and status of conservation
- Existing upcoming meetings as opportunities for consultation
- Links with European initiatives to rationalize the collections.

The Group agreed that it would be important to have representative(s) in the Wheat/Rye /Triticale Strategy Advisory Group (see below, Collaboration with the Trust).

Short presentations

Short presentations were given by the representatives of Italy (Marzia Cattaneo, ISC), Portugal (Benvindo Martins Maçãs, ENMP) and Turkey (E. Firat, AARI) *(full reports are included in Part II).*

Conclusion

Presentation and correction of the draft report

The draft report was presented to the participants and approved with minor modifications.

Election of the Chair and Vice-Chair

Annick Le Blanc having informed the Group that, owing to forthcoming changes in her professional career, she could not continue with her responsibilities as Chair of the Wheat Working Group, L. Maggioni asked the Group whether they had any candidate to propose. Two proposals were made: Z. Bulińska and I. Faberová proposed G. Kleijer, and L. Bondo proposed O. Díaz. Both candidates confirmed that they were interested and a vote took place. G. Kleijer was elected by majority.

The newly elected Chair thanked the Group and said that he was looking forward to helping the Group in its progress for the implementation of the agreed workplan. He particularly emphasized the importance of making progress with the central database, as an essential tool for all the Working Group's activities.

He also stressed the importance and the opportunity to strengthen relationships with the ECP/GR Steering Committee in the future, thanks to his membership in that committee as National Coordinator for Switzerland.

He then thanked A. Le Blanc for her past involvement and all her hard work throughout the years and for the organization of this meeting, and the ECP/GR Secretariat for its continuing support.

Finally, he asked I. Faberová whether she would take on the role of Vice-Chair for the Group and she accepted, with the consent of the rest of the Group.

Collaboration with the Trust

After the election of the WG Chair, the Group wished to discuss a possible reply to the invitation from the Global Crop Diversity Trust to nominate representatives from the WG who could help in the definition of the global strategy for Wheat/Rye/Triticale, possibly as members of the Strategy Advisory Group.

Different opinions were expressed by the Group members regarding the opportunity to designate someone with genebank management experience and/or with good knowledge of the crop from the breeder's perspective. The Group took into consideration the specific questions the Strategy Advisory Group will have to address, as well as the importance of linking the European conservation strategy (which is likely to evolve from the AEGIS project) with the global strategy. Overall, the Group agreed that the Chair (G. Kleijer) and the Vice-Chair and database manager (I. Faberová) will be the recommended representatives of the Working Group. However, it was also specified that other areas of strong expertise could be tapped in Europe and an evident source was available from the Nordic Gene Bank. Moreover, it was agreed that the Secretariat should inform the Trust whether any member of the Wheat Working Group was already planning to attend the 7th International Wheat Conference in November 2005 in Argentina. B. Maças informed the Group that he will attend this conference.

Closing remarks

The next meeting of the WG is planned for 2007, as part of the Cereals Network meeting, during which the three Cereal Working Groups (*Avena*, Barley and Wheat) plan to meet jointly. An offer to hold this meeting in Turkey was made by E. Firat and acknowledged with thanks by the Chair, with the comment that it will have to be discussed with the other Cereals Working groups.

Among the various social activities kindly organized by the local hosts in the charming city of La Rochelle and its surroundings, the visit to a private fossil collection made the Group reflect on the passing of Time…

PART II. PRESENTATIONS AND PAPERS

National collections

Status of wheat collections in Armenia

Alvina Avagyan
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Introduction
Wheat growing in Armenia has a very long-standing tradition. The area under wheat in 2004 was 128 705 ha, i.e. 39.6% of the arable land in use.

Activities related to *ex situ* conservation of wheat genetic resources in Armenia started in 1981, when the Plant Genetic Resources (PGR) Laboratory was established at the Armenian Agricultural Academy on the initiative of Prof. P.A. Ghandilyan. Today wheat genetic resources collections are maintained mainly in the Armenian Agricultural Academy (PGR Laboratory) and the Scientific Centre of Agronomy and Plant Protection of the Ministry of Agriculture. There is a small seed collection of wild wheats in the Institute of Botany of the National Academy of Science. In total, the wheat collections contain 2740 accessions, including 423 breeding lines, 2005 advanced cultivars (hybrids and/or lines), 67 local cultivars and landraces, and 245 wild species. Scientific institutions holding seed collections receive funding for the collecting and studying of samples from the state budget in the framework of current research programmes.

Collecting
The enhancement of the genetic diversity of the collection through collecting missions is one of the priorities. Itineraries of research expeditions are planned on the basis of data from former surveys and of information available from the literature. During the field missions in 2003-2004, 167 accessions of wild wheats were collected by the PGR Laboratory.

Storage
There is no national genebank for long- or medium-term conservation of PGR seed collections in Armenia. Seed samples of wheat (as well as of other crops) are currently stored in thick cardboard boxes or kept in paper bags under non-controlled temperature and moisture conditions. The Ministry of Agriculture, with financial support from ICARDA (the International Center for Agricultural Research in the Dry Areas), plans to establish facilities for medium-term conservation at national level.

Safety-duplication
Safety storage facilities are also lacking. The collection as a whole has been not duplicated at genebanks abroad, but 582 accessions of wheat are stored in the N.I. Vavilov Research Institute of Plant Industry (VIR, St. Petersburg). Materials collected during joint missions are also stored at other genebanks. Some accessions will be repatriated after the national genebank has been established.

Regeneration status
Stored accessions with low germination rates or only a small amount in the collection are regenerated. Sometimes several wild species are rejuvenated in glasshouses. The volume of field multiplication and regeneration is not large, and it varies from year to year, depending on the amounts of newly collected material, overall regeneration needs and the germination rates of the stored material. Owing to the shortage of technical and financial resources, many accessions require urgent regeneration.

Characterization and evaluation

Evaluation of the wheat collection is carried out by specialists working at the research institutions which keep seed collections. Evaluation and characterization of accessions are based on morphological, biological, disease resistance and productivity traits, but not all data are computerized. The most frequently evaluated parameters are the following: elements of yield structure (plant height, number of spikelets in the ear, 1000-kernel weight, number of kernels in the ear, etc.), time of heading, winter hardiness, resistance to prevalent diseases, resistance to lodging and sometimes protein content.

Availability of the material and institutional responsibilities

The stored genetic material can be transferred to research and educational institutions within the country and freely distributed to breeders and scientists or exchanged with other seed collections upon request. Material transfer agreements and prior informed consent mechanisms have been not developed yet for use in Armenia.

Four institutions deal with wheat genetic resources in Armenia, each responsible for different species or seasonal types and for kinds of research work:

- Armenian Agricultural Academy: collecting missions, morphological, physiological and cytogenetic studies of accessions, selection of the most potentially valuable forms for breeding, use of wild wheat relatives in breeding programmes, field trials;
- Scientific Centre of Agronomy and Plant Protection: breeding, preliminary agronomic evaluation and basic ecogeographical evaluation of winter wheat;
- Gyumri Breeding Station: breeding, field trials on spring and winter wheat; and
- Institute of Botany: taxonomy, collecting missions, morphological, anatomical and cytological studies.

Status of wheat genetic resources in Azerbaijan

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Azerbaijan, which is characterized by a wide variety of climates and soils, is the host to 16 species of wheat (*Triticum* L.). These include three wild species (*T. araraticum* Jakubz., *T. boeoticum* Boiss. and *T. urartu* Thum. ex Gandil.), which are mainly found on the Great Caucasian and Lesser Caucasian Mountains in the middle and low hill zones (e.g. in Aghsu, Shamakhi and Nakhichivan regions).

Two institutes deal with the protection of wheat collections in *ex situ* conditions (30 species): the Genetic Resources Institute (GRI) of the Azerbaijan National Academy of Sciences and the Scientific Research Institute of Agriculture (SRIA) of the Ministry of Agriculture. The GRI has coordinating functions and has carried out the National Inventory of *ex situ* collections. Some accessions have been lost for various reasons (mainly the lack of suitable conservation conditions and shortage of financial resources). Some seeds or accessions have lost their regeneration ability. Intermediate research materials have been defined. The results of the inventory are recorded in a database.

The genebank for medium-term conservation established at the SRIA holds in its working collections 5045 wheat accessions; these include 550 advanced local varieties and landraces. The remainder of the accessions are research materials obtained from ICARDA (International Center for Agricultural Research in the Dry Areas), CIMMYT (International Maize and Wheat Improvement Center) and VIR (N.I. Vavilov Research Institute of Plant Industry, St. Petersburg).

As of June 2005 the GRI collection contains 833 wheat accessions (mostly from Azerbaijan), including 451 landraces and wild species, 368 local cultivars, and 14 introduced cultivars from Iran, Syria, France, The Netherlands, etc. The collecting areas so far explored cover most regions of the country. The GRI wheat collection is being continually enriched through expeditions carried out by the Bioecology Laboratory and the Grain Cereals and Legume Laboratory, and through exchanges.

In the related laboratories of the GRI (e.g. Biochemistry, Physiology, Technology, etc.) evaluation and characterization of wheat accessions are carried out using international descriptors. The database located at the GRI contains passport data for 913 accessions of the genus *Triticum* L. The records include 79 accessions of wild species and 318 local varieties. The most frequently represented species are *T. aestivum* L. (665 accessions, including var. *lutescens* (116 accessions), var. *erythrospermum* (88), var. *ferrugineum* (86), and others), *T. durum* Desf. (166), *T. dicoccum* Schuebl. (12) and *T. boeoticum* Boiss. (9).

In the last growing season wheat was sown on 770 000 ha and the average crop yield was 2.5t/ha. The most frequently sown wheat varieties are ‘Azamatli-95’, ‘Gilchigsiz-1’, ‘Vugar’, ‘Alinja-84’ and ‘Giymatli 2/17’, but others are also grown. Measurements are being carried out on wheat *in situ*, on-farm and *ex situ*.

Status of the wheat collection in Bulgaria[82]

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The base collection of wheat maintained at the Institute of Plant Genetic Resources (IPGR) in Sadovo consists of 9454 accessions of bread wheat (*T. aestivum* L.), 2182 accessions of durum wheat (*T. durum* Desf.) and 785 accessions of other *Triticum* species (Table 1). The evaluation of accessions starts with their registration in the collection. The current collection is the result of more than 30 years of experimental work.

Table 1. Status of wheat collections maintained in the National genebank of Bulgaria (1977-2005)

Species	No. of accessions stored in the genebank*	Status of the germplasm			
		Bulgarian origin (breeding material and local forms)	Received from abroad	Unknown	Evaluated by descriptors
Triticum aestivum L.	9454 (8127)*	1050	3177	5227	8540
Triticum durum Desf.	2182 (1893)*	1034	431	717	1859
Triticum spp.	785 (577)*	15	289	481	110
Total	**12421**	**2099**	**3897**	**6425**	**10509**

* between brackets: number of accessions under long-term storage conditions

Accessions originate from all continents where wheat is grown. This guarantees a large variation within and among the genotypes which comprise the collection. The *T. aestivum* collection consists of accessions originating from Bulgaria, France, Germany, Russia, Ukraine and the USA. The durum wheat collection consists of about 50% local germplasm and 50% introduced from abroad (Italy, France, Russia, Spain, Turkey and the USA).

The wheat breeding programmes in Bulgaria have always focused on high productivity, genotype plasticity and resistance to stress factors. Because of climatic anomalies occurring in the last few years there has been a significant increase in the interest in accessions possessing these characters. Proper evaluation is therefore crucial.

In total 1497 cultivars and lines of bread wheat received from abroad during 1991-1995 have been evaluated and described according to the IPGRI descriptors (Table 2).

Among the 600 accessions of bread wheat evaluated for the raw protein content, 75 have a high protein content. Among the 500 accessions examined for flour sedimentation value, 92 have a high sedimentation value. Regarding ripening time, 42 accessions are characterized as early. Eleven accessions are above the country standard for certain productivity characters.

The ISTA (International Seed Testing Association) method for polyacrylamide gel electrophoresis (PAGE) of gliadins was used for cultivar identification in the framework of a project supported by the National Science Fund. We evaluated 52 wheat cultivars and 47 breeding lines originating from Bulgaria. The results were entered into a database using Vilber-Lourmat Bio 1D++ software.

In the last five years the utilization of the Bulgarian wheat collection in free exchange was as follows: 440 accessions were sent abroad and 55 were distributed to breeding programmes within the country.

[82] See also: "Status of the durum wheat collection in Sadovo, Bulgaria", pp. 140-141.

Table 2. Grouping of the Bulgarian wheat collection (*Triticum aestivum* L.) according to the variation in the agronomic characters evaluated

	Values	Minimum value	Mean value	Maximum value
1.	Plant height (cm) Number of accessions	<80 814	80.1-110.0 464	>110.0 219
2.	Ear length (cm) Number of accessions	<7.5 758	7.6-10.5 517	>10.5 222
3.	Number of productive ears per plant Number of accessions	<2.5 764	2.6-3.5 517	>3.5 589
4.	Number of spikelets per spike Number of accessions	<20 1203	20.1-26.0 288	>26 6
5.	Number of kernels per ear Number of accessions	<25 755	25.1-35.0 473	>35 269
6.	Kernel row weight per ear (g) Number of accessions	<1.4 1387	1.5-2.0 96	>2.0 14
7.	1000- kernel weight (g) Number of accessions	<38 1394	38.1-46.0 93	>46 10
8.	Raw protein content (%) Number of accessions	<12.6 405	12.7-17.0 120	>17.0 75
9.	Sedimentation (cm) Number of accessions	<40 217	41-55 191	>55 92

The wheat collection in the Czech Republic

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The wheat collection in the Czech Republic consists of domestic and foreign materials, and is composed of cultivated accessions which are mainly of European origin. The Research Institute of Crop Production (RICP) in Prague is responsible for the wheat collection within the National Programme. The size of the wheat collection held at RICP has reached 10 018 accessions. Nearly 60% of this amount are the winter wheat accessions, which are of the most interest in the region. Tables 1 and 2 show the composition of the Czech wheat collection.

Table 1. Overview of the Czech wheat collection

Status	Status of samples*					Total	% of total collection
	U	W	LR	AC	BM		
Passport	26	158	663	6414	2757	**10018****	100
Characterized/evaluated	24	21	349	5144	1817	**7355**	73.42
Storage							
Active	25	52	641	6361	2737	**9816**	97.99
Base	0	0	25	243	431	**699**	6.98
Safety-duplication	2	1	38	415	288	**744**	7.43

* U = unknown; W = wild; LR = landraces; AC = advanced cultivars; BM = breeding material
* genetic stocks (265 accessions) are excluded

Table 2. Accessions of domestic origin in the Czech wheat collection

Status	Status of samples*					Total	% of total collection
	U	W	LR	AC	BM		
Passport	0	0	70	208	478	**756**	7.55
Characterized/evaluated	0	0	28	198	348	**574**	7.80
Storage							
Active	0	0	70	207	471	**748**	7.62
Base	0	0	23	190	404	**617**	88.27
Safety-duplication	0	0	33	149	212	**394**	52.96

* U = unknown; W = wild; LR = landraces; AC = advanced cultivars; BM = breeding material

Revision

A thorough revision of the collection was carried out in 2004. Seed availability from the users' point of view was the main criterion of the check. The category "genetic stocks" which are not available for distribution, and other unavailable material, were excluded from the regular collection. Therefore, the total of accessions slightly decreased in comparison to 2003, despite the regular continuous receipt of additions to the collection.

Characterization and evaluation

The processing of characterization and evaluation data progressed considerably. All new accessions are characterized and evaluated regularly during their preparation for the seed collection. When necessary, older accessions are evaluated within regular regenerations. The synthesis of older characterization and evaluation data and their conversion into electronic form has been done recently. Identification methods based on the gliadin and glutenin composition and utilization of molecular markers (microsatellites) were intensified.

