European Cooperative Programme for Crop Genetic Resources Networks

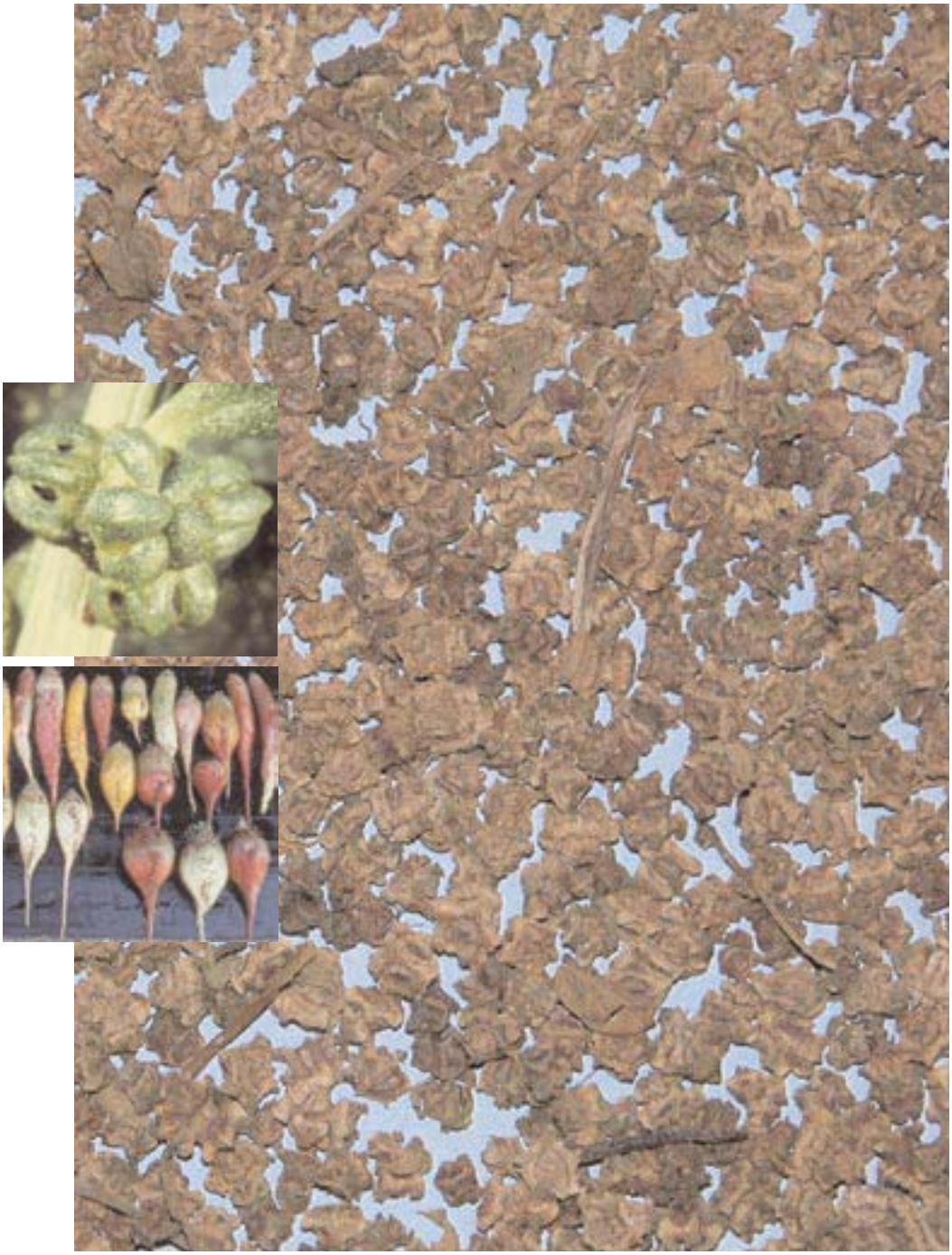
ECP/GR

Report of a Working Group on *Beta* and World *Beta* Network

IPGRI

Second joint Meeting, 23–26 October 2002, Bologna, Italy

L. Frese, C. Germeier, E. Lipman and L. Maggioni, *compilers*



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The International Plant Genetic Resources Institute (IPGRI) is an independent international scientific organization that seeks to advance the conservation and use of plant genetic diversity for the well-being of present and future generations. 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 three programmes: (1) the Plant Genetic Resources Programme, (2) the CGIAR Genetic Resources Support Programme and (3) the International Network for the Improvement of Banana and Plantain (INIBAP).

The international status of IPGRI is conferred under an Establishment Agreement which, by January 2003, 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 ten 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, vegetables, grain legumes, fruit, minor crops, industrial crops and potato) 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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Cover photos: Seeds and maturing fruits of *Beta vulgaris*, courtesy of © L. Frese, BAZ, Braunschweig, Germany / Diversity of beet roots, courtesy of © E. Biancardi, ISCI-Sezione di Rovigo, Italy.