Core collections

Core collections in both the winter and spring wheat sub-collections were developed separately. The selection of accessions for the core was made according to morphology, taxonomy, pedigree analysis and microsatellites in the framework of parallel research projects.

Safety-duplication

Safety-duplication is in progress in collaboration with the genebank of the Research Institute for Plant Production (RIPP) in Piešťany (Slovakia). About 52% accessions of domestic origin are stored as safety-duplicates.

Documentation

The wheat collection is fully documented for passport data. The present proportion of characterized/evaluated accessions reached 73.4 %, with an average of about 30 descriptors per accession.

The Estonian wheat collection [83]

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Long-term preservation of the Estonian wheat collection is carried out by the genebank of the Jõgeva Plant Breeding Institute (JPBI). The mandate of the genebank is to collect and preserve the most outstanding varieties and breeding material of Estonian origin.

The Estonian wheat collection consists of material from the following institutions:

1. Jõgeva Plant Breeding Institute
   - varieties of Estonian origin
   - breeding material with special characteristics, of Estonian origin
   - varieties of foreign origin used in breeding programmes (small amount of seeds).

2. Department of Gene Technology of the Tallinn University of Technology
   Collection of diploid and tetraploid wheat accessions provided by the Vavilov Institute (VIR, St. Petersburg). Species which are accessible sources of genes for use in wheat improvement as donors of new genes for disease resistance, higher protein content, etc. Methods of monosomic aneuploid analysis and molecular genetics techniques were used for the localization and identification of the powdery mildew genes in these wheat lines. The most valuable wheat lines have been sent to the genebank with evaluation and characterization data.

3. Repatriation from other genebanks: the Vavilov Institute and the Nordic Gene Bank.

Accessions of the Estonian wheat collection
The long-term collection contains 284 accessions (52% winter wheat and 48% spring wheat) (Table 1).

Table 1. The Estonian long-term wheat collection

Status of sample	No. of accessions
Varieties of Estonian origin	9
Advanced cultivars	128
Breeders' material	146
Wild	1
Total	**284**

A breeder's field collection with more than 2000 wheat accessions is held by the Jõgeva PBI.

Safety-duplicates
According to the agreement between the Jõgeva PBI and the Nordic Gene Bank (NGB) in 1999, safety-duplicates of the most valuable accessions are preserved in the NGB.

[83] See also "Preservation and utilization of cereal genetic resources in Estonia", pp. 142-145.

Regeneration status

Since the genebank was established only six years ago and the material held in it is from 1998 or later, there has been no need for regeneration as yet, except for material repatriated from other genebanks. Five wheat accessions repatriated from VIR and two from the NGB were regenerated at the Jõgeva PBI during 2002–2005.

Characterization and evaluation activities

Characterization and evaluation of the varieties and breeding lines preserved in the genebank in long-term storage were conducted by the Jõgeva PBI. Biological and agronomic traits were tested in field trials and quality analyses made in the laboratory of the institute. Characterization of 57 wheat lines has been carried out at the Tallinn University of Technology (Department of Gene Technology).

Availability of material

The material is freely available. The database with passport data is accessible on the Internet (http://www.jpbi.ee/index.php/387/).

Wheat genetic resources in France

Annick Le Blanc[1] and Jean Koenig[2]

[1] *Collection Nationale Céréales à Paille, GEVES - Domaine du Magneraud, Surgères, France*

[2] *Institut National de la Recherche Agronomique (INRA) – UMR 1095 – Amélioration et Santé des Plantes, Clermont-Ferrand, France*

A very large collection of wheat genetic resources is conserved by INRA in Clermont-Ferrand, but a network, led by GEVES, which brings together public and private research and breeding institutes (according to the strategy elaborated within the framework of the French National Charter for the Conservation of Genetic Resources), is responsible for the management of the accessions, which is the official priority in the international context.

In the near future, this organization may be changed: INRA may then manage all the seeds (conservation, regeneration, distribution) while the network partners would participate in the collection, evaluation and use; the whole structure will still be overseen by a steering committee.

Description of the wheat collection

Total number of wheat accessions : 11 965, of which 5889 are managed by the French small seed cereal cooperative network; 70% of these are of *Triticum aestivum*.

About 50% of this material is of French origin. Among those of foreign origin, about 80% are from Europe.

Most of the collection can be classed as landraces or obsolete cultivars, breeding lines or scientific material and recent cultivars. There are a few lines classed as wild and collected material.

Evaluation and description of wheat genetic resources

Each year the network dispatches to various members a number of genotypes from the Collection, or new genotypes proposed for this Collection, so that they can be described more precisely and eventually used directly in breeding programmes.

In the course of regeneration, accessions have been described according to the list of descriptors recommended by the ECP/GR Wheat Working Group: awnedness, grain colour, glume colour, glume hairiness, spike density and plant height. This has been done particularly thoroughly for the INRA wheat core collection (about 400 accessions).

INRA itself, during 2000 to 2002, evaluated its entire collection for agromorphological characters, such as heading date, plant height, frost resistance, kernel weight, awnedness, and pest and disease susceptibility. Computerization of these data is in progress.

Seed and data access

Data are computerized in a centralized database named ERGE, developed by GEVES on Access software.

Access to the National Collection is unrestricted and free of charge, which is especially useful for reciprocal exchanges between genebank partners, breeders and research institutes around the world. Fifty to 100 seeds per accession are supplied depending on the quantity available.

Objectives in the near future

- Improve the system (conservation, multiplication, distribution, database management, etc.)
- Make an inventory of durum wheat and wheat-related species collections in France
- Carry on the minimum description of the collection
- Carry on computerization
- Include molecular descriptors
- Carry out quality assurance requirements in order to obtain accreditation as a Gene Bank according to the ISO 9001 Standard.

Wheat genetic resources in Germany

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Establishment of a federal central genebank *(ex situ)* for agricultural and horticultural cultivated plants (contributed by L. Frese and H. Knüppfer)

A merger took place of the genebank collections of the Federal Centre for Breeding Research on Cultivated Plants (BAZ) and of the Institute of Plant Genetics and Crop Plant Research (IPK). The whole collection is now managed by the IPK genebank in Gatersleben.

- **Status of the merger**

The IPK genebank is developing a new genebank information system, GBIS, which contains already the passport data of the former BAZ genebank holding. The BAZ genebank will also contribute its characterization and evaluation data as well as updated observations made according to the IPGRI descriptor list for wheat and to UPOV. This task has been completed for 22 172 accessions and 171 characters of wheat.

All wheat accessions have been transferred from BAZ to IPK. They are integrated in the federal genebank and are available to users.

- **Present species composition of the wheat collection (Table 1)**

The collection contains 53% landraces and wild species, and 47% cultivars and lines. Regarding seasonal growth types, 41% are winter wheats, 58% spring wheats and 1% intermediate forms or the seasonality is unknown.

Table 1. Number of accessions of the most frequent *Triticum* species (>20)

Species	No. of accessions
T. aestivum L. em. Fiori et Paol.	12554
T. aethiopicum Jakubz.	624
T. araraticum Jakubz.	60
T. boeoticum Boiss. em. Schiem.	114
T. carthlicum Nevski	78
T. dicoccoides (Körn. ex Aschers. et Graebn.) Schweinf.	96
T. dicoccon Schrank	521
T. durum Desf.	1579
T. macha Dekapr. et Menabde	39
T. monococcum L.	153
T. polonicum L.	76
T.* sp. (accessions not yet determined)	**11251**
T. spelta L.	195
T. sphaerococcum Perciv.	74
T. turanicum Jakubz.	31
T. turgidum L.	135
T. urartu Thum. ex Gandil.	58

* Accessions referred to as "*Triticum* sp." are recent acquisitions (mostly from the former BAZ collection). They will be taxonomically re-determined.

National evaluation programme for plant genetic resources of cereals (EVA II) [84]

- **Management**

Federal Centre for Breeding Research on Cultivated Plants, Institute of Epidemiology and Resistance Resources, Aschersleben.

- **Aims**

Establishment of a standardized evaluation system of the main cereals (wheat, barley) to provide breeders with genotypes resistant to the most important diseases and with relevant scores from up to 27 sites and from one or more years. The data are available on the Internet via the information system www.genres.de/eva.

- **Cooperating partners**

- 6 public research centres and institutes
- 19 private breeding companies

- **Origin of evaluated samples of winter and spring wheat from 2001 to 2005**

Breeders' lines	192
Genebank accessions	112
Foreign cultivars	183

About 200 genebank accessions are evaluated annually. After pre-selection for agronomic and resistance traits they are included in EVA II for tests at different locations. The data are transferred to ZADI (German Centre for Documentation and Information in Agriculture, Bonn), analyzed and included in the information system.

[84] See also "German Network for the evaluation and use of disease resistance in cereals (EVA II)", pp. 205-210.

Status of the national wheat collections in Hungary

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Institute for Agrobotany (TABI), Tápiószele, Hungary

Institutional responsibilities

In Hungary, the Institute for Agrobotany, Tápiószele (TABI) bears the overall responsibility for the maintenance of wheat genetic resources. TABI receives full governmental budgetary support via the Ministry of Agriculture and Rural Development, and all its main tasks are related to plant genetic resources activities. It is thus responsible for the development and maintenance of the Hungarian field crop and vegetable genebank collections. The TABI wheat collection consists of 8290 accessions of 24 *Triticum* species (Table 1).

Table 1. The wheat collection at the Institute for Agrobotany, Tápiószele (TABI)

Species	No. of accessions
T. aestivum L.	7380
T. durum Desf.	417
T. monococcum L.	174
T. spelta L.	87
T. dicoccon Schrank	59
T. turgidum L.	37
T. dicoccoides (Körn. ex Aschers. et Graebn.) Schwein	22
*T. timopheevii (*Zhuk.) Zhuk.	22
T. boeoticum Boiss.	19
T. carthlicum Nevski	18
14 other species	<10

Within the country five other institutions (mainly breeding institutions or universities) are involved in wheat genetic resources activities. A great part of their working collections (2750 accessions) is deposited in the National Base Collection (NBC), which is also established and operated at TABI.

Development / collecting

Since its founding in the middle of the past century, the TABI wheat genebank collection has been continuously developing. In the first decade of its history a major part in the increase in the numbers of stored accessions resulted from field collecting missions in the country. In the last five years 38 accessions have been introduced from direct collecting in Hungary and in the Carpathian valley. Nowadays the main sources for the development of the collection are seed exchange (including the repatriation of wheat samples of Hungarian origin from other genebanks) and the breeders' donations from their working collections. Special attention has also been paid to the collection of ecotypes of *Aegilops cylindrica* Host., which is an aboriginal wheat wild relative species found in Hungary (75 accessions collected).

Regeneration status

The accessions which require urgent regeneration because of decreasing viability or depleted seed stocks are multiplied as necessary each year, but the overall volume of field multiplication and regeneration changes from year to year according to the results of introduction or collecting activities.

Characterization and evaluation activities

The descriptor lists for the characterization of the TABI wheat collection include 64 characters. Although characterization has been a routine activity at TABI since the beginning of the 1980s, a relatively large number of wheat accessions (those which were deposited earlier into the storage chambers) still need to be characterized. Because of budgetary problems, the detailed evaluation is done at a restricted level.

Documentation

Data management (passport, characterization and genebank management data) is fully computerized but the updating and the thorough overhaul of the more than 30 year-old TABI databases are under way.

Storage

The TABI wheat collection is managed according to international genebank standards. After careful field multiplications, viability tests and drying to agreed standards, the wheat seed samples are stored in the active and base collection chambers. The storage temperature is 0°C in the active and -20°C in the base collection storage rooms.

Safety-duplication

One third of wheat collection is duplicated within TABI. A large portion of the accessions, which really deserve safety-duplication, is duplicated within the country, but at present there is no special programme for the safety-duplication of the whole collection abroad, or at another Hungarian institution.

Availability of material

TABI's own materials are freely available to users, though with seed samples of limited size. The accessions deposited in the NBC are at the disposal of the persons or institutions who placed them there.

Status of the Irish National Wheat Collection

Barry O'Reilly

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Collection

The Department of Agriculture and Food maintains the national genebank collection of wheat accessions at its Variety Testing Station at Backweston, Leixlip, Co. Kildare. The national collection is in the initial stage of its development and contains approximately 30 wheat accessions at present. Some of these are of Irish origin but the main collection comprises selections of Ethiopian landrace wheats with high protein content. A small number of old Irish varieties of wheat are conserved *in situ* by NGOs.

Collecting

The collection was established in July 2002. No new accessions have been added to the collection since then. Work to expand and develop the National wheat genebank is ongoing.

Storage

Approximately 500 g of each wheat accession are kept under refrigeration at the National Crop Variety Testing Centre, Backweston, Leixlip, Co. Kildare.

Regeneration status

The wheat collection is regenerated in the field every three years. At present, as the numbers of accessions is still quite small, the viability of the collection is monitored through regular germination testing.

Characterization and evaluation

The Ethiopian landrace wheats ("Farmers Selection") in the collection are generally variable and lack homozygosity. Only few of these wheats have been characterized and evaluated so far.

Availability of material

Samples of wheat from the national collection are available to other institutions and organizations.

Collections of Triticum *and* Aegilops *species in genebanks in Israel*

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There are four major collections of *Triticum* and *Aegilops* species in Israel. One is in the Israeli Genebank for Agricultural Crops managed by the Ministry of Agriculture and three are owned and managed by their institutions. The status of the collections is shown in Table 1.

Table 1. *Aegilops* and *Triticum* collections in Israeli genebanks

Species	Holding institute						
	Israeli Gene Bank, Bet-Dagan	Institute for Cereal Crops Improvement, Tel-Aviv		Institute of Evolution, University of Haifa		Weizmann Institute of Science, Rehovot	
	No. acc.	No. acc.	No. pops.	No. acc.	No. pops.	No. acc.	No. pops.
Aegilops							
bicornis		498	11		4	16	
biuncialis	1	121	-		4	50	
kotschyii	2	176	5		24	39	
longissima	25	1695	37		30	38	
ovata	1	422	4		24	63	
searsii	9	255	5		8	30	
sharonensis	18	2196	40		12	18	
speltoides	1	1394	25		5	132	5
triuncialis	1	118	-		4	63	
variabilis	1	1096	22		54	102	
Triticum							
dicoccoides	534	2370	62	1664	>25	142	12
aestivum	1966	ca. 1000				404	
durum	115					429	

The Israeli Gene Bank (IGB), Bet-Dagan collection

Curator: Dr R. Hadas (rihadas@volcani.agri.gov.il).

In addition to those listed in the table, IGB holds a few accessions of various subspecies and varieties of different wild, primitive and modern *Triticum* species. The accessions were contributed by different individuals and their availability for seed distribution depends on the terms agreed by the donors. Seeds are stored in cold rooms (-15°C, 15% RH) and regenerated as required.

The Institute for Cereal Crops Improvement (ICCI), Tel-Aviv University collection

Curator: Dr J. Manistersky (jacobm@post.tau.ac.il).

Seed distribution policy: collaboration. The collection consists of 10341 accessions from 11 species that are stored in cool rooms (7-12°C, 35-40% RH) and regenerated as required (all accessions have viable seeds). Most of the accessions were evaluated for response to leaf rust, some also for response to yellow rust and stem rust and some *T. dicoccoides*, *Ae. sharonensis* and *Ae. bicornis* for response to powdery mildew. *T. aestivum* accessions are differential lines for pathogen race differentiation.

Institute of Evolution, University of Haifa collection

Curator: Dr A. Beharav (beharav@research.haifa.ac.il).

The *T. dicoccoides* collection represents accessions from a wide range of ecological conditions in Israel and neighbouring countries and was evaluated for various traits (information from Prof. E. Nevo at nevo@research.haifa.ac.il). Seeds are stored in cool rooms (4-10°C, 10% RH). The *T. dicoccoides* collection is regenerated every 12 years. *Aegilops* seeds were collected in 1992 (original seeds). Seed distribution policy: collaboration.

Department of Plant Sciences, the Weizmann Institute of Science, Rehovot collection

Owner: Prof. M. Feldman (moshe.feldman@weizmann.ac.il).

In addition to the list in Table 1 there are also various genetic stocks including mutants, aneuploids, amphiploids and substitution and addition lines. The *T. durum* collection includes landraces. Seeds are stored in dry freezers (-18°C). The collection is regenerated occasionally. Seed distribution: upon request.

Wheat genetic resources at the Experimental Institute for Cereal Research, Italy

Marzia Cattaneo and Gaetano Boggini

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Italian wheat breeding has a very long and significant tradition: its most celebrated personality was the famous geneticist Nazareno Strampelli, who started wheat breeding work in Italy at the end of the 19th century and anticipated Borlaug's "green revolution" in our nation. He is regarded as the intellectual father of a large family of important Italian breeders who continued (and are still continuing) this activity, with increasing success. He can be considered the originator of a large number of cultivars which have spread all over the world, becoming the progenitors of several fundamentally important cultivars which have largely been grown until now in the most important cereal-growing countries of the world (Argentina, Australia, China, Russia, East European states, USA, etc.).

The Experimental Institute for Cereal Research (Istituto Sperimentale per la Cerealicoltura, ISC) stores collections of different cereal species of interest in its various Sections. The *Triticum* accessions which it maintains are shown in Table 1.

Table 1. Sections of the ISC maintaining *Triticum* species

ISC Section	Main species of *Triticum* held	Approximate no. of accessions
S. Angelo Lodigiano	*T. aestivum*	4475
	T. monococcum (subsp. *monococcum* and *boeoticum*)	1500
Roma	*T. aestivum* and *T. durum*	300
Foggia	*T. durum* and *T. spelta*	550
Catania	*T. durum* and *T. aestivum*	310
Total		**7135**

To assemble the different *Triticum* collections present in our country, in the 1980s the ISC section of S. Angelo Lodigiano started tracking, recovering and growing accessions from both public and private groups in order to preserve and describe them, as summarized in Table 2. About 4500 accessions, particularly of *T. aestivum* and to some extent of *T. durum*, with duplicates in some cases, were collected.

All these accessions have been regenerated in the field and characterized by morphological descriptors for plant, ear and seeds, according to both the IPGRI and National Register protocols. Part of this material has also been transferred to the Bari Germplasm Institute.

Table 2. Italian public institutions and private companies which contributed wheat accessions to ISC

Origin of accessions	Approximate no. of accessions
Public institutions	
Istituto Sperimentale per la Cerealicoltura (ISC), S. Angelo Lodigiano	2000
Istituto di Genetica e Sperimentazione Agraria N. Strampelli, Lonigo (Vicenza)	720
Dipartimento di Agronomia Generale e Coltivazioni Erbacee, Università degli Studi di Firenze	100
Private companies	
Società Produttori Sementi, Bologna	510
Dekalb, Settore Italiano Frumenti, Treviso	500
Amministrazione M.A. di Frassineto, Fontarronco	240
Sementi Samoggia, Bologna	215
Società Italiana Sementi (SIS) Foraggera, Badia Polesine	105
Federconsorzi, Roma	85
Total	**4475**

In a second stage, other species of *Triticum,* mostly from foreign institutions, were added to the collection. *Triticum monococcum*, with about 1450 accessions, *T. dicoccum* and *T. spelta*, with 250 accessions, are the most frequently represented species in this new part of the collection.

During the last ten years our aim has also been to collect and describe the wheat varieties bred by Nazareno Strampelli, utilizing up-to-date biochemical and molecular methods.

Broad bibliographical research allowed us to recover the descriptions of 77 Strampelli bread wheat varieties. In collaboration with national and international institutions, over 200 samples believed to belong to Strampelli's materials were gathered (Table 3). They were fingerprinted by means of storage proteins and molecular methods (AFLP). The results of the analyses reduced to 86 the number of verified accessions, representing 53 varieties. Some varieties, in fact, were present as several different biotypes, which were slightly diverging for biochemical or morphological characteristics. All the analyses were also performed on six relevant progenitor lines which had been used by Strampelli in his breeding programme.

Table 3. Institutions which sent germplasm bred by N. Strampelli and total number of evaluated and confirmed accessions (duplicates are included).

Institution	Total no. of evaluated accessions	Total no. of confirmed accessions
Istituto Sperimentale per la Cerealicoltura (ISC), Roma, Italy	61	44
Centro Ricerche e Sperimentazione per il Miglioramento Vegetale (CERMIS), Tolentino (MC), Italy	11	7
Ente Nazionale per le nuove tecnologie, l'Energia e l'Ambiente (ENEA), Roma, Italy	32	26
Istituto del Germoplasma, Bari, Italy	8	8
Istituto di Genetica e Sperimentazione Agraria "N. Strampelli", Lonigo (Vicenza), Italy	2	1
Scuola Superiore S. Anna, Pisa, Italy	6	2
Various seed companies, Italy	12	9
Australian Winter Cereals Collection, Tamworth, NSW, Australia	35	25
Crop Research Institute, Academy of Agricultural and Forestry Sciences, Ningxia, China	7	4
N.I. Vavilov Institute of Plant Industry (VIR), St. Petersburg, Russia	21	12
USDA National Small Grains Collection, Aberdeen, Idaho, USA	14	8
Total	**209**	**146**

The results of this extensive project, which highlight again the amplitude of Strampelli's research, are presented in a CD-ROM (CRA-ISC 2004) containing the article "*Le varieta' di frumento tenero costituite da Nazareno Strampelli: descrizione morfologica, agronomica, biochimica, molecolare e tecnologica. Rivisitazione scientifica di una pagina di storia italiana" (Bread wheat varieties developed by Nazareno Strampelli: morphological, agronomic, biochemical, molecular and technological description. Revisiting a historical page of Italian history)"* and the "*Schede descrittive delle 53 varietá" (Description of the 53 varieties)*. Four articles in English (three by the researchers of the S. Angelo Lodigiano Section, and one in collaboration with the N.I. Vavilov Institute in St. Petersburg), reporting specific facets of the complex research carried out on Nazareno Strampelli bread wheat germplasm, and which were originally presented at international conferences are also included, as well as a copy of the original book reporting Strampelli's work during his active years (Strampelli 1932).

For the coming years, our programme includes the documentation of passport data for all accessions, a better subdivision and characterization of the Italian varieties to distinguish them from the foreign accessions, and the improvement and if possible the completion of the collection of Strampelli's material.

In Italy other institutions must also be mentioned for their interesting work on *Triticum*, made in order to prevent the loss of biological material and to preserve biodiversity. In particular the group of researchers of the Istituto di Genetica e Sperimentazione Agraria N. Strampelli ("N. Strampelli" Institute for Genetic and Agricultural Experimentation) of Lonigo (Vicenza) not only evaluated the accessions of *Triticum*, but also the local populations of *Zea mays*, and has even described the history of these important crops in northeast Italy (Veneto region). The results are reported in a book and a CD-ROM, with articles, tables and photographs of accessions (Bressan *et al.* 2003).

Other projects have been carried out by researchers of the CERMIS (Centro Ricerche e Sperimentazione per il Miglioramento Vegetale = Research and Experimentation Centre for Plant Improvement, Tolentino) and of the St. Anna Superior School (Pisa), who gave special attention to old local populations grown in Central Italy. Some private companies and breeders, universities and regional authorities also maintain small collections.

The status of the Bari Germplasm Institute collection was reported in 2003 by Perrino.[85]

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[85] See "Wheat germplasm collections in the Bari Genebank, Italy", pp. 148-153.

Status of wheat genetic resources conservation and utilization in Latvia

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Plant genetic resources (PGR) activities in Latvia were started only after the collapse of the former Soviet Union. The Latvian Gene Bank of Cultivated Plants was established in 1998 at the Institute of Biology, University of Latvia (Salaspils) in the framework of the Nordic-Baltic PGR project (Rashal 1999, 2002). The mandate of the genebank covers only accessions of Latvian origin, with one small exception.

Seeds in the Latvian Gene Bank of Cultivated Plants are stored according to internationally accepted standards. Seeds of both the basic and active parts of the collections are stored in commercial deep freezers. Safety-duplicates of the most important Latvian accessions are stored in the Nordic Gene Bank according to a bilateral agreement (Anonymous 1999). All accessions preserved in the Latvian Gene Bank are divided into three priority groups according to their status: 1) varieties, 2) advanced breeders' lines, and 3) genetic stocks. The numbers of seeds stored in the Latvian Gene Bank depends on the priority group of an accession (Table 1).

Table 1. Number of seeds per accession in the Latvian Gene Bank of Cultivated Plants

Priority group	Base collection	Active collection	Safety-duplicate collection (Nordic Gene Bank)
1	10000	5000	2000
2	2500	2500	-
3	< 1000	< 1000	-

The Latvian Gene Bank operates as a centre for the Latvian PGR network. Multiplication, evaluation and characterization are carried out by experts in particular crops, mainly in the plant breeding stations. Wheat multiplication and evaluation/characterization, as well as the maintenance of the working collection is done at the State Stende Plant Breeding Station. The first trials with wheat were started at Stende Plant Breeding Station in 1923. Local material and wheat varieties from foreign countries were investigated. During the Soviet period, working collections were created through the Vavilov Institute in St. Petersburg (VIR). When the national Latvian PGR programme was initiated in the mid-1990s, the collection of wheat was inventoried. All available varieties of Latvian origin and some advanced breeders' lines were accepted for long-term preservation in the genebank (Table 2). Unfortunately, no Latvian wheat landraces survived.

Table 2. Wheat (*Triticum aestivum)* accessions in the Latvian Gene Bank of Cultivated Plants

Crop	No. of accessions
Spring wheat	
- varieties (1920s-1950s)	2
- breeders' lines	9
Winter wheat	
- varieties (1920s-1940s)	6
- varieties (1980s)	2
- varieties (1990s)	6
- breeders' lines	26
- traditional varieties of foreign origin	2
Total	**53**

Along with the evolution and characterization of wheat genetic resources for conventional breeding, new breeding activities and the assessment of selection criteria for organic breeding were started at the State Stende Plant Breeding Station in 2002. Organic farming is a comparatively new and increasingly important direction for agriculture in Latvia. The lack of appropriate wheat genotypes selected for productivity under low input agriculture is a major limiting factor for further breeding work.

For commercial use in organic farming, cultivars need to fulfil both general requirements (high yield potential, baking quality, disease resistance) and specific criteria (efficient utilization of fertilizing elements during the growth period, effective plant competition with weeds, stability of the main traits under varying environmental conditions). Eight winter wheat varieties - 'Krista', 'Sakta', 'Banga' (Latvia), 'Pamjati Fedina' (Russia), 'Ibis' (Germany), 'Cobra' (Poland), 'Belina' and 'Garmonia' (Belarus) - were tested in low input conditions. Grain yield and stability, winter hardiness, resistance against the main diseases, protein content and quality, falling number, lodging, plant height and several morphological traits were evaluated. There was clear evidence that local varieties are more suitable for growing under organic conditions. Accessions from the 1950s and 1960s (both varieties and breeding lines) can be used as a source material for breeding wheat varieties suitable for organic farming.

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Status of the winter wheat collections in Lithuania [86]

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All winter wheat accessions are kept in the active collections of the Lithuanian Institute of Agriculture (LIA). Since 1995 the collections have been increased by the addition of new material received from other institutions or obtained from breeding programmes.

In 2005 the collection contained 15 winter wheat varieties of Lithuanian origin. The Nordic Gene Bank (NGB) has provided facilities for long-term seed storage at LIA. Seventy-two winter wheat accessions of Lithuanian origin (old varieties, breeding lines, mutants) have already been placed under long-term conservation (10 000 seeds per accession). Eight winter wheat accessions of Lithuanian origin have been placed in the long-term safety-duplication collection in the base collection of the genebank of the N.I. Vavilov Research Institute of Plant Industry (VIR).

Table 1. Winter wheat collections at the Lithuanian Institute of Agriculture, 2005

Sample status	No. of accessions
Varieties	440
Breeding lines, mutants, genetic stocks, infraspecific taxa	235
Varieties of Lithuanian origin	15*
Total	**690**

* 8 accessions are duplicated at VIR

Most of the Lithuanian winter wheat accessions were described in the *Catalogue of Lithuanian Plant Genetic Resources* (Būdvytytė *et al.* 1997). In 1998 material was prepared for the Baltic plant genetic resources catalogue; it will include only varieties and lines of Baltic origin.

The Lithuanian Institute of Agriculture has an active winter wheat collection which is mainly used for breeding purposes. It is not stored in long-term seed storage. The number of accessions is not constant. Since 1989 all winter wheat varieties received at the Lithuanian Institute of Agriculture have been officially collected and maintained. The number of accessions at LIA currently amounts to 690. Every year, about 200 accessions are planted and evaluated in experimental fields. In order to maintain high seed viability, the varieties need to be regenerated every three years.

Our future plans include continuation of the collection, preservation, identification, characterization, evaluation and documentation of the accessions, and extension of cooperation and exchange of genetic material with other holders of plant genetic resources.

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[86] See also “Wheat genetic resources in Lithuania”, pp. 162-166.

Current status and utilization of wheat genetic resources in Macedonia FYR

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Introduction
The main wheat breeding activities in Macedonia (FYR) are concentrated at the Institute of Agriculture in Skopje. The wheat collection is maintained in collaboration with the Faculty for Agricultural Sciences and Food, Department for Genetics and Plant Breeding. The wheat breeding programme and the establishment of the working collection were started in 1970. In 1996 evaluation of the wheat collection was carried out using IPGRI descriptors. The collection contains 200 accessions of *Triticum aestivum* and 265 accessions of *T. durum*. Basic information data have been collected and processed, but are still incomplete, due to some missing passport data.

This report will focus on the status of the active collection of *T. aestivum* and of the base collection which has been partially assessed for grain moisture and protein contents.

Current status of wheat genetic resources and their utilization
Before 1996, the complete *T. aestivum* collection was reproduced every year under field conditions. The existing cold chamber for medium-term conservation allows us to reduce the number of accessions in the field each year.

The active collection consists of approximately 60-70 accessions that are commonly used in breeding programmes as the parental components in hybridization. Beside yearly regeneration, some assessments are usually carried out in the active collection, such as recording phenological data, morphological and productive characters, etc. In the last few years, the main aim in wheat breeding has been to attain high baking quality accompanied by good yielding ability; therefore some Hungarian varieties of A_1 and A_2 quality groups have been included in the active collection as well as the other local accessions.

The base collection is stored in a cold chamber (2°C). In July 2005, the grain humidity values of 62 accessions ranged from 12.3 to 13.3%, which indicates good conditions for storage. The same accessions were also examined for dry matter protein content in the laboratory: the values ranged between 13.5 and 20%. In 28 of the 62 accessions, the protein content was higher than 15.6%, which provides a good choice of potential parents in further breeding programmes for high baking quality.

Further activities
The following activities are planned for the future:
- Completion of the examination of a number of M_6 generation lines (derived from gamma-ray mutagenically treated wheat varieties) and inclusion of the best ones in the base collection;
- Setting up of suitable conditions for the repatriation of the collection of wheat landraces originating from Macedonia, currently held by USDA (United States Department of Agriculture);
- Improvement of PGR data computerization in order to make the data available to the international research community;
- Work on the National Programme for genebank activities.

The wheat collection at the Nordic Gene Bank

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The Nordic Gene Bank (NGB) is a regional institute under the Nordic Council of Ministers. The region includes the following Nordic countries: Denmark, Finland, Iceland, Norway and Sweden. The NGB collection currently contains a total of 1677 accessions of the genus *Triticum*, including different species and subspecies (Table 1). This material has been used in pre-breeding programmes worldwide and also in some phylogenetic studies.