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PART I. DISCUSSION AND RECOMMENDATIONS

Introduction

Opening of the meeting

Paolo Ranalli, Director of the Istituto Sperimentale per le Colture Industriale (ISCI), hosting the meeting, welcomed the participants and wished them a nice stay in Bologna. He thanked Lothar Frese, Lorenzo Maggioni and Giuseppe Mandolino for their help in the organization of the meeting and wished the Group a fruitful meeting.

Lothar Frese, Chairman of the ECP/GR Working Group on *Beta*, opened the meeting and welcomed the participants of the ECP/GR Working Group and World *Beta* Network meeting. He thanked P. Ranalli and G. Mandolino who had agreed to host the meeting and to take care of the local organization. He also thanked the ECP/GR Secretariat for the financial support and the excellent assistance during the planning of this meeting. He stressed that the planning of the meeting was initiated by the BAZ Gene Bank in Braunschweig but finally executed by ISCI and the ECP/GR. Thanks to the excellent communication between the three institutions the organizing team experienced no problems.

In contrast to the previous meetings, the organizing committee and the *Beta* Coordinating Committee of the World *Beta* Network decided not to actively search for additional funds to facilitate the participation of experts from non-European countries. As a consequence countries from outside Europe were under-represented. On the other hand, five European countries (Hungary, Slovakia, Slovenia, Ukraine and F.R. Yugoslavia) had been invited for the first time to confer with the Group. Three countries sent representatives and were specifically welcomed by the Chairman (Hungary, Slovenia and Ukraine). The Chairman expressed the wish to include a broader range of European countries, especially those located in the main distribution area of the genus, and experts from North Africa and Asia. It has always been ECP/GR policy to involve non-European countries as observers in ECP/GR Working Groups discussions and activities. The Chairman suggested that FAO/IPGRI should provide easily accessible funds to facilitate the participation of these experts.

L. Frese regretted the absence of other invited participants – representatives from Azerbaijan (Z. Akparov), France (B. Desprez) and USA (L. Panella) – who were unable to attend.

In 1999 the Group received offers from Poland and Italy to host a meeting. The Chairman, together with a group of sugar beet breeders, decided to convene the meeting in Italy, where research on breeding for resistance is ongoing. In addition, investigations into the genetic diversity of the sea beet populations growing along the northern part of the Adriatic seashore are currently under way at the host institute and the Group was eager to learn about the research results at first hand.

The Chairman said the purpose of the meeting was to improve the management and utilization of *Beta* genetic resources. Meetings are necessary to review the workplan approved in 1999 and to develop a new workplan for the next period. He emphasized that the Working Group contributes to the global efforts for the sustainable management and use of plant genetic resources. *Beta* is a genus native to Europe. Europe is therefore specifically obliged to maintain the genetic resources of cultivated beets and their wild relatives. The ECP/GR *Beta* Working Group along with the World *Beta* Network partners have to support the genus *Beta* as there is no other institution interested in the genetic resources of *Beta*. This emphasizes the importance of the Group.

The Chairman then explained the proposed agenda and said that an exchange of research results and the elaboration of a workplan for the next three years were the major aims of this 3-day meeting.

General briefing on ECP/GR

Lorenzo Maggioni, ECP/GR Coordinator, welcomed the participants to the second joint meeting of the ECP/GR Working Group on *Beta* and the World *Beta* Network and briefly summarized the objectives and mode of operation of the cooperative programme. He then mentioned the activities carried out during Phase VI of the programme (1999-2003) within the framework of the Industrial Crops and Potato Network. These included two meetings of the Network Coordinating Group and two meetings respectively of the Potato and *Beta* Working Groups. *Ad hoc* meetings were also held on two occasions to discuss *Beta* core collections and flax genetic resources in Europe. He then gave a brief account of the outcomes of the mid-term meeting of the ECP/GR Steering Committee, held in St. Petersburg, Russian Federation, on 14-17 October 2001. In this occasion, a task force working on the definition of a model Material Transfer Agreement for the European region was encouraged to continue its effort and a statement was made recommending that an extended list of crops be considered for the establishment, by the FAO Commission on PGRFA, of a multilateral system for access and benefit-sharing. Regarding sharing of responsibilities in Europe for the conservation of genetic resources, the Steering Committee recommended that the possible practical options be analyzed in more detail and that the definition of genebank quality standards receive careful attention.

In order to develop a strategy for the next Phase (VII), two task forces composed of a few Steering Committee members were established to discuss (1) the impact on PGR of recent developments in science, technology and international policy; and (2) how genebanks might implement relevant international agreements and their impact on their operation. A questionnaire sent to all Working Group Chairs and National coordinators is being used to sound out opinions on the future priorities and mode of operation of ECP/GR, to be defined during the Steering Committee meeting planned for October 2003.