Table 1. *Triticum* species preserved at the Nordic Gene Bank

Species	No. of accessions
Triticum sp.	171
Triticum aestivum	
subsp. *aestivum*	1324
subsp. *compactum*	11
subsp. *macha*	2
subsp. *spelta*	21
subsp. *sphaerococcum*	4
Triticum monococcum	
subsp. *aegilopoides*	7
subsp. *monococcum*	59
Triticum timopheevii	
subsp. *armeniacum*	1
subsp. *timopheevii*	10
Triticum turgidum	
subsp. *carthlicum*	3
subsp. *dicoccoides*	8
subsp. *dicoccon*	21
subsp. *durum*	15
subsp. *paleocolchicum*	1
subsp. *polonicum*	4
subsp. *turanicum*	1
subsp.*turgidum*	14
Total	**1677**

The NGB wheat collection consists of 221 cultivars and 38 landraces of Nordic origin (Table 2). This collection has been evaluated for different morphological characters, such as awnedness, ear density and emergence, growing time, lodging, lower glume hair, plant growth habit, plant height, as well as for susceptibility to several fungus diseases (e.g. powdery mildew, leaf rust, yellow rust and septoria). The results are available on the Internet at http://www.ngb.se/sesto.

Table 2. Status of samples in the NGB wheat collection

Country of origin	Cultivars	Landraces	Total
Denmark	24	1	25
Finland	29	6	35
Norway	19	4	23
Sweden	138	21	159
Other countries	11	6	17
Total	**221**	**38**	**259**

Beside the ordinary wheat collection, NGB conserves other special *Triticum* collections:

1. the wild Triticeae collection, which consists of a number of accessions collected in different geographical areas of Europe, China and in North and South America, comprising 1286 accessions of wild and locally cultivated species from different genera. *Triticum* is represented by 69 accessions of *Triticum aestivum*, *T. monococcum* subsp. *aegilopoides* and *T. turgidum* subsp. *durum*. The genera *Hordeum, Secale, Aegilops, Elymus, Roegneria, Agropyron* and *Brachypodium* are also included in this sub-collection;
2. the collection of Near Isogenic Lines, developed by Professor James Mac Keys at the Swedish University of Agricultural Sciences, consists of 222 lines derived from backcrosses utilizing Nordic wheat parents. This material provides valuable gene sources especially for improving disease resistance in wheat; and
3. the Haslund-Christensen collection, which includes 22 *Triticum* accessions collected in Afghanistan during the 1940s.

The NGB distributes these seeds and information about the material to all interested researchers and breeders free of charge.

The wheat genetic resources collection in Poland

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The wheat genetic resources collection is one of the most important collections maintained in the Polish genebank, which is hosted by the Plant Breeding and Acclimatization Institute at Radzików near Warsaw. It represents a substantial share of the genetic resources material which is under the management of the National Crop Genetic Resources Conservation Programme in Poland, the overall responsibility for which is entrusted to the Crop Genetic Resources Center in Radzików. The programme is financed by the Ministry of Agriculture. The Centre provides controlled storage facilities (-18°C and 0°C), organizes collecting missions, holds central databases and leads national and international cooperation. The Programme is based on multi-institutional input. Three universities, nine branch institutes, seven experimental stations, and the Botanical Garden of the Polish Academy of Science are all responsible for various aspects of the conservation of crop collections.

The wheat genetic resources collection consists of 10 327 accessions of spring and winter types belonging to 20 species (see Table 1), mostly of *Triticum aestivum* and *T. durum.*

Table 1. Species composition of the Polish wheat genetic resources collection

***Triticum* species**	**In storage**	**Collected material**	**Total**
aestivum	8064	110	8174
aethiopicum	36		36
araraticum	4		4
boeoticum	18	14	32
compactum	17		17
dicoccoides	7		7
dicoccum	44	6	50
durum	1823	5	1828
karamyschevii	1		1
kiharae	1		1
macha	5		5
militinae	1		1
monococcum	18	7	25
persicum	13		13
polonicum	12		12
spelta	60		60
sphaerococcum	5		5
timopheevii	18	1	19
turgidum	33	3	36
vavilovii	1		1
Total	**10181**	**146**	**10327**

Most accessions are of foreign origin. They come from 53 countries from all over the world. However most of them represent the European wheat genepool. Accessions received from the USA and the Former Soviet Union are relatively well represented. Out of all accessions, 4171 are old and modern cultivars of which 345 are of Polish origin (Table 2).

Table 2. Number of wheat cultivars received from 19 countries

Country	No. of cultivars	Country	No. of cultivars
Germany	637	Portugal	100
France	385	Austria	98
USA	382	Canada	97
Russia	276	Hungary	92
Italy	232	The Netherlands	84
Australia	158	Argentina	81
Czech Republic	149	Bulgaria	69
Sweden	139	Former Yugoslavia	61
Great Britain	109	Kenya	54
		Spain	54

Collecting missions carried out over the last ten years to Iran, Albania, Romania, Bulgaria, Ukraine and the Czech Republic have made significant contributions to the wheat collection. Conservation of the wheat genetic resources collections is divided among three institutions. They conduct evaluation, reproduction and the regeneration of accessions. Spring and wheat accessions are maintained by the Plant Breeding Stations located in Strzelce and in Konczewice and the *Triticum durum* accessions by the Institute of Genetics and Plant Breeding of the Agriculture Academy in Lublin. Wild *Triticum* and related species are maintained by the Crop Genetic Resources Center in Radzików.

Wheat genetic resources accessions are characterized and evaluated with regard to resistance to pathogens (mildew, rusts, *Septorium, Fusarium* and leaf diseases), parameters of plant emergence, tillering, heading, lodging, seed maturity, length of the vegetation period, plant height, ear size and 100-kernel weight.

Identification, characterization, evaluation and multiplication and regeneration of *Aegilops* accessions are carried out in Radzików. At present the collection of *Aegilops* includes 19 species, of which 217 accessions of 9 species were collected during collecting missions in Ukraine, Iran, Turkey, Albania, Russia and Bulgaria (Table 3). All results of agronomic evaluation as well as available additional information are provided to our partners and breeders on request.

Table 3. Status of the Polish *Aegilops* genetic resources collection

Aegilops species	In storage	Collected material	Total
biuncialis	17	38	55
columnaris	4		4
crassa	2	1	3
cylindrical	68	72	140
geniculata	36	7	43
juvenalis	1		1
kotschyi	4		4
longissima	3		3
lorentii	9		9
neglecta	10	2	12
ovata	7	17	24
speltoides	13		13
squarrosa	1		1
tauschii	13	19	32
triaristata	3	1	4
triuncialis	94	60	154
umbellulata	1		1
variabilis	1		1
ventricosa	2		2
Total	**314**	**217**	**531**

Wheat genetic resources in Romania[87]

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In Romania, the national *Triticum* collection comprises 3234 accessions kept by six breeding institutions (Strãjeru *et al.* 2000; Strãjeru and Vasilescu 2003) and by the Suceava Genebank.

Today, 1319 accessions of 12 *Triticum* species are stored in the active and base collection of the Suceava Genebank (Table 1). The storage temperature complies with standard conditions for long- and medium-term.

Table 1. *Triticum* species in the active and base wheat collections, Suceava Genebank

Species	(2n)	No. of accessions
T. monococcum L.	14	51
T. dicoccoides Koern. ex Schweinf.	28	6
T. dicoccon (Schrank) Schübl		5
T. durum Desf.		4
T. carthlicum Nevski		1
T. polonicum L.		3
T. timopheevii Zhuk.		5
T. turgidum L.		5
T. persicum L.		1
T. aestivum L.	42	1231
T. spelta L.		6
T. vavilovii Jakubz		1
Total		**1319**

The collection is used for characterization, evaluation of important agronomic traits, and plant breeding. For the characterization of the *Triticum* collection the standard IPGRI descriptor list and a list developed independently are used.

Evaluation has been made of 353 accessions for morphophysiological characters and 251 accessions have been studied for their biochemical properties.

Research has also been carried out on the influence of ultrasonic treatments on some biochemical descriptors.

We use a database information system for the management of the *Triticum* collection. Some information about the collection is accessible through the Internet (www.svgenebank.ro) and in EURISCO.

Our regeneration capacity is limited, and this may present, in the future, a potential risk for the satisfactory maintenance of the *Triticum* collection.

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[87] See also "Wheat genetic resources in Romania", pp. 171-174.

The wheat collection at the Vavilov Institute: status 2005 and perspectives for further development

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The Vavilov Institute of Plant Industry in Russia is responsible for the collection, long-term conservation, study and sustainable use in breeding programmes of genetic resources of wheat and its wild relatives. The start of the development of the wheat collection dates back almost one century. The collection comprises more than 37 000 accessions collected worldwide. These include current and obsolete wheat varieties, primitive forms and wild species.

The collection is enriched annually by 100-150 accessions which possess valuable traits or fill gaps in the phenotypic and genotypic variability of the wheat species. Significant efforts are focused on the following:

- ensuring appropriate safety storage of the accessions under standard conditions;
- development of landrace classification based on study of DNA markers;
- improvement of the amount and quality of the information about each of the accessions;
- supply of material with useful traits to users for inclusion as parental forms in crosses and for the development of new varieties.

The main purposes of the research activities are to facilitate the use of the collection and provide basic information about it, and to increase efficiency and accuracy of the selection of accessions with the required traits for basic research and for wheat breeding.

The wheat genetic resource collection in the Slovak Republic [88]

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The Slovak wheat collection is organized according to the growth habit of the accessions in sub-collections of winter and spring wheat. It currently includes 4154 accessions: 3663 of winter wheat (88.1%) and 491 of spring wheat (11.9%).

Characterization and evaluation of wheat genetic resources

The wheat accessions are evaluated under field conditions at the Research Institute of Plant Production (RIPP) experimental station. The aims are: collecting and conservation; characterization and evaluation according to the standard descriptors (morphological characteristics, phenological stages, evaluation of yield characters, disease resistance and postharvest quality analyses); and selection of suitable genotypes for breeding programmes.

The evaluation system is based on a general methodology and is divided into three steps; following this procedure, 400-500 wheat samples are evaluated every year.

1. The first year of evaluation serves for the reproduction of small samples and a preliminary evaluation.
2. The second step of evaluation allows us to obtain description data. Samples (ca. 80-100 genotypes) are evaluated as two replicates over two years. Data on morphological and phenological characters, baking quality and resistance to the most frequent diseases are stored in databases.
3. In the third step of this evaluation the most promising genetic resources are recommended for breeding.

The characters and material studied are shown in Table 1.

Future and priorities

Samples of wheat genetic resources and related information are provided by the Gene Bank of the RIPP Piešťany according to the principles of the Convention on Biodiversity and of the International Treaty on PGRFA. In 2003, 768 samples of wheat genetic resources were provided to local users and 68 samples were sent abroad.

The further development and extension of the wheat collection in the Slovak Republic is enabling the breeders to make full use not only of existing genetic resources, but also of the newest varieties with their valuable accumulated properties and characters.

In recent years the RIPP has played an important role in genetic and breeding research on wheat. Research has dealt with the evaluation of the collected wheat genetic resources for morphological and yield characters and analyses of DNA markers, resistance genes *Lr19* and *Lr24* to wheat rust (*Puccinia recondita* f.sp. *tritici*) and alleles of the *Glu-1* locus controlling good breadmaking quality. The selection process includes electrophoretic analyses of these proteins and detection of the uniformity of newly bred lines.

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[88] See also "Activities and current status of the national wheat collection in the Slovak Republic", pp. 175-178.

Table 1. Survey of characterization and evaluation of wheat genetic resources in Slovakia

Characters	No. of accessions			
	Landraces	Breeding material	Advanced cultivars	Total
Plant - tuft shape	30	882	1215	2127
Plant – height	20	940	1261	2221
Stem - length of the upper internodes	27	805	1093	1925
Stem – thickness	27	834	1151	2012
Stem – fullness	27	864	1219	2110
Stem - waxy bloom highest internode	16	834	1139	1989
Stem - colour of the upper internodes	30	921	1293	2244
Flag - leaf position	30	921	1289	2240
Flag leaf - length	30	866	1199	2095
Flag leaf - width	30	855	1146	2031
Flag leaf - waxy bloom	30	855	1148	2033
Leaf - ligule presence	30	897	1204	2131
Leaf - length of auricles	30	896	1205	2131
Spike - colour	30	895	1201	2126
Spike - waxy bloom	16	666	908	1590
Spike - position	15	765	1069	1849
Spike - branchiness	16	750	1008	1774
Spike - shape	23	834	1126	1983
Spike - length	24	598	903	1525
Spike - density	14	240	226	480
Spike - awns or scurs	13	474	725	1212
Awns or scurs at tip of ear: length	16	548	623	1187
Glume - colour	12	450	698	1160
Glume - indumentum	12	452	699	1163
Caryopsis - shape	24	459	687	1170
Caryopsis - surface	24	455	685	1164
Caryopsis - colour	24	463	698	1185
Vegetation - character	51	1723	2378	4152
Winter - hardiness	20	855	995	1870
Lodging - resistance	20	898	1131	2049
Powdery mildew - plant - resistance	21	903	1134	2058
Powdery mildew - spike - resistance	21	749	906	1676
Stripe rust - resistance	20	778	917	1715
Brown rust - resistance	21	779	929	1729
Septoria disease - resistance	21	704	812	1537
Fusarium head blight - resistance	21	731	852	1604
Stand - number of spikes	15	460	542	1017
Stand - grain yield preliminary	14	225	221	460
1001 grain mass	21	783	961	1765
Spike - grain mass	15	459	542	1016
Spike - number of grains	15	459	545	1019
Spike - number of spikelets	15	461	545	1021
Spikelet - number of grains	15	460	540	1015
Grain - texture	1	135	63	199
Grain - crude protein content	15	405	445	865
Flour - wet gluten content	14	440	526	980
Gluten swelling	14	302	464	780
Flour - baking quality	1	267	397	665
Flour - sedimentation test	14	240	253	507

Status of the ex situ *wheat collection at the CRF-INIA (Spain)* [89]

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Conservation

As of July 2005, the CRF-INIA wheat collection holds a total of 2912 accessions (2910 in the active collection and 1826 accessions in the base collection). The majority of accessions are Spanish landraces, obtained from expeditions or breeders' collections. The composition of both collections according to species is shown in Table 1.

Table 1. Taxonomic composition of the CRF wheat collection (numbers of accessions)

Species	Base collection		Active collection	
	Total	Spanish landraces	Total	Spanish landraces
T. monococcum	16	16	20	17
T. timopheevi	3	-	6	-
T. turgidum	773	609	1106	566
T. aestivum	1034	657	1778	868
Total	**1826**	**1282**	**2910**	**1451**

Collecting

In the last five years only 8 accessions of Spanish wheat landraces have been collected, owing to the replacement of local varieties by commercial cultivars.

Regeneration status and availability of material

The criteria for regeneration or multiplication of the collection are that germination should be below 85%, or there should be less than 2000 seeds in the active collection. Priority is given to the Spanish landraces. At present, a total of 37 wheat accessions have a germination rate below 85% (including 10 Spanish landraces) and 417 have less than 2000 seeds in the active collection (including 13 Spanish landraces). A total of 1818 entries are available, 1009 have a limited availability, and 85 are not available.

Characterization

The agromorphological characterization is usually carried out during the multiplication of the accessions. At least 13 descriptors are recorded in the field and in the laboratory. The number of accessions with characterization data is as follows:

- *T. monococcum*	20
- *T. timopheevi*	3
- *T. turgidum*	557
- *T. aestivum*	466

Some molecular data (gliadins and glutenins) are also available for about 800 accessions.

[89] See also "Current status of the wheat collection maintained at the CRF-INIA (Spain) and research activities", pp. 179-183.

Wheat genetic resources in Switzerland – Update 2005 [90]

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Over the last two years the wheat collection of the Federal Research Station for Plant Production of Changins (RAC), now called Agroscope RAC Changins, Federal Agricultural Research Station, was increased by 187 accessions, mostly of *Triticum aestivum.* The total is now 7445 accessions. The passport data and the available evaluation data of these accessions will be introduced into the National Database before the end of 2005 and will be included in the European Wheat Database and in EURISCO. About 95% of the wheat collection is in long-term storage, but seed samples will remain available of course to *bona fide* users. The other accessions are in medium-term storage. Seed multiplication will be carried out for these accessions and they will also be put into long-term storage.

A new project for the evaluation of the Swiss *T. spelta* landraces started in 2005, carried out by the private company Getreidezüchtung Peter Kunz in collaboration with RAC. Agronomic characteristics as well as quality traits and disease resistance are being observed. This project is financed by the National Plan of Action for the conservation and sustainable use of plant genetic resources for food and agriculture of the Swiss government.

90 See also "Wheat genetic resources in Switzerland", p. 184.

Status of the wheat genetic resources programme in Turkey

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Turkey is one of the origins and diversity centres for the major cereals, including wheat. Wild ancestors of cultivated wheat species are widely distributed in Turkey. Wheat species found in Turkey have a wide range of variation, for both wild relatives and landraces of cultivated species or primitive cultivars. Diploid cultivated einkorn, *Triticum monococcum*, and tetraploid emmer wheat, *Triticum dicoccum,* are now only found on a small scale in cultivation. Their wild ancestors (wild einkorn, *Triticum boeoticum*, and wild emmer, *Triticum dicoccoides)* are also found, either in mixed populations or in separate habitats. A considerable diversity of *Aegilops* species is found in Turkey. The early sites for findings of domesticated plants, dated 7000-5000 BC, confirm that Turkey is a centre of origin for wheat (Firat and Tan 1998).

These valuable wheat genetic resources of Turkey started to be explored and utilized in 1930. Systematic collection, conservation (both *ex situ* and *in situ*) and utilization activities started in the 1960s within the framework of the National Plant Genetic Resources Programme (NPGRP). The Aegean Agricultural Research Institute (AARI) is responsible for the national coordination of NPGRP.

Surveys/collecting, multiplication/regeneration and utilization activities are organized by plant groups (cereals, food legumes, forages, industrial crops, vegetables, fruit trees and grapes, ornamental plants, medicinal and aromatic plants, and endemic plants).

Wheat genetic resources activities are conducted within the framework of NPGRP. *Ex situ* conservation activities have been undertaken since 1964. The collected seed material is preserved in cold storage at the National Gene Bank at AARI, where the facilities are designed according to international standards for long- and medium-term storage for the base and active collections; working samples are kept in short-term storage. In addition, base collections are stored in Ankara at the Field Crop Central Research Institute for safety-duplication. The wheat genetic resource collections consist of a total of 5763 accessions, comprising wild (1931 accessions) and cultivated species (3832 accessions). During the past four years, 239 *Triticum* accessions were regenerated and multiplied.

In situ and on-farm conservation are also conducted within the framework of NPGRP. Various *in situ* conservation projects are being run, dealing with the conservation of wild relatives of crop species in their natural habitat and the maintenance of landraces on farms. Efforts for *in situ* conservation of relatives of crop species were started within the framework of a project supported by the Global Environment Facility and the Turkish Government in 1993. Various sites were identified as Gene Management Zones for wild wheat. One of the most important outputs of this project is the publication of the National *In Situ* Conservation of Plant Genetic Diversity in Turkey. The project has also aimed to integrate *in situ* conservation with the existing *ex situ* conservation programme of Turkey. The Project on *In Situ* (On-Farm) Conservation of Landraces in the Northwest Transitional Zone of Turkey was started in 1999. This project was proposed and carried out on the basis of the National Plan, given the priorities for the crop species and regions that are considered as needing urgent conservation. The objective of the project is to search out the possibilities for on-farm conservation of hulled wheat and also legume landraces grown in the provinces of the northwestern transitional zone of Turkey, with the active participation of the farmers (Tan 2002).

A new initiative on participatory landrace improvement will start in the coming year, jointly with the National Agricultural Research Systems (NARS) of Turkey, the University of California, EMPRAPA (Empresa Brasileira de Pesquisa Agropecuária, Brazil), CIMMYT (Centro Internacional de Mejoramiento de Maíz y Trigo, Mexico) and ICARDA (International Center for Agricultural Research in Dry Areas, Aleppo, Syria), to maintain the landraces on farm in two sites in the west (Kutahya) and east (Sivas) transitional regions.

In 1999-2002 a total of 81 hulled wheat seed samples collected in the northwestern transitional zone of Turkey and a total of 726 *T. turgidum durum* accessions collected from various regions of Turkey in 2002-2003 were characterized using the descriptor lists of IPGRI.

A newly proposed and accepted project aims to improve the Fe and Zn content of wheat varieties by using wild wheat genetic resources in Turkey. The wheat genotypes including *Triticum dicoccoides*, *T. boeoticum, T. monococcum, T. dicoccum, T. durum, T. aestivum, Aegilops speltoides* and *Ae. tauschii* held in the AARI Seed Gene Bank will be screened for Fe and Zn content and genotypes with high levels of Fe and Zn will be used in breeding programmes to transfer "Fe and Zn genes" into widely grown Turkish wheat cultivars via marker-assisted selection. This project was formulated with the participation of Sabanci University and will be supported by the State Planning Organization, the General Directorate of Agricultural Research of the Ministry of Agriculture and Rural Affairs, Çukurova University, CIMMYT–Ankara and two private companies.

Documentation is one of the main functions of the NPGRP for both *ex situ* and *in situ* activities. A database management system exists for documentation of both *ex situ* and *in situ* conservation information, including the wheat collections. Since the *in situ* conservation programme is complementary to *ex situ* conservation, the two databases, including wheat collection information, are linked and complementary to each other. A Geographic Information System (GIS) is available to evaluate the quantitative and spatial data gathered especially from survey and inventory activities (Tan and Tan 1998).

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The Ukrainian collections of wheat and triticale genetic resources [91]

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The wheat and triticale collections of the Ukrainian National Plant Genebank have been established and maintained by several institutions located in different climatic regions so as to provide for their ecological investigation and reliable maintenance: the V.Y. Yurjev Institute of Plant Production (Kharkiv), the Ustimivs'ka Experimental Station of Plant Production (Poltava region), the Breeding and Genetics Institute (Odessa), the Myronivs'kiy Wheat Institute (Kyiv region) and the Southern Region Agricultural Research Institute (Kherson).

The collections contain a total of 20 626 wheat accessions of 23 natural species and a number of synthetic forms, and 3288 triticale accessions (Table 1).

Table 1. Composition of the national wheat and triticale collections of Ukraine

Type of material	Holding institute	No. of accessions		
		Winter and intermediate	Spring	Total
Bread wheat (*T. aestivum* L. em. Fiori et Paol.)	Yurjev Plant Production Institute	4903	2800	7703
	Ustimivs'ka Experimental Station	2421	-	2421
	Breeding and Genetics Institute	4686	-	4686
	Myronivskiy Wheat Institute	1810	1190	3000
	South Region Agricultural Research Institute	327	-	327
Total bread wheat		**14147**	**3990**	**18137**
Durum wheat (*T. durum* Desf.)	Yurjev Plant Production Institute	96	1112	1208
	Breeding and Genetics Institute	286	-	286
	Myronivskiy Wheat Institute	-	521	521
Total durum wheat		**382**	**1633**	**2015**
Neglected wheat species	Yurjev Plant Production Institute	**35**	**250**	**285**
Synthetic forms (amphidiploids)	Yurjev Plant Production Institute	**11**	**72**	**83**
Wild wheat relatives	Yurjev Plant Production Institute	**98**	**8**	**106**
Triticale (x *Triticosecale* Wittmack)	Yurjev Plant Production Institute	1616	920	2536
	Ustimivs'ka Experimental Station	470	282	752
Total triticale		**2086**	**1202**	**3288**

All accessions are evaluated and characterized for traits of economic value, both in the field and in the laboratory.

A large number of accessions have been selected for high productivity in combination with other valuable traits: early ripening, resistance to lodging, resistance to diseases and pests, large size, plumpness and desirable form of the grain, etc. Researches on plant immunity to diseases are carried out in an infective environment.

One of the most important traits for winter wheat in Ukraine is winter hardiness. It is evaluated in conditions similar to natural field conditions, i.e. exposure to frost in a special freezing chamber, where the critical temperatures for destruction by frost are determined.

[91] See also "Wheat and triticale genetic resources in Ukraine", pp. 186-192.

The cultivars from Ukraine ('Borovyk-Balkan', 'Yuzhnyi 1', 'Bilosnizhka', 'Luganchanka', 'Driada 1', etc.) and Russia ('Donskoy Syurpriz', 'Viktoria 95', 'Novosibirskaya 32', etc.) have the highest frost hardiness. New cultivars ('Vasylyna', 'Volodarka', 'Dykanyka', 'Vdala', 'Zemlyachka', etc.) can endure the critical temperature in the period of maximal hardening (CTPMH) down to –19°C. Among triticale cultivars the following should be mentioned: 'Popsuyevs'ke', which endured CTPMH –21°C, and 'Soyuz', 'Bulat' and 'Svytyaz' (-20°C).

The second trait complex of great importance is technological, in particular breadmaking grain quality, and for durum wheat also macaroni baking quality. The following traits are studied: grain contents (moisture, protein, gluten, starch, carotenoids, essential aminoacids, non-proteic nitrogen); aminoacid and fractionated (by electrophoresis) composition of grain protein; sedimentation and gluten quality indexes, bread loaf volume, common breadmaking value, etc. In 2004 more than 15 000 biochemical and technological analyses were carried out. The spring bread wheat cultivars 'Voronyezhskaya 6', 'Prokhorovka', 'Kharkivs'ka 34', 'Kharkivs'ka 18', 'Rannya 93' and others were distinguished by their superior breadmaking characters. Among the winter bread wheat cultivars were found some carriers of the gliadin alleles *1A4, 1B1* and *1D4* which positively influence flour quality: 'KS89WGRC4', 'K85W663-9-3-1', 'KAREN', 'REDLAND', 'Te3915', etc. In spring wheat, 'DESC', 'F7ME2EM.9Y90', 'CETTIA', 'L501', 'L592', 'Kinel'skaya 60', 'Klara', etc. are sources of good breadmaking qualities.

Breadmaking grain quality of triticale is a special problem. It is determined by the genomes of wheat, rye and their interaction. The study of a wide diversity of triticale genotypes permitted us to select about 30 spring samples having a good complex of these qualities, close to those of wheat.

Based on research results, various collections have been built (base, trait, special, working, educational collections). This increases the efficiency of the utilization of germplasm samples in breeding, science, training, ecological, production and other programmes, and facilitates users' access to the diversity available in the collections.

With this goal, samples which are the sources of valuable traits and which represent various types of collections are distributed to users. In 2004, about 2800 samples were distributed. The transfer is performed on the basis of a Material Transfer Agreement accepted by the international community.

The germplasm in the collections is actively used as the initial material for wheat and triticale breeding. In breeding institutions located in temperate regions (Yuryev Institute of Plant Production, Myronivka Wheat Institute, Donyetsk Institute of Agroindustrial Production, Institute of Agriculture, etc.), preference is given to samples of local origin or created in neighbouring regions of Russia because they are well adapted to harsh climatic conditions (primarily winter cold and drought). Institutes of the southern region (Breeding and Genetics Institute, Southern Region Agricultural Research Institute, etc.) widely use both local and foreign germplasm.

The material is included in programmes of intraspecific and wide hybridization and also in mutagenic treatment, for which the Institute of Plant Physiology and Genetics (Kyiv) has a leading role. Wide utilization of wild wheat relatives and related neglected cultivated species is carried out in the Breeding and Genetics Institute, the Myronivka Wheat Institute and the Yuryev Institute of Plant Production. It is planned to use, in particular, representatives of the wild genera *Aegilops*, *Thynopyrum* and *Elymus,* cultivated species *Triticum dicoccum, T. ispahanicum, T. polonicum, T. petropavlovskyi,* etc., artificial amphidiploids *T. kiharae, T. miguschovae, T. monococcum-T. dicoccum, T. durum-Ae. tauschii,* and others.

Proteomic research on wheat and its relatives is carried out in the Breeding and Genetics Institute, Yuryev Institute of Plant Production, Myronivka Wheat Institute, Institute of Agroecology and Biotechnology, Institute of Plant Physiology and Genetics and other institutions. The Southern Biotechnology Center carries out genomic research under the leadership of Prof. Yury Sivolap (Odessa).

New directions of breeding for grain quality being are developed in Ukraine, particularly for "superstrength flour" for breadmaking; high starch content and low protein content for cookies; "waxy" forms with a high amylopectin ratio in starch for food films. Triticale is used in breadmaking.

The wheat germplasm of the Ukrainian Genebank is documented in the Information System "Plant Genepool". In order to collaborate with breeders and researchers throughout the world and exchange genepool samples, most of the passport database is included in the European Catalogue EURISCO (Table 2).

Table 2. Documentation of accessions in Ukrainian passport database and in EURISCO

Crop	No. of accessions	
	Passport database	EURISCO
Bread wheat	6463	5991
Durum wheat	1192	1159
Neglected wheat species	222	222
Synthetic forms - amphidiploids	27	-
Triticale	2209	1778

The National Centre for Plant Genetic Resources of Ukraine carries out the registration of valuable samples and collections of genetic resources, issuing special certificates which attest the authority. It is performed on the basis of special regulations approved by the Ukrainian Academy of Agrarian Sciences.

All the collections are put in long-term storage. If earlier the accessions were stored at uncontrolled temperatures, a freezing chamber with controlled temperature (–20°C) is now available. A duplicate collection is maintained at +4°C in the Ustymivs'ka Experimental Station; all institutions keep active collections in short-term storage under uncontrolled conditions.

Research

Evaluation of Triticum monococcum *for resistance to fungal pathogens with special emphasis on prehaustorial resistance to leaf rust*

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At the Institute of Epidemiology and Resistance Resources, up to now 348 accessions of *Triticum monococcum* obtained from different genebanks and plant breeders have been screened for resistance. The collection is being continuously enlarged by new accessions. *T. monococcum* and other wild relatives of wheat contain a wide range of valuable characters, including disease resistance to many pathogens, which can be transferred to polyploid wheat (*Triticum durum*, *T. aestivum*). We are mainly interested in a special type of resistance to leaf rust (*Puccinia triticina*), which was described as prehaustorial resistance (Anker and Niks 2001). In addition, the screening is also concerned with resistance to tan spot (*Drechslera tritici-repentis*), powdery mildew (*Blumeria graminis* f. sp. *tritici*), stripe rust (*P. striiformis*) and eyespot (*Tapesia yallundae*).

Prehaustorial resistance to leaf rust was detected in 13 accessions (3.7%). It is characterized by the absence or a drastic reduced formation of haustoria, although haustorium mother cells are initiated. Because of the reduced number of haustoria the infection unit will not form a spore-producing pustule and no hypersensitivity reactions appear. Testing was carried out by artificial inoculation with five rust isolates in a growth chamber at 18ºC and 14 hours light. Prehaustorial resistance was determined using three characters: (a) haustorium mother cells were counted 48 hours after inoculation; (b) haustoria were counted 56 hours after inoculation; and (c) the infection type was screened 10 days after inoculation. The infection structures within the leaf tissue were recorded by the use of both fluorescence microscopy and phase contrast microscopy. For the description of symptoms on the leaf surfaces, the scale of McIntosh *et al.* (1995) was applied, which uses the infection type classes 0, 1 and 2; 0 means resistant without any disease symptoms, 1 is moderately resistant with weakly sporulating pustules and 2 is moderately susceptible with spore production. Other infection types (e.g. 3 and 4 with amply sporulating pustules) were not found on *T. monococcum*.