A brief account was also given on the progress of the EU-funded project EPGRIS 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 CCDBs. EURISCO is expected to gradually develop and become the most complete and reliable source of passport data in Europe.[1] The catalogue will carry 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 Multicrop Passport Descriptor List (MCPDv2), finalized in December 2001 (http://www.ipgri.cgiar.org/publications/pubfile.asp?ID_PUB=124).

Report of the Working Group Chair

The Chair reported on the six fields of activities discussed by the Working Group (WG) during its first meeting held at Broom's Barn, United Kingdom in 1999. A major recommendation was to redesign the International Data Base for *Beta* (IDBB) following the concept introduced by C. Germeier. This work is completed to a large extent and the debugging work is in progress. Characterization and evaluation data of the GENRES

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[1] Update at time of publication: EURISCO was launched officially at the Final Conference of the EPGRIS Project, 11-13 September 2003, Prague, Czech Republic. A demo version of the catalogue is available at http://eurisco.ecpgr.org/

CT 95-42 project have been included in the new database as well as characterization data recorded by VIR in the framework of the ECP/GR-funded *Beta* project. Data from the University of Kraków and the Gene Bank in Prague will progressively be added. Members of the WG will be approached later and requested to provide datasets they wish to make available to the user community. A significant improvement of the database is that the origin of all IDBB data is now understandable for the users by providing names and addresses of the partners/institutions that conducted the individual characterization and evaluation work.

In the year 2000 C. Germeier spent several days with the database experts of GRIN at Beltsville (USA) and discussed in detail possibilities of merging the US and European evaluation data. In principle it is possible to merge the two sets of information. The main problem is the limited work capacity available at the BAZ Gene Bank for this additional task.

In 1999 the WG had noted that it would be helpful to analyze characterization and evaluation data with GIS software and requested the IDBB managers to provide the IDBB with appropriate software. No actions have been undertaken to implement this recommendation. The development of the new database and the data input have first priority, the analyses of the data with GIS has second priority and will therefore be done later. The WG Chair explained that GENRES CT95-42 funds were shifted from the IPK budget to the BAZ budget. This money was used to extend a contract for a scientist who assisted C. Germeier in the development of database modules. The extra budget was also used to prepare an on-line taxonomic guide of the genus *Beta*.

The identification of duplicates is part of the work programme of the EU project GENRES CT95-42. The WG Chair explained that there are fewer groups of duplicates than indicated by similar sounding accession names. The large group of probable duplicates (PRD) of the "Egyptian flat-round" type for example must be divided into a number of morphologically distinct subgroups. The accessions grown in the field at Braunschweig were also investigated by means of molecular markers at the University of Birmingham. In general it can be concluded that there are fewer duplicates than expected.

A task force to look into the preliminary Synthetic *Beta* core collection and to further develop it was convened at Cappelle-en-Pévèle (France) on 30 September 2000. The WG Chair submitted a proposal to ECP/GR to fund this meeting. The proposal was approved and facilitated the participation of B.V. Ford-Lloyd, L. Panella and A. Tan in the meeting. The *ad hoc* group produced a report which can be downloaded from the *Beta* WG Web page as a PDF file (see http://www.ecpgr.cgiar.org/Workgroups/beta/beta.htm).

The concept of a hierarchical and differential genebank[2] seed stock management developed by the BAZ Gene Bank was used to elaborate a database structure required to manage sharing of responsibilities within a European Working Group. The Chair explained that this work has been completed only recently and that most of the actions planned in the field of task-sharing can be commenced now. He stated that the communication between the IDBB and the national collection curators would start within about two years.

The WG had suggested elaborating a genebank quality standard. Trust in each other's collection management procedures was considered vital for sharing responsibilities. Amongst other aspects, seed production procedures determine the quality of a genebank. The WG chair has distributed a *Beta* seed production manual which describes the cultivation

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[2] Bücken, S. and L. Frese. 1999. Differential and hierarchical seed stock management – a new alternative for the management of large-sized genebank holdings. Pp. 96-101 *in* Implementation of the Global Plan of Action in Europe – Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture. Proceedings of the European Symposium, 30 June–3 July 1998, Braunschweig, Germany (T. Gass, L. Frese, F. Begemann and E. Lipman, compilers). International Plant Genetic Resources Institute, Rome, Italy.

methods applied by the BAZ Gene Bank. Curators of partner genebanks were requested to produce similar documents.

The WG had recommended in 1999 to search for opportunities for *in situ* conservation of wild species. Except for Turkey, none of the European countries have developed specific *in situ* management plans and actions for *Beta*. The Chairman reported that the USDA/ARS (contact: L. Panella) has repeatedly expressed interest in a *B. nana* survey. The USDA/ARS would be willing to co-fund plant explorations in Greece and the Greek Gene Bank is in principle prepared to assist a mission. However, concrete actions have not been undertaken due to time constraints. On the occasion of a GENRES *Brassica* meeting (Córdoba, Spain) the WG chair addressed the issue of *in situ* management of wild *Beta* species during a visit to the Botanical Garden of Córdoba. The Garden is engaged in raising public awareness of plant genetic resources and is willing to act as contact address. It seems to have the competence for nature conservation projects on the Canary Islands, the main distribution area of the section *Procumbentes*.

Update on National Collections

(Available full papers are included in Part II)

Belarus

Anna Svirshchevskaya (Institute of Genetics and Cytology, Belarus National Academy of Sciences, Minsk) provided a written report on the status of *Beta* genetic resources in Belarus. Beet is traditionally grown in Belarus for sugar production and as a fodder and vegetable crop. The beet germplasm collection is divided between three institutes of the Belarus National Academy of Sciences (Belarus Research Institute of Arable Farming and Fodders (BRIAFF) in Zhodino; Belarus Research Institute of Vegetable Crops (BRIVC) in Samohvalovichi; and Institute of Genetics and Cytology (IGC) in Minsk) and the Belarus Regional Experimental Breeding Station for Sugar beet near Nesvizh (BREBSS). The collections include: (i) populations and old cultivars from former USSR (mainly from the Ukraine, Russian Federation and Latvia) cultivated in recent decades in the country; (ii) commercial cultivars and components for commercial hybrids arising from local breeding activities in Belarus; (iii) germplasm of wild species (mainly sources of genes for disease resistance) from VIR (St. Petersburg, Russian Federation); (iv) material arising from existing breeding programmes; and (v) germplasm produced by biotechnological means—doubled haploid (DH) and dihaploid lines.

The report also provides information on the Belarus national programme "Creation of the National Genetic Fund for economically important plants" initiated in 2000 with funding for 6 years, and in which 10 research and educational institutions participate. Activities related to beet germplasm characterization and evaluation, seed processing and storage, research and international cooperation are presented.

China

Yahuai Ma, from the Sugar Beet Research Institute of the Chinese Academy of Agricultural Science (ISB-CAAS) presented an overview of *Beta* genetic resources in China. Several organizations are involved in activities on *Beta,* including institutes of CAAS (ISB, Institute of Vegetables and Flowers, Institute of Crop Genetic Resources) and others. A map of sugar beet and leaf beet planting areas in China was presented. *Beta* resources collected by the Institute of Vegetables and Flowers and by ISB amount to 231 and 1288 accessions respectively. Main research issues for *Beta* in China include checking for differences between

material; evaluation of disease resistance; exchange of data between breeders and international organizations and development of methods for routine work.

Czech Republic

A report was received before the meeting from Zdeněk Stehno, Vera Chytilová and Iva Faberová on "*Beta* collection in the Czech Republic in the period 2000-2002". During the last three years, attention has been paid to increasing seed availability, especially of garden beet, characterization and evaluation. Few accessions of *Beta vulgaris* var. *altissima (Beta vulgaris* subsp. *vulgaris* Sugar Beet Group*)*[3] were multiplied in the framework of the EU- and ECP/GR-funded project GENRES CT95-42. Evaluation of 118 accessions of salad beets (*Beta vulgaris* var. *vulgaris*) *(Beta vulgaris* subsp. *vulgaris* Garden Beet Group*)* showed a great variability in the shape and colour of the beet root, with the following root shapes observed: flat (cultivar 'Egyptska plocha'), circular (cv. 'Detroit'), cylindrical (cv. 'Cylindra') and conical (cv. 'Dobbie's Purple'). A different intensity of skin and root flesh colour could also be found as well as some cultivars with orange skin colour ('Severnaja oranzevaja'). Cultivar 'Nutting's' has an interesting nut flavour when eaten fresh. The collection of 27 accessions of Swiss chards (*Beta vulgaris* var. *cicla*) *(Beta vulgaris* subsp. *vulgaris* Leaf Beet Group*)* includes cultivars with various leaf colours from yellow-green ('Gelber Krauser'), light green ('Lyoner') to dark green ('Poise Verte A Carde Blanche') and red colour ('Rhubarb Chard'). The surface of the leaf blade, length and colour of petiole also show high variability.

Germany

Ute Wehres presented the situation in Germany on behalf of L. Frese. The Convention on Biodiversity became national law in 1993. On the basis of the CBD as well as the Global Plan of Action a National Programme for Plant Genetic Resources has been approved by the Ministry of Consumer Protection, Food and Agriculture and published in September 2002. As a consequence of this programme the whole *ex situ* holding of the BAZ Gene Bank including *Beta* will be transferred to the IPK genebank at Gatersleben. From October 2002 users are requested to order *Beta* accessions from the IPK genebank only. The IPK genebank will work on the optimization of *ex situ* management procedures, including the search for duplicates and the development of a "molecular passport" for outcrossing species.