The 13 genotypes selected for a high level of prehaustorial resistance are shown in Table 1. They are arranged according to their mean number of haustoria. For comparison, two susceptible types are also listed. For both lines provided by plant breeders the country of origin is unknown. The accessions PI 272560, PI 518452 and PI 428158 were described already by Anker and Niks (2001) as highly resistant.

Single plants of seven accessions (Table 2) had been selfed for three years to ascertain homozygosity. In factorial crosses between 3 highly resistant, 1 moderately resistant and 3 susceptible genotypes the genetic basis of leaf rust resistance was studied. Replicated resistance tests under different environmental conditions showed that prehaustorial resistance has a high heritability (h^2 = 0.89**). The different parameters used to measure the resistance are significantly correlated: number of haustorium mother cells vs. scores = 0.99**, number of haustoria vs. scores = 0.95**, number of haustorium mother cells vs. number of haustoria = 0.95**. Because of the strong correlation, only the number of haustorium mother cells is used in the current evaluation programme for leaf rust resistance.

Table 1. Selected accessions of *T. monococcum* with a high level of prehaustorial resistance to leaf rust and two susceptible control lines

Accession no.	Scientific name / line designation	Origin	Mean number of haustoria
PI 272560	var. *monococcum*	Hungary	0.3
PI 518452	var. *monococcum*	Spain	0.4
PI 428158	var. *monococcum*	Great Britain	0.4
PI 167526	var. *monococcum*	Turkey	0.7
TRI 645/76	var. *vulgare*	Greece	0.8
BGRC 42017	var. *macedonicum*	Albania	1.0
PI 427927	var. *monococcum*	Iran	1.2
2006	Saffra 6		1.2
TRI 2125/91	var. *vulgare*	Bulgaria	1.5
7041	var. *laetissimum*	Armenia	1.9
TRI 577/81	var. *hornemannii*	Germany	2.2
2011,2	Saffra 12		2.3
TRI 00620	var. *macedonicum*	Albania	2.5
37351	var. *albohornemannii*	Germany	10.3
36594	var. *hornemannii*	Germany	13.3

Table 2. Characterization of *T. monococcum* lines used as parents for factorial crosses

Genotype	Mean number of haustorium mother cells	Mean number of haustoria	Score of infection type
Female parents			
PI 272560	2.4	0.2	0
7041	4.9	1.8	0
7038	5.9	2.6	0
Male parents			
2651	7.1	4.4	1
36554	12.7	7.4	2
37351	13.1	10.3	2
36594	16.2	13.1	2

In all crosses analyzed up to now the segregation ratios suggest that the resistance is simply inherited and is controlled by recessive and dominant genes, respectively (Table 3). Distinct classes were observed in F_2–generations and the progeny of each F_2-plant was retested in order to verify the phenotypic data. Tests for allelism to detect identity of resistance genes are in progress. Zhang *et al.* (1992) and Bai *et al.* (1998) also reported on major gene controlled inheritance of resistance, whereas Anker and Niks (2000) identified a complex resistance and quantitative trait loci.

After phenotyping, from all F_2-plants the DNA was extracted for molecular analyses. The objective is to localize the genes for prehaustorial resistance and to develop molecular markers for their marker-assisted transfer to tetraploid and hexaploid wheat. The availability of molecular markers is the prerequisite for the successful introgression of these genes.

Table 3. Selected crosses between susceptible and resistant genotypes of *T. monococcum*, segregation ratios and genetic basis of resistance

Cross parents		No. of F_2-plants	Segregation ratios	χ^2 test probability	Genetic basis of resistance
Resistant	Susceptible				
7038	36554	107	9:4:3	0.75 – 0.50	2 recessive genes
7038	36594	153	9:4:3	0.75 – 0.50	2 recessive genes
7041	37351	80	9:3:3:1	0.75 – 0.50	2 recessive genes
PI 272560	37351	158	27:18:9:6:4	0.25 – 0.10	2 dominant genes 1 or 2 recessive genes
PI 272560	2651	116	9:3:3:1	0.75 – 0.50	2 dominant genes

Several examples for the transfer of leaf rust resistance from *T. monococcum* to *T. aestivum* (Knott and Zang 1990; Cox *et al.* 1994; Murphy *et. al.* 1999; Cox *et al.* 1999) without the help of molecular markers are known. Kuraparthy *et al.* (2001) transferred a resistance gene linked to a microsatellite marker. By the use of monosomic analysis Hussien *et al.* (1998) localized three genes of resistance derived from *T. monococcum* in wheat lines on chromosomes 1A, 5A and 6A. In all papers mentioned the effects of resistance genes were not studied before to see whether they are of the prehaustorial type.

Prehaustorial resistance to leaf rust is a new type of resistance not yet occurring in German wheat cultivars. It reacts unspecifically to the different pathotypes and does not develop hypersensitivity reactions or sporulating pustules. After being transferred to wheat it can be handled easily in breeding, because of its simple inheritance. Prehaustorial resistance will contribute effectively to the durability of resistance to leaf rust in wheat cultivars, provided the expression of genes is the same as in *T. monococcum*.

In addition to the resistance to leaf rust, *T. monococcum* can also be used as the source for resistance to other pathogens. Some selected lines with different resistance combinations are presented in Table 4. Their use in breeding could enable the transfer of combined resistance to *Triticum durum* and *T. aestivum*. Apart from disease resistance, *T. monococcum* is also a rich source of novel variability for other traits of economic importance, e.g. high protein content, high yellow pigment content, water use efficiency, salt tolerance and sprouting resistance.

Table 4. Lines of *T. monococcum* carrying genes of resistance to different pathogens

Genotype	Leaf rust	Stripe rust	Tan spot	Powdery mildew
TRI 645/76	r	r	r	r
TRI 1988/76	r	r	r	r
BGRC 42007	r	r	r	r
7038	r	r	r	s
BGRC 42017	r	r/m	r	s
37351	s	r/m	r	r
7041	r	r/m/s	r	r
PI 272560	r	r/m/s	r	s
TRI 577/81	r	r/m/s	r	r
36594	s	r/s	r	r

Legend: r = resistant, m = moderately resistant, s = susceptible; for stripe rust the reactions were different depending on the pathotype; for tan spot and mildew pathotype mixtures were used.

References

Anker, C.C. and R.E. Niks. 2000. Genetics of prehaustorial resistance to wheat leaf rust in diploid wheat. Acta Phytopath. et Entomol. Hungarica 35:23-30.

Anker, C.C. and R.E. Niks. 2001. Prehaustorial resistance to the wheat leaf rust fungus, *Puccinia triticina*, in *Triticum monococcum* (s.s.). Euphytica 117:209-215.

Bai, D., D.R. Knott and J.M. Zale. 1998. The inheritance of leaf and stem rust resistance in *Triticum monococcum* L. Canad. J. Plant Sci. 78:223-226.

Cox, T.S., R.G. Sears, B.S. Gill and E.N. Jellen. 1994. Registration of KS91WGRC11, KS92WGRC15, and KS92WGRC23 leaf rust-resistant hard red winter wheat germplasms. Crop Sci. 34:546-547.

Cox, T.S., R.G. Sears, B.S. Gill, T. Hussien, R.L. Bowden and G.L. Brown-Guedira. 1999. Registration of KS96WGRC34 leaf rust-resistant hard red winter wheat germplasm. Crop Sci. 39:595.

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Knott, D.R. and H.T. Zang. 1990. Leaf rust resistance in *durum* wheat and its relatives. Pp. 311-316 *in* Wheat Genetic Resources: Meeting Diverse Needs (J.P. Srivastava and A.B. Damania, eds). John Wiley, Chichester, UK.

Kuraparthy Vasu, Harjit Singh, S. Singh, Parveen Chhuneja and H.S. Dhaliwal. 2001. Microsatellite marker linked to a leaf rust resistance gene from *Triticum monococcum* L. transferred to bread wheat. J. Plant Biochem. Biotech. 10:127-132.

McIntosh, R.A., C.R. Welling and R.F. Park. 1995. Wheat rusts: an atlas of resistance genes. CSIRO, Australia and Kluwer Academic Publishers, Dortrecht, The Netherlands.

Murphy, J.P., S. Leath, D. Huynh, R.A. Navarro and A. Shi. 1999. Registration of NC96BGTA4, NC96BGTA5, and NC96BGTA6 wheat germplasm. Crop Sci. 39:883-884.

Zhang, H.S., R.E. Niks, R.G. Dekens and H.H. Lubbers. 1992. Inheritance of pre- and posthaustorial resistance to wheat leaf rust in diploid wheat. Pp. 208-210 *in* Cereal Rusts and Mildews - Proceedings of the 8th European and Mediterranean Cereal Rusts and Mildews Conference, 8-11 September 1992, Weihenstephan, Germany (F.J. Zeller and G. Fishbeck, eds). Vortrage fur Pflanzenzuchtung 24.

Nitrogen use efficiency of bread and durum wheat and triticale

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Introduction

Nitrogen is one of the main abiotic factors limiting cereal production. According to the new rules of the Common Agricultural Policy, there are some restrictions on the application of nitrogen to the land in order to reduce the environmental risks of agriculture. The objectives of this study were: 1) to evaluate genetic progress on nitrogen use efficiency and the tolerance to nitrogen deficiency of modern genotypes of bread wheat, durum wheat and triticale compared to that of old varieties of bread and durum wheat; and 2) to study the effect of nitrogen stress on the expression of grain yield and quality traits.

Material and methods

A 2-year (2002-03 and 2003-04) field experiment was established with 25 genotypes, which included 12 bread wheats, 8 durum wheats and 5 triticales (Table 1), under four fertilization regimes (Table 2), and in the presence or absence of fungicides, under irrigation.

Table 1. Genotypes of bread wheat, durum wheat and triticale used in the study (2002-03 and 2003-04)

Bread wheat	Durum wheat	Triticale
Pirana (old variety)	Lobeiro (old variety)	Alter
Mocho de Espiga Ruiva (landrace)	Amarelejo (old variety)	Rhino–3/Bull–1-1
TE 9406	Colosseo	Fahad 8-1 * 2 // Hare
Côa	Iride	Pollmer 2. 3. 1
Almansor	Celta	CMH77A.1024 / 2 * YO
Guadalupe	Marialva	
Sorraia	Preco	
Golia	Silver 14/Moewe	
TE 9712		
TE 9713		
TE 9714		
TE 9715		

Table 2. Treatments

1.	N = 180 / P_2O_5 = 120 / K_2O = 120
2.	N = 0 / P_2O_5 = 120 / K_2O = 120
3.	N = 180 / P_2O_5 = 0 / K_2O = 0
4.	N = 0 / P_2O_5 = 0 / K_2O =0

Results

Nitrogen stress resulted in very severe yield reductions compared to the non-stressed situations. The yield was reduced by 55% in the bread wheat, 57% in durum wheat and 61% in triticale (Table 3).

Table 3. Grain yield (kg/ha) of bread wheat, durum wheat and triticale across different treatments

Treatment	Grain yield (kg/ha)		
	Bread wheat	Durum wheat	Triticale
N=180 / P=120 / K=120 /+ Fungicide	4266	4260	5677
N=180 / P=120 / K=120 / Without fungicide	3779	3945	5360
N=180 / P=0 / K=0	3467	3569	5326
N=0 / P=120 / K=120	2322	2105	2482
N=0 / P=0 /K=0 / Without fungicide	1926	1817	2250

Modern genotypes showed similar performance to the old ones under stress conditions, providing evidence that there has been no progress due to genetic breeding on nitrogen use efficiency (Tables 4, 5 and 6). Wheat breeding conducted under high nitrogen fertility conditions has produced germplasm with high response to nitrogen, while no selection pressure was applied for nitrogen use efficiency. Other breeding strategies considering low nitrogen or alternating low and high nitrogen conditions during the selection of segregating populations and grain yield evaluations could result in germplasm with improved nitrogen use efficiency.

Table 4. Grain yield (kg/ha) of the 12 bread wheat genotypes

Genotype	Grain yield (kg/ha)				
	N=180 / P=120 / K=120 / + Fungicide	N=180 / P=120 / K=120 / Without fungicide	N=180 / P=0 / K=0	N=0 / P=120 / K=120	N=0 / P=0 / K=0 / Without fungicide
Pirana	4251 abc[1]	3692 ab	3471 abc	2424 abc	1872 a
M.Espiga Ruiva	1800 d	1530 c	1714 d	1728 c	1444 a
TE 9406	5310 a	3936 ab	3752 ab	2174 bc	1721 a
Côa	4518 abc	4205 a	3807 ab	2232 bc	2239 a
Almansor	5015 ab	4876 a	4222 a	2592 ab	2318 a
Guadalupe	3605 bc	3204 ab	2399 cd	3117 a	2034 a
Sorraia	4750 abc	4713 a	4216 a	2702 ab	2254 a
Golia	3659 bc	3455 ab	3586 abc	2454 abc	2198 a
TE 9712	4187 abc	3577 ab	3359 abc	2147 bc	1353 a
TE 9713	3278 c	2375 bc	2660 bcd	1754 c	1396 a
TE 9714	5562 a	4946 a	4026 a	2214 bc	1811 a
TE 9715	5257 a	4842 a	4393 a	2325 bc	2466 a

Table 5. Grain yield (kg/ha) of the 9 durum wheat genotypes

Genotype	Grain yield (kg/ha)				
	N=180 / P=120 / K=120 / + Fungicide	N=180 / P=120 / K=120 / Without fungicide	N=180 / P=0 / K=0	N=0 / P=120 / K=120	N=0 / P=0 / K=0 / Without fungicide
Lobeiro	1965 b	1833 b	1564 c	2207 ab	2026 a
Amarelejo	1651 b	1968 b	1310 c	1438 b	604 b
Colosseo	4508 a	4271 a	4215 ab	2605 a	2058 a
Iride	5413 a	5338 a	5041 a	2047 ab	1946 a
Celta	4860 a	3933 a	4666 ab	2148 ab	2295 a
Marialva	5208 a	4590 a	3560 b	2014 ab	1815 a
Preco	5495 a	4657 a	4779 ab	2370 a	2098 a
Silver14/ Moewe	4282 a	4973 a	3414 b	2009 ab	1695 a

Table 6. Grain yield (kg/ha) of the 5 triticale genotypes

Genotype	Grain yield (kg/ha)				
	N=180 / P=120 / K=120 / + Fungicide	N=180 / P=120 / K=120 / Without fungicide	N=180 / P=0 / K=0	N=0 / P=120 / K=120	N=0 / P=0 / K=0 / Without fungicide
Alter	4979 b	5057 a	5101 bc	2358 a	2633 a
Rhino-3/Bull-1-1	5360 ab	4542 a	4557 c	2296 a	2121 a
Fahad8-1*2//Hare	6197 a	5845 a	5796 ab	2798 a	2155 a
Pollmer 2.3.1.	5813 ab	5697 a	5262 ab	2324 a	2153 a
CMH77A.1024/…	6034 a	5659 a	5916 a	2634 a	2188 a

Protein content was also very dependent on the nitrogen supply. Modern and old genotypes had similar capacity to mobilize nitrogen to the grain, showing no differences under nitrogen stress (Table 7).

Table 7. Protein content (%)

Treatment	Protein content (%)		
	Bread wheat	Durum wheat	Triticale
N=180 / P=120 / K=120	12.11	12.55	10.24
N=180 / P=0 / K=0	12.55	12.76	11.04
N=0 / P=120 / K=120	9.42	9.85	8.98
N=0 / P=0 / K=0	9.68	9.98	9.33

APPENDICES

Appendix I. List of useful Web sites

Armenia	http://www.cac-biodiversity.org/arm/arm_database.htm
Azerbaijan	http://www.cac-biodiversity.org/aze/aze_database.htm
Bulgaria	http://www.genebank.hit.bg/
Czech Republic	http://www.vurv.cz/index.php?lang=en
Estonia	http://www.jpbi.ee/index.php/216/ http://tor.ngb.se/sesto/index.php?scp=est
France	http://www.brg.prd.fr/brg/ecrans/vegetales_An.htm
Georgia	http://www.cac-biodiversity.org/geo/geo_projects.htm
Germany	http://www.ipk-gatersleben.de/en/
Hungary	http://www.rcat.hu/english/english.htm
Ireland	http://www.tcd.ie/Botany/GHI/irishcerealvars.html
Israel	http://www.agri.gov.il/Depts/GeneBank/Genebank.html
Italy	http://www.cerealicoltura.it/
Latvia	http://tor.ngb.se/sesto/index.php?scp=lva
Lithuania	http://www.lzi.lt/
Macedonia (FYR)	http://www.fao.org/documents/show_cdr.asp?url_file=/DOCREP/005/Y2722E/y2722e0w.htm
Netherlands	http://www.cgn.wur.nl
NGB	http://www.ngb.se/Databases/
Poland	http://www.ihar.edu.pl/gene_bank/about.html
Portugal	http://www.iniap.min-agricultura.pt/default.aspx?uni=6
Romania	http://www.svgenebank.ro/
Russian Federation	http://www.vir.nw.ru
Slovakia	http://www.vurv.sk
Spain	http://www.inia.es/sapportal/guest/guest
Switzerland	http://www.agroscope.ch/inde.html
Turkey	http://www.aari.gov.tr/main-aari.html
Ukraine	http://www.fao.org/documents/show_cdr.asp?url_file=/DOCREP/005/Y2722E/y2722e17.htm

Other useful links:

IPGRI Internet links directory	http://www.ipgri.cgiar.org/links/select.asp
EWDB	http://genbank.vurv.cz/ewdb/
EURISCO	http://eurisco.ecpgr.org/

Appendix II. The European Wheat Database (EWDB) – Status 2005

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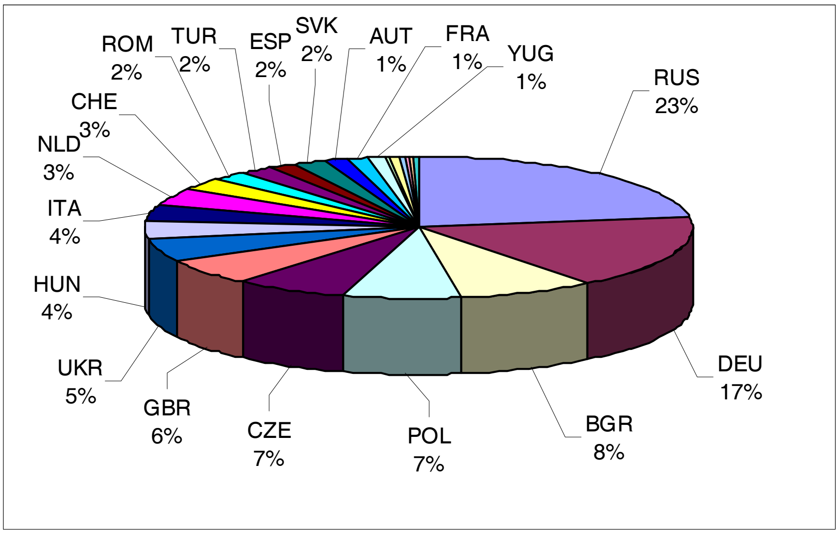
Research Institute of Crop Production (RICP), Prague-Ruzyne, Czech Republic

(Tables and figures from the presentation given during the meeting - see text in Part I, pp. 238-239).

Passport data in the EWDB per contributing country

Country	No. of records
RUS	34808
DEU	25494
BGR	12237
POL	10397
CZE	10259
GBR	9461
UKR	7372
HUN	6300
ITA	6161
NLD	5315
CHE	4366
ROU	3234
TUR	3046
ESP	2814
SVK	2616
AUT	2174
FRA	1949
YUG	1504
ISR	620
SWE	614
LVA	566
AZE	396
PRT	176
GRC	170
GEO	146
ARM	143
CYP	80
LTU	47
IRL	32
BLR	19
EST	8
Total	**152524**

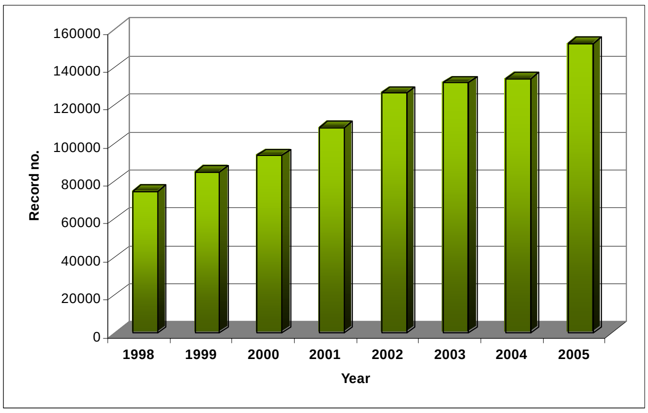
EWDB - proportion of contributors (152 524 records)



Number of records in the EWDB, 1998-2005

Year	No. of records
1998	74703
1999	84694
2000	93569
2001	108229
2002	126427
2003	131896
2004	134099
2005	152524

Increase in EWDB record number



Contributing institutions

Code*	Contributor	No. of records
RUS001	N.I. Vavilov Research Institute of Plant Industry St. Petersburg	34808
DEU146	Genebank, Inst. for Plant Genetics and Crop Plant Research (IPK) Gatersleben	16757
BGR001	Institute of Plant Introduction and Genetic Resources 'K. Malkov' Sadovo	12237
POL003	Plant Breeding and Acclimatization Institute Blonie, Radzikow near Warsaw	10397
CZE122	Genebank Dept., Research Institute of Production Prague 6 - Ruzyne	10259
GBR011	John Innes Centre Norwich Research Park Norwich, Norfolk NR4 7UH	9461
DEU001	Federal Research Center for Agricult.(FAL) Braunschweig	8737
UKR001	Yurjev Institute of Plant Breeding Kharkov	7219
HUN003	Institute for Agrobotany Tapioszele	5461
NLD037	Centre for Genetic Resources, the Netherlands (CGN) Wageningen	5315
ITA266	Istituto Sperimentale per la Cerealicoltura S. Angelo Lodigiano (MI)	5005
CHE001	Station Federale de Recherches Agronomiques de Changins Nyon	4362
TUR001	Plant Genetic Resources Dept. Aegean Agricultural Research Inst. Izmir	3046
ESP004	Centro de Recursos Fitogeneticos Alcala de Henares, Madrid	2814
SVK001	Research Institute of Plant Production Piestany	2616
FRA051	Unite experimentale du Magneraud GEVES Surgeres	1949
YUG002	Institute for Field and Vegetable Crops, Faculty of Agriculture Novi Sad	1478
ROM007	Genebank of Suceava, Judetul Suceava	1319
AUT001	Agrobiology Linz - Austrian Agency of Health and Foodsafety / Seed Co Linz	1311
HUN020	Agricultural Research Institute Hungarian Academy of Sciences Martonvasar	839
ROM001	Agricultural Research Station Turda, Judetul Cluj	684
AUT011	Austrian Agency of Health and Food Lwvie - Institute of Plant Product Vienna	640
ISR002	Israel Gene Bank for Agricultural Crops, Agricultural Research Org. Bet Dagan	620
SWE002	Nordic Gene Bank Alnarp	614
LVA010	Plant Genetics Laboratory Institute of Biology Salaspils	566
ITA079	Istituto Sperimentale per la Cerealicoltura - Sez. Operativa Foggia	547
ROM008	Agricultural Research Station Simnic	488
ROM028	Agricultural Research Station Suceava	371
AZE015	Azerbaijan National Academy of Sci Genetic Resources Institute Baku	350
ITA226	Istituto Sperimentale per la Cerealicoltura Catania	310
ITA349	Istituto Sperimentale per la Cerealicoltura Roma	299
ROM026	Agricultural Research Station Podu Iloaiei-Iasi	243
AUT005	Genebank Tyrol Tyrolean Government Innsbruck, Tirol	222
PRT005	Banco de Germoplasma - Genetica Estacao Agronomica Nacional Oeiras	176
GRC035	Nat. Agric. Res. Foundation -Direc Int. Relat., Document. and Info. Athens	170
UKR008	Ustimovskaya Experimental Station for Plant Cultivation Globino dist.	115
ARM002	Armenian Agricultural Academy Yerevan	111
ROM002	Genetic Resources Dep. - Research Inst. for Cereals and Ind. Crops Fundulea	97
CYP004	Agricultural Research Institute Plant Genetic Res. and Herbarium Nicosia	80
GEO013	N.Ketskhoveli Institute of Botany Tbilisi	79
GEO001	Scientific Research Institute of Farming Mtskheta, Tserovani	66
LTU001	Lithuanian Institute of Agriculture Dotnuva-Akademija, Kedainiai D	47
AZE003	Agricultural Research Institute 370098 Baku	46
UKR002	Plant Breeding and Genetics Inst. Odessa	33
IRL029	Department of Agriculture, Food and Rural Development, Leixlip, Co. Kildare	32
ROM023	University of Agricultural Science s and Veterinary Medicine Timisoara	32
YUG040	Agricultural and Technological Research Centre Zajecar	26
ARM005	Institute of Botany, National Acad emy of Sciences of Armenia Yerevan	23
BLR011	Belarus Research Institute of Arable Farming and Fodders Zhodino, Minsk	19
ARM006	Scientific Center of Agronomy and Plant Protection Echmiadzin	9
EST001	Jogeva Plant Breeding Insitute Jogeva	8
UKR003	Mironovskyi Institute for Wheat Breeding and Seed Production, Kiev reg	5
CHE071	Schweizer Bergheimat Lucerne	4
AUT025	Research Station for Special Crops Wies 88	1
GEO007	Mtskheta Selection Station Village Tsilkani, Tserovani, M	1
	Total	**152524**

* Romanian institutions are still coded “ROMxxx” (the FAO INSTCODE table has not yet been updated to reflect the change in the ISO country code from ROM to ROU).

Comparison between EURISCO and the EWDB

The table below shows that as of March 2005, some records were missing in EURISCO and /or the EWDB (value = 0 in the table). Updates resulting from the download from EURISCO into the EWDB (September 2005) are indicated by shaded cells.

Country ISO Code	Country name	No. of records in		
		March 2005		September 2005
		EURISCO	EWDB	EWDB
ARM	Armenia	144	0	143
AUT	Austria	2099	2077	2174
AZE	Azerbaijan	397	0	396
BEL	Belarus	0	19	19
BGR	Bulgaria	12400	12237	12237
CYP	Cyprus	80	80	80
CZE	Czech Republic	11035	10259	10259
EST	Estonia	72	0	8
FRA	France	1967	1949	1949
GEO	Georgia	146	0	146
DEU	Germany	17216	25494	25494
GRC	Greece	0	170	170
HUN	Hungary	7844	6300	6300
IRL	Ireland	32	0	32
ISR	Israel	620	0	620
ITA	Italy	0	0	6161
LVA	Latvia	18	566	566
LTU	Lithuania	38	7	47
NLD	Netherlands	5531	5315	5315
NGB	Nordic Countries	1374	614	614
POL	Poland	0	10397	10397
PRT	Portugal	176	0	176
ROU	Romania	3234	0	3234
RUS	Russian Federation	34253	34808	34808
SVK	Slovakia	2629	2616	2616
ESP	Spain	2840	2814	2814
CHE	Switzerland	6867	4366	4366
UKR	Ukraine	7373	0	7372
GBR	United Kingdom	9462	9461	9461
TUR	Turkey	0	3046	3046
YUG	Serbia and Montenegro	0	1504	1504
	Total	**127847**	**134099**	**152524**
	Missing records	**15136**	**12050**	**none**

List of updates of passport information since 2003

1. Bulgaria: new IDs for the wheat collection + 2203 new recs. EURISCO by-product (revised data in standardized form, assessed new unique national identifiers)

2. Appended from EURISCO

NI	No. of records
ARM	143
AZE	396
GEO	146
IRL	32
ISR	620
PRT	176
ROU	3234
UKR	7372
Total	**12119**

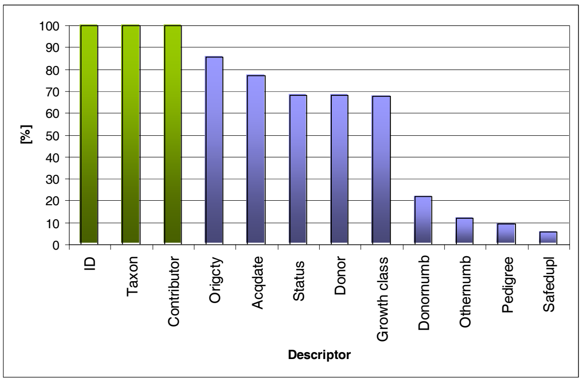
3. Other updates by WWG members

ITA	6161
AUT	97
EST	8
LTU	40

Total updates: **20 358 records**

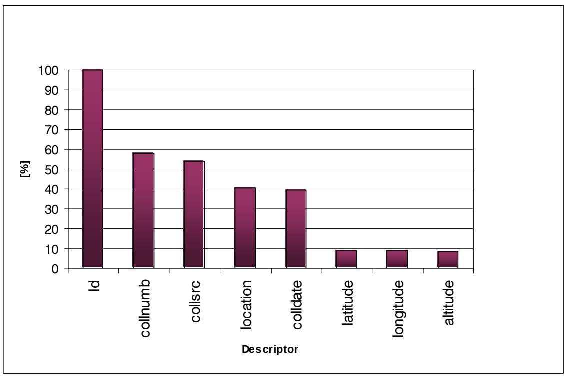
Completeness of passport data (152 524 records)

Passport data descriptor	% of records	No. of records
ID	100	152524
Taxon	100	152524
Contributor	100	152524
Origcty	86	130450
Acqdate	77	117384
Status	68	103968
Donor	68	103914
Growth class	68	103160
Donornumb	22	33343
Othernumb	12	18676
Pedigree	10	14611
Safedupl	6	8680



Completeness of collecting data (39 397 records)

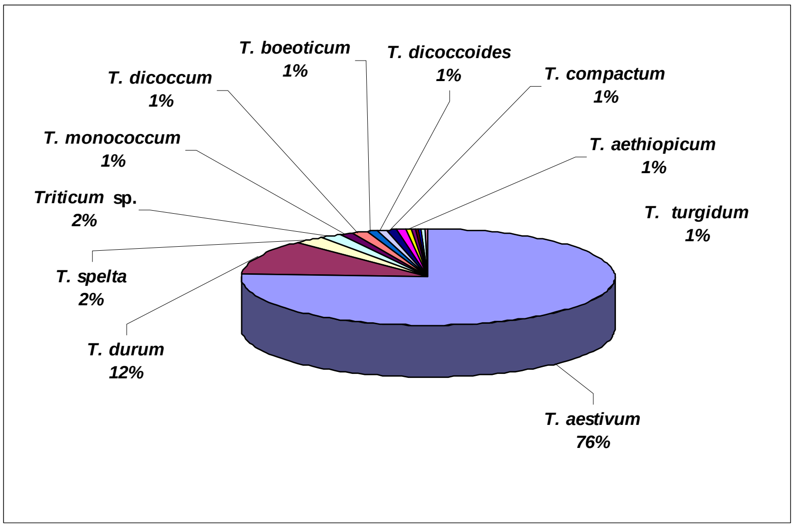
Collecting data	% of records	No. of records
Id	100	39379
Collnumb	58	22754
Collsrc	54	21319
Location	41	16042
Colldate	40	15566
Latitude	9	3581
Longitude	9	3536
Altitude	8	3280