The German *Beta* holding amounts to 2293 accessions (section *Beta* 76%, section *Corollinae* 21%, section *Nanae* and *Procumbentes* 3%). The collection is being characterized and evaluated using the IPGRI Descriptors for *Beta*. The characterization and evaluation data of the BAZ Gene Bank *Beta* holding form a subsample of the data documented by the IDBB. Currently the IDBB contains 16397 characterization and 5248 evaluation data items.

After the merger of the two holdings and the respective databases is complete the BAZ Gene Bank will assume new tasks in the field of plant genetic resources management. The BAZ will continue to manage the IDBB and will provide input into the ECP/GR Working Group on *Beta* and the WBN as in the previous years.

One of the new tasks consists of the development of germplasm management strategies that complement *ex situ* activities. The Institute of Ecology, Ecotoxicology and Ecochemistry

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[3] For clarity and consistency, where necessary the nomenclature proposed by Lange *et al.* (1998) and adopted by the WBN has been inserted in the text.
Lange, W., W.A. Brandenburg and Th.S.M. De Bock. 1998. Proposal for a new taxonomical classification of the cultivated forms of beet, *Beta vulgaris* L. Pp. 16-22 *in* International *Beta* Genetic Resources Network. A report of the 4th International *Beta* Genetic Resources Workshop and World Beta Network Conference held at the Aegean Agricultural Research Institute, Izmir, Turkey, 28 February-3 March 1996. International Crop Network Series 12. (L. Frese, L. Panella, H.M. Srivastava and W. Lange, eds). International Plant Genetic Resources Institute, Rome, Italy.

of the RWTH Aachen started with a GMO risk assessment study in 1993. Within this framework the institute has made an inventory of *Beta vulgaris* subsp. *maritima* populations growing on the Baltic Sea shore in Germany. The research results can be used as a baseline required to establish *in situ* management activities. The states of the Federal Republic of Germany have the formal competence to run *in situ* management programmes. The BAZ will have the responsibility to initiate activities, develop methodologies and to assume a coordinating role.

Discussion and recommendation

In reply to a question from G. Poulsen, L. Frese explained that the concept of a molecular passport proposed by the IPK genebank involves the possibility of describing populations with molecular markers and therefore to use molecular techniques to check the genetic integrity of individual accessions after seed multiplication.

G. Poulsen remarked that the definition of acceptable natural levels of genetic variation and drift during seed multiplication was a very important issue and recommended that it be dealt with by a task force of the Working Group on *Beta*.

Hungary

Attila Simon (Institute for Agrobotany, Tápiószele) presented general background information on the Institute and genebank activities. The Hungarian *Beta* collection held at the institute includes 301 accessions, including 133 of Hungarian origin. All the *Beta* accessions are stored in the active collection, while 21% of the samples (63) are kept in the base collection. *Beta* landraces total 88 accessions (34%) and are maintained in the base collection. The accessions in the collection were received from 15 countries, with most (219) coming from Hungarian institutes. Passport, evaluation and genebank management data of the PGR maintained by the Institute are computerized. Hardware and software have been updated regularly. The database structure is based on genebank standards and takes into account the recommendations of FAO/IPGRI. The volume of *Beta* field multiplication and regeneration varies from year to year according to the changes in the collection resulting from introduction or collecting activities. During multiplication special attention is paid to isolation. In the case of landraces multiplication is also carried out according to a "backyard multiplication system". Characterization and evaluation are based on the *Descriptors for Beta* published by IBPGR/CGN in 1991, complemented by a few additional traits. Almost half of the *Beta* collection has been characterized. Characterization data are available for 57% of the landraces.

Iran

Mohammad Nasser Arjmand (Iranian Sugar Factories Syndicate, Tehran) presented a report on the collection and characterization of beet landraces and *in situ* conservation of *Beta lomatogona* in Iran.

The collection and evaluation of *Beta* germplasm has recently received increased attention in Iran owing to the need for biotic and abiotic resistance/tolerance genes and concern about loss of germplasm due to gradual elimination of natural habitats. The Sugar Beet Seed Institute (SBSI) holding the *Beta* Gene Bank in Iran carried out a national project in 1998-2002 to collect and characterize *Beta* germplasm, with expeditions programmed each year. During the past five years, *Beta* germplasm, especially landraces, was collected in different provinces. Characterization of beet landraces was carried out and the results showed a great variation both between and within the populations. Cytological analysis revealed that all accessions studied were diploid. Each year multiplication of about 25 accessions was conducted.

The population size of wild beet (*Beta lomatogona),* surveyed several times in the past years, is apparently decreasing in a number of localities due to severe drought, land management changes and overgrazing, suggesting the need for protection of this species. The exploration mission could not find any plants of *B. lomatogona* in 1999 and drew attention to this. To establish *in situ* conservation, pericarp caps of fruit balls of *B. lomatogona* were removed manually and sown in April 2000 in the greenhouse in Karadj in one-litre pots filled with sterile soil. 150 well-developed plants were transported to Ardabil and transplanted to the prepared plot. Seeds were harvested in bulk in August 2002. The plants are kept in the research station of Ardabil. This project is funded by the Scientific Research Council.