Origin of accessions in the EWDB

Proportion of countries of origin	Proportion of donor countries
59% countries of origin= Europe 26% non European 15% not known	55% countries of origin= Europe 11% non European 34% not known

Taxonomic composition of the EWDB



Documentation of safety-duplicates in the EWDB

EWDB total wheat records	Country	No. of safety-duplicates	Location of safety-duplicates
34808	RUS		
25494	DEU		
12237	BGR		
10397	POL		
10259	CZE	718	SVK
9461	GBR		
7372	UKR	2512	UKR
6300	HUN		
6161	ITA		
5315	NLD	141	AUT
4366	CHE	1510	DEU
3234	ROU	1050	ROU
3046	TUR		
2814	ESP	8	RUS
2616	SVK	132	CZE
2174	AUT	2	DEU, RUS
1949	FRA	1949	FRA
1504	YUG	103	HRV, HUN, YUG
620	ISR		
614	SWE	442	NOR
566	LVA		
396	AZE		
176	PRT		
170	GRC		
146	GEO	2	DEU, RUS
143	ARM	16	RUS
80	CYP	80	ITA
47	LTU	7	RUS
32	IRL		
19	BLR		
8	EST	8	SWE
Total = 152524		**8680**	

Inclusion of characterization data in the EWDB

(for the first six descriptors = awnedness, grain colour, glume colour, glume hairiness, spike density, plant height)

Country	Passport	Characterization
AUT	2174	756
CZE	10259	7178
ESP	2814	948
EST	8	8
LTU	47	40
RUS	34808	1594
Total	**50110**	**10524**

Passport data and characterization data

Country	Passport	Characterization
ARM	143	
AUT	2174	756
AZE	396	
BGR	12237	
BLR	19	
CYP	80	
CZE	10259	7178
DEU	25494	
ESP	2814	948
EST	8	8
FRA	1949	
GBR	9461	
GEO	146	
GRC	170	
HUN	6300	
CHE	4366	
IRL	32	
ISR	620	
ITA	6161	
LTU	47	40
LVA	566	
NLD	5315	
POL	10397	
PRT	176	
ROU	3234	
RUS	34808	1594
SVK	2616	
SWE	614	
TUR	3046	
UKR	7372	
YUG	1504	
Total	**152524**	**10524**

Update since 2003: 5030 rec. sets

Appendix III. Workplan for the delivery of characterization data to the EWDB manager

Descriptors 1 to 6 mentioned in the table below are defined as follows:

1. awnedness
2. grain colour
3. glume colour
4. glume hairiness
5. spike density
6. plant height

N.B. The table below includes all data available at time of publication. Further updates, including commitments made by the countries that have not yet responded, will be available on the Web page of the Wheat Working Group (http://www.ecpgr.cgiar.org/Workgroups/wheat/wheat.htm).

Country	Current status (% of collection already documented)	Workplan	
		Descriptors to be documented and deadline	**% of collection**
Armenia	0	descriptors 1 to 5 by end 2006	ca. 10%
Austria	60%	descriptors 1 to 6 for 220 accessions not yet documented (Genebank Tyrol), by beginning of 2006	95%
Azerbaijan	25%	descriptors 1 to 6 by November 2007	75%
Czech Republic	72%	descriptors 1 to 6 by end 2007	75%
Estonia	4%	descriptors 1 to 6 by end October 2006	80%
France	0	descriptors 1 and 6 by end 2005 others only for core collection (372 var.) by end 2005 whole collection by end 2006	100% 5% 100%
Georgia	0	descriptors 1 to 6 by end 2006	40%
Germany	70%	descriptors 1 to 5 by end 2007	80%
Greece	3%	descriptors 1 to 6 by the end 2005	52%
Hungary	3%	data of the most original Hungarian accessions, acquired until 1965 – by end 2007	5%
Ireland	0	descriptors 1 to 6 by end 2006	100
Israel	descriptors not applicable to *Aegilops*		
Italy	0	by end 2007: descriptors 1 to 6 for ca. 1995 acc. (1250 *T. aestivum*, 295 *T. durum* and 450 other species (*monococcum, spelta,* etc.) + descriptors 2, 3, and 6 for ca. 60 acc.	ca. 35%

Country	Current status (% of collection already documented)	Workplan	
		Descriptors to be documented and deadline	**% of collection**
		(*T. durum*)	
Lithuania		descriptors 1 to 6 by end 2006	90%
Macedonia FYR	0	descriptors 1 to 6 by end 2007	30%
Netherlands	0	descriptors 2, 5 and 6 by end 2005	40%
NGB	descriptor 1 and 6: 80% descriptors 2, 3, 4, 5: 0%	remaining data by October 2007	100%
Portugal	15%	descriptors 1 to 6 by end 2006	40%
Romania	descriptors 5 and 6: 10% descriptors 1, 2, 3, 4: 0%	descriptors 1 to 6 by end 2010	25%
Russian Federation	4.5%	descriptors 1 to 6 by end 2006	5%
Spain	33%	descriptors 1 to 6 by end 2006	36%
Switzerland		descriptors 1 to 5 = October 2006 descriptor 6 (plant height) = October 2005	70%
Turkey	20% (1274 accessions)	descriptors 1 to 6 by October 2007	75%
Ukraine	40%	descriptors 1 to 6 by end 2005	90%

Appendix IV. Agenda

Second Meeting of the ECP/GR Working Group on Wheat
22-24 September 2005, La Rochelle, France

Wednesday 21 September
Arrival of participants

Thursday 22 September

8:00	*Departure from the hotel to the Youth Hostel*
8:30 – 8:40	• Opening of the meeting, welcome
8:40 – 9:00	• Brief self-introduction of the participants
	• Approval of the agenda
9:00 – 9:30	• Briefing on ECP/GR Phase VII (*L. Maggioni)* • Briefing on international events (*L. Maggioni and J. Koenig)*
9:30 – 10:30	• Networking activity on wheat and EWDB: stock taking (*A. Le Blanc and I. Faberová)*
10:30 – 11:00	*Coffee break*
11:00 – 12:30	• Networking activity on wheat and EWDB: stock taking *(continued)*
12:40 – 13:45	*Lunch*
14:00 – 15:00	• Networking activity on wheat and EWDB : stock taking *(continued)*
15:00 – 15:30	*Coffee break*
15:30 – 16:30	• Presentation and discussion on AEGIS (*introduced by J. Koenig)*
16:30	*Departure from the Youth Hostel to the hotel*
17:00	*Short reception in Town Hall*
18:00	*Visit of La Rochelle in carriage*
19:30	*Free time for dinner in La Rochelle*

Friday 23 September

8:00	*Departure from the hotel to Le Magneraud, by bus*
	• Welcome to GEVES (*Bruno Richard, Head of the Variety Testing Unit)*
9:30 – 10:30	• Presentation and discussion on COST 860 – SUSVAR (sustainable low input cereal production *(introduced by G. Kleijer)*
	• Establishment of a new workplan for the Wheat Working Group (*introduced and animated by A. Le Blanc and I. Faberová*)
10:30 – 11:00	*Coffee break*
11:00 – 13:00	• Establishment of a new workplan for the Wheat Working Group *(continued)* - Discussion and Recommendations
13:00 – 14:30	*Lunch*
14:30 – 15:00	• The Global Crop Diversity Trust and the ECP/GR Wheat Working Group (*L. Maggioni*)
15:00 – 17:00	*Visit of GEVES*
17:00	*Departure from Le Magneraud to Aigrefeuille*
17:30 – 19:30	*Visit of a fossil collection*
20:00	*Return to hotel in La Rochelle - Free time for dinner*

Saturday 24 September

8:30	*Departure from the hotel to the Youth Hostel*
9:00 – 10:00	• Short presentations *(Marzia Cattaneo, Italy; Benvindo Martins Maçãs, Portugal; and E. Firat, Turkey)*
10:00 – 15:00	• Drafting of the report *(Free time for delegates not involved in the drafting)*
12:30 – 13:30	*Lunch*
15:00 – 17:00	• Presentation and correction of the draft report • Election of the Chair and Vice-Chair • Closing remarks
17:00	*Departure to the hotel*
	Free time
19:30	*Official dinner in La Rochelle*

Sunday 25 September

Departure of participants

Appendix V. List of participants

Second Meeting of the ECP/GR Working Group on Wheat
22-24 September 2005, La Rochelle, France

N.B. The composition of the Working Group is subject to changes. The latest update can be found on the Wheat Working Group Web page (http://www.ipgri.cgiar.org/networks/ecpgr/contacts/ecpgr_wgwh.asp).

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ACRONYMS AND ABBREVIATIONS

AARI	Aegean Agricultural Research Institute, Izmir, Turkey
AEGIS	A European Genebank Integration System
AFLP	Amplified fragment length polymorphism
AGES	Österreichische Agentur für Gesundheit und Ernährungssicherheit GmbH (Austrian Agency for Health and Food Safety), Austria
ARI	Agricultural Research Institute, Nicosia
AWCC	Australian Winter Cereals Collection
AWG	*Avena* Working Group (ECP/GR)
BAZ	Bundesanstalt für Züchtungsforschung an Kulturpflanzen (Federal Centre for Breeding Research on Cultivated Plants), Braunschweig, Germany
BCC	Barley Core Collection
BRC	Biological Resource Centre
BRG	Bureau des ressources génétiques (Board for Genetic Resources), France
BWG	Barley Working Group (ECP/GR)
BYDV	Barley yellow dwarf virus
BYMV	Barley yellow mosaic virus
CBD	Convention on Biological Diversity
CERMIS	Centro Ricerche e Sperimentazione per il Miglioramento Vegetale (Research and Experimentation Centre for Plant Improvement), Tolentino, Italy
CGIAR	Consultative Group on International Agricultural Research
CGN	Centre for Genetic Resources, the Netherlands
CIMMYT	Centro Internacional de Mejoramiento de Maíz y Trigo (International Wheat and Maize Improvement Center), Mexico (CGIAR)
CIP	Centro Internacional de la Papa (International Potato Center), Peru (CGIAR)
CNCG	Cereals Network Coordinating Group (ECP/GR)
CNR	Consiglio Nazionale delle Ricerche (National Research Council), Italy
CRA	Consiglio per la Ricerca e la Sperimentazione in Agricoltura (Agricultural Research Council), Italy
CRF	Centro de Recursos Fitogenéticos (Centre for Plant Genetic Resources) (INIA), Alcalá de Henares, Spain
EADB	European *Avena* Database
EBDB	European Barley Database
ECCDB	European Central Crop Database
ECP/GR	European Cooperative Programme for Crop Genetic Resources Networks
ENMP	Estação Nacional de Melhoramento de Plantas (National Plant Breeding Station), Elvas, Portugal
EPGRIS	European Plant Genetic Resources Information Infra-Structure
ESDB	European *Secale* Database
ETDB	European Triticale Database
EU	European Union
EUFORGEN	European Forest Genetic Resources Programme
EURISCO	European Internet Search Catalogue (EPGRIS project)
EWDB	European Wheat Database
FAO	Food and Agriculture Organization of the United Nations, Rome, Italy

GEF	Global Environment Facility
GEVES	Groupe d'Etude et de contrôle des Variétés et des Semences (Varieties and Seeds Study and Control Group), France
GIS	Geographical information system
GIWGR	Global Inventory of Wheat Genetic Resources
GMO	Genetically modified organism
GPA	Global Plan of Action
GRDC	Grains Research and Development Corporation, Australia
GRI	Genetic Resources Institute, Azerbaijan National Academy of Sciences, Baku, Azerbaijan
GRIN	Genetic Resources Information System (USA)
GWIS	Global Wheat Information System
IBGS	International Barley Genetics Symposium
IBV	Information Centre for Biological Diversity (ZADI), Bonn, Germany
ICARDA	International Center for Agricultural Research in the Dry Areas, Aleppo, Syria (CGIAR)
ICCI	Institute for Cereal Crops Improvement, Tel Aviv, Israel
ICIS	International Crop Information System
IDG	Istituto del Germoplasma (Germplasm Institute), Bari, Italy
IER	Institute of Epidemiology and Resistance, Aschersleben, Germany
IGB	Israeli Gene Bank for Agricultural Crops, Bet-Dagan, Israel
IGER	Institute of Grassland and Environmental Research, Aberystwyth, United Kingdom
IGV	Istituto di Genetica Vegetale (Institute of Plant Genetics), Italy
INIA	Instituto Nacional de Investigação Agrária (National Institute for Agrarian Research), Portugal
INIA	Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (National Institute of Food and Agriculture Investigation and Technology), Spain
INRA	Institut National de la Recherche Agronomique (National Agronomic Research Institute), France
INRA	Institut National de la Recherche Agronomique (National Agronomic Research Institute), Morocco
IPGR	Institute for Plant Genetic Resources, Sadovo, Bulgaria
IPK	Institut für Pflanzengenetik und Kulturpflanzenforschung (Institute for Genetics and Plant Breeding), Gatersleben, Germany
IRIS	International Rice Information System
ISC	Istituto Sperimentale per la Cerealicoltura (Experimental Institute for Cereal Research), Italy
ISSR	Inter-simple sequence repeat
IU	International Undertaking
IWGRN	International Wheat Genetic Resources Network
JIC	John Innes Centre, Norwich, United Kingdom
JPBI	Jõgeva Plant Breeding Institute, Jõgeva, Estonia
LIA	Lithuanian Institute of Agriculture, Dotnuva, Lithuania
LUA	Lithuanian University of Agriculture, Kaunas, Lithuania
MCPD	Multi-crop Passport Descriptors (FAO/IPGRI)

MTA	Material Transfer Agreement
NAGREF	National Agricultural Research Foundation, Greece
NCPGRU	National Centre for Plant Genetic Resources of Ukraine, Kharkiv, Ukraine
NGB	Nordic Gene Bank, Alnarp, Sweden
NGO	Non-governmental organization
NPGS	National Plant Germplasm System (USDA-ARS)
NSGC	National Small Grains Collection (USDA-ARS)
OECD	Organisation for Economic Co-operation and Development
PAGE	Polyacrylamide gel electrophoresis
PBAI	Plant Breeding and Acclimatization Institute, Radzików, Poland
PCR	Polymerase chain reaction
PGR	Plant genetic resources
PGRFA	Plant genetic resources for food and agriculture
QTL	Quantitative trait loci
RAC	Station Fédérale de Recherches Agronomiques de Changins (Federal Research Station for Plant Production of Changins), Nyon, Switzerland
RAPD	Random amplified polymorphic DNA
RFLP	Restriction fragment length polymorphism
RICP	Research Institute of Crop Production, Prague, Czech Republic
RIPP	Research Institute of Plant Production, Piešťany, Slovak Republic
SCRI	Scottish Crop Research Institute, Dundee, United Kingdom
SIDA	Swedish International Development Agency
SINGER	System-wide Information Network for Genetic Resources (CGIAR)
SNP	Single nucleotide polymorphism
SSR	Simple sequence repeat
TABI	Institute for Agrobotany, Tápiószele, Hungary
UNDP	United Nations Development Programme
UNEP	United nations Environment Programme
UPOV	Union pour la Protection des Obtentions Végétales (International Union for the Protection of New Varieties of Plants), Geneva, Switzerland.
USAID	United States Agency for International Development
USDA	United States Department of Agriculture
USDA-ARS	United States Department of Agriculture - Agricultural Research Service
USDA-MAP	United States Department of Agriculture-Marketing Assistance Project in Armenia
VIR	N.I. Vavilov Research Institute of Plant Industry, St. Petersburg, Russian Federation
VU	Vilnius University, Lithuania
WWG	Wheat Working Group (ECP/GR)
ZADI	Zentralstelle für Agrardokumentation und -information (German Centre for Documentation and Information in Agriculture), Bonn, Germany

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