Lithuania

Rima Tamošiūnienė (UAB Agrofirma "Sėklos") indicated that there are three institutions responsible for the national *Beta* collection in Lithuania: the Lithuanian Institute of Agriculture (LIA, Akademija) (long-term storage), the Lithuanian Institute of Horticulture (LIH, Babtai), and UAB Agrofirma "Sėklos" (headquarters in Vilnius, breeding laboratory in Akademija).

The long-term storage genebank currently contains 9 red beet accessions (all Lithuanian varieties and 3 new stable breeder's lines) and 7 accessions of fodder beet. The working collection of red beet (*Beta vulgaris* var. *conditiva* Alef.) *(Beta vulgaris* subsp. *vulgaris* Garden Beet Group*)* is located at LIH. Since 1999 it has increased by more than 40 accessions. The red beet accessions maintained in the working collections includes breeder's lines (characterized by high yield, earliness and bigermity) and foreign varieties (sources of earliness, root type, monogermity, etc.). The accession of red beet landraces collected in 1996 near Vilnius in the village of 40 Totoriu was found to be a valuable source of bolting and disease resistance.

Since 2001 the collection, evaluation and use of sugar and fodder beet accessions are based at the UAB Agrofirma "Sėklos". This company is also responsible for pre-breeding work, breeding activities and primary seed production of the registered Lithuanian fodder beet varieties and landraces. In 2000-2001 the working collection of fodder and sugar beets included 30 accessions. 17 accessions were obtained from VIR. In 2002 the collection consists of 26 accessions (5 of them sugar beet with CMS) for further selection and use in the breeding process.

Nordic Countries

Gert Poulsen (Nordic Gene Bank, Alnarp, Sweden) indicated that NGB's mandate on *Beta* species includes *Beta vulgaris* subsp. *cicla (*Swiss chard) *(Beta vulgaris* subsp. *vulgaris* Leaf Beet Group*), B. vulgaris* subsp. *maritima* (wild beet), *B. vulgaris* var. *alba* (fodder beet) *(Beta vulgaris* subsp. *vulgaris* Fodder Beet Group*), B. vulgaris* var. *altissima* (sugar beet) *(Beta vulgaris* subsp. *vulgaris* Sugar Beet Group*)* and *B. vulgaris* var. *conditiva* (beetroot) *(Beta vulgaris* subsp. *vulgaris* Garden Beet Group*)*. The NGB *Beta* collection currently includes a total of 105 accessions, including 60 accessions accepted for long-term conservation (44 from Denmark and 16 from Sweden). The distribution of accessions according to type of sample is as follows: 91 cultivars, 6 breeding lines, and 11 wild types. The region is located on the northern limit of growth (*limes borealis*) of wild beets. A diversity study on these populations is being carried out in collaboration with Risø Research Centre in Denmark.

Accessions are stored in the base collection and in the active collection at -20°C after drying to 5-7% moisture content. Safety-storage is subject to natural conditions at -4°C. Characterization data are available for most of the material and 40 accessions of fodder beets have been characterized using isozymes. All material can be found on the NGB homepage

(www.ngb.se). Characterization data have not been fully published yet. The IDBB contains 272 records from Nordic material. NGB material is presently available without any restrictions to *bona fide* users.

Poland

On behalf of Leonarda Dalke (Plant Breeding and Acclimatization Institute, Research Division Bydgoszcz), Kamilla Kuzdowicz presented an overview of the Polish *Beta* collection, located in Bydgoszcz. It consists of wild *Beta* species, old varieties, breeding material and cultivated beets from Poland and abroad, material received from international expeditions, and local populations. The collection comprises 300 accessions (112 sugar beet, 156 fodder beet and 32 wild forms of accessions of sections *Beta*, *Corollinae* and *Procumbentes*).

Collecting of beet materials aims to save the genepool of old multigerm cultivars. The use of hybridization methods based on CMS lines led to the narrowing of the genetic base in the new cultivars. Wild species and local populations are important sources of resistance to disease, pest and abiotic factors.

Evaluation is carried out in Konczewice for agricultural characters and in Bydgoszcz for morphological, cytological features, seed quality and seed germination tests. It follows the Descriptor List for *Beta.* Part of the collection is evaluated *in vitro* for two economically important beet diseases (*Aphanomyces cochlioides* Drechsler and *Cercospora beticola* Sacc.)

Passport, characterization and evaluation data are documented and stored in the collection and sent to the National Centre for Plant Genetic Resources in Radzików. Part of the data has been sent to the IDBB.

The *Beta* collection is kept in long-term storage in Radzików, in glass jars at -15°C and 5-8% moisture content. After 10-20 years long-term storage the accessions revealed still very good germination and need no multiplication.

Some of the accessions are stored in Bydgoszcz under medium-term storage as a working collection. Information and seed samples are distributed freely. A quarantine certificate is necessary for sending samples abroad. The collected and evaluated germplasm is used in sugar and fodder beet breeding and in several research programmes.

Romania

Ioan Gherman (Research and Production Station for Sugar Beet and Sweet Substances, Braşov) reported on the Romanian *Beta* collections. Holders are the Research Institute for Potato and Sugar Beet Braşov, Sugar Beet Research Station Roman, Breeding Beet Laboratory Fundulea and Agricultural Research Station Lovrin. Most of the germplasm is preserved in working collections. A small part is kept as safety-duplicates at Suceava Genebank under medium- and long-term conditions. The *Beta* collection consists of indigenous and foreign sugar beet monogerm and multigerm varieties; breeding materials (diploid and tetraploid monogerm and multigerm); indigenous and foreign fodder beet and garden beet varieties; breeding material of fodder beet; and wild species. Only two wild species are represented: *Beta vulgaris* subsp. *maritima* L. (annual) and *Beta trigyna* Wald (perennial). There are also landraces of garden beet and fodder beet in farmers' gardens in the hills. The collection currently consists of 858 accessions.

The short-term collection is preserved as seeds in breeding centres where morphological, physiological and biochemical studies and evaluations are conducted. Biochemical descriptors are used for secondary evaluation. The existing germplasm is used for gene stocks maintenance; creation of resistant genitors, especially to *Cercospora beticola* and *Rhizomania*; and creation of new highly productive varieties (high sugar content and high juice purity).

Conditions for long-term storage are not available. After 4-5 years' storage, the germination rate is reduced and 20% of the collection needs to be regenerated each year.

Financial resources allocated to the *Beta* germplasm resources programme are insufficient to allow evaluation and characterization. There is no standardized national database. Each holder has evaluated its own breeding material according to its own priority objectives and therefore some of the descriptors used differ.

Breeding for disease resistance, especially for *Cercospora beticola* and *Rhizomania* is one of the major objectives. Breeding lines and hybrids that combine tolerance to *Cercospora* and *Rhizomania* have been selected by screening in heavily infested fields. Selection of germplasm tolerant to drought and scorching heat is also important because of the very high summer temperatures and drought conditions in southern Romania.

Objectives for the expansion of the *Beta* collection include: acquisition of newly registered varieties; evaluation of the collection and its preservation as duplicates in medium- or long-term conditions in Suceava Genebank; collecting of leaf beet and garden beet and fodder beet germplasm from farmers' vegetable gardens; and collecting wild species in the southern part of the country.

Russian Federation

Tatiana Piskunova (VIR, St. Petersburg) reported on the VIR *Beta* collection started in 1924 from material collected by N.I. Vavilov. It currently comprises a total of 2882 accessions including wild species, primitive forms, landraces, cultivars, hybrids, mutant forms, self-pollinated lines, accessions with marker characters, genetic sources with identified genes and donors.

Most of the accessions are characterized for 24 descriptors according to the international *Beta* descriptor list and evaluated for major commercial traits. Characterization and evaluation of the collection has been carried out in three experiment stations situated in different geographical zones of the country. Evaluation is carried out for three years. The data obtained are then compared to estimate the accessions' ecogeographic variability and to determine their genetic potential. Four sources of the most important characters (monogermicity, bolting resistance and resistance to diseases) have been identified.

VIR *Beta* databases currently contain passport and conservation data. Characterization and evaluation data need to be computerized. The results of tests for resistance to black root (258 accessions) and bolting resistance (535 accessions) are published in special catalogues.

Every year about 200 accessions are distributed to Russian research institutes, national breeding centres, foreign genebanks and breeders. Requests from foreign users are fulfilled according to the availability of accessions. The distribution of small seed samples of new breeding lines, donors of most important commercial traits, is restricted.

Regeneration of the beet accessions is carried out when seed viability decreases to 50-60% and multiplication when seed stock is below 1000 seeds. Regeneration takes place at five experiment stations (585 accessions every year).

The base collection is preserved in medium-term storage at +4°C in the National Seed Storage at the Kuban experiment station (Krasnodar region) and in long-term storage at -10°C in the VIR genebank. The active collection is stored at room temperature in St. Petersburg at the Department of Vegetable and Cucurbit crops. A duplicate active collection is placed for storage at +4°C in a special room.

Three collecting missions were organized on the territory of Russia in 1996-2002, resulting in a total of 28 collected samples of beet accessions.

Activities planned for the future include: multiplication of collected accessions for long-term storage; screening of the collection and identification of genetic sources of the most important characters; creation of evaluation databases; collecting and exchange.

Slovenia

Vladimir Meglič (Crop and Seed Science Department of the Agricultural Institute of Slovenia, Ljubljana) gave an overview of the organization of PGR activities in Slovenia within the Slovenian Plant Genetic Resource Programme (SPGR). The institutions participating in the SPGR are the Biotechnical Faculty of the University of Ljubljana, the Agricultural Institute of Slovenia (AIS) and the Institute for hop and brewery in Zalec. The AIS maintains a fairly large *ex situ* collection of vegetables, winter wheat, grasses and clovers, fodder crops, small fruit, grapevine and grain legumes. The *Beta* collection is part of fodder and vegetable crops and consists of 46 accessions including *Beta maritima* (2) (*Beta vulgaris* subsp. *maritima*), *B. vulgaris* var. *rapacea* (fodder beet) *(Beta vulgaris* subsp. *vulgaris* Fodder Beet Group*)* (9), *B. vulgaris* var. *altissima (*sugar beet*) (Beta vulgaris* subsp. *vulgaris* Sugar Beet Group*)* (18), *B. vulgaris* var. *conditiva* (red beet) *(Beta vulgaris* subsp. *vulgaris* Garden Beet Group*) (12)* and *B. vulgaris* var. *cicla (*mangold) *(Beta vulgaris* subsp. *vulgaris* Leaf Beet Group*)* (5). Efforts for the broadening of the *Beta* collection and consists of 46 accessions including *Beta maritima* (2), *B. vulgaris* var. *rapacea* (fodder beet) (9), *B. vulgaris* var. *altissima (*sugar beet*)* (18), *B. vulgaris* var. *conditiva* (red beet) *(12)* and *B. vulgaris* var. *cicla (*mangold) (5). Efforts for the broadening of the *Beta* collection with fodder and wild species are ongoing. Regarding documentation, an initiative was taken up to establish an information and database management system for the Slovenian Gene Bank. Each institution holds a database for its working collections on a crop basis. With a need for a uniform and centralized documentation and information system, a computer program was used to unite four separate databases that will enable easier and faster access to the complete information for all users, better management of germplasm resources in the Central Plant Gene Bank and exchange of information with other ECP/GR and EUFORGEN genebank databases. *Beta* accessions are documented for IPGRI minimum passport descriptors.

The current area cultivated under *Beta* in Slovenia is 10 000 ha for sugar beet, 1800 ha for fodder beet and 150 ha for red beet and mangold. The EU quotas would make Slovenia a net importer of sugar.

Turkey

Ayfer Tan (Aegean Agricultural Research Institute (AARI), Menemen, Izmir) reported on the activities related to *Beta* genetic resources in Turkey, which are part of the National PGR Research Programme (NPGRRP). The wild species of *Beta* sect. *Beta* and *Beta* sect. *Corollinae* are widely distributed in Turkey. Landraces of beet (leaf and root beets) are also still widely grown by farmers. The beet genetic resources project deals with both wild and cultivated local races of beet. The AARI, as the national coordination centre, coordinates activities on beet genetic resources (survey, collection, *ex situ* and *in situ* conservation, characterization/evaluation, multiplication/regeneration and documentation). While previous activities were mostly focused on *ex situ* conservation of wild beets, present activities are mainly collection, conservation and keeping an inventory of local races of vegetable beets and *in situ* conservation of wild and local races, and identification of a beet core collection using molecular markers (biochemical characterization). Breeding programmes are increasingly using the existing collections. The national *ex situ* collection is stored at AARI national genebank and the safety-duplicates are stored at the Field Crop Central Research Institute in Ankara.

Ukraine

Oleh Slyvchenko (Institute for Sugar Beet, Ukrainian Academy of Agrarian Science (ISB-UAAS), Kiev) indicated that *Beta* germplasm research activities in the Ukraine are carried out by UAAS as part of the National Plant Genetic Resources Programme. The ISB collection

currently contains more than 360 accessions representing 12 species of *Beta*. Six sugar beet breeding stations also have their own local *Beta* germplasm collections with a broad spectrum of accessions (950) obtained from conventional breeding programmes. However until today Ukraine seemed to be "unknown territory" as regards national *Beta* genetic resources. For example, only one accession of *Beta trigyna* from the Crimean Peninsula was present in the collection and no detailed information was available from scientific literature. A new project started in 2001 within the framework of the European Science Foundation Programme "*Assessment of the Impacts of Genetically Modified Plants*". Germplasm collection and local wild beet habitat examination have been carried out in the Black Sea region. As a result, the ISB collection increased by 7 new *Beta vulgaris* subsp. *maritima* and 10 *B. trigyna* accessions from the Crimean Peninsula. Some weed beet infestation has been identified, probably as a result of gene flow between cultivated and wild beet accessions. The problem has occurred during 20 years of conventional sugar beet seed production in Crimea and the Odessa region.

A recent study examined wild beet accessions of Ukrainian origin. Allozyme diversity was assayed on 7 accessions collected in 2001 and compared with other beet accessions. The first conclusion from the allozyme analysis is that Ukrainian sea beets are genetically quite distinct from European sea beets. The results clearly revealed significantly greater genetic diversity among Ukrainian sea beet accessions in comparison with other European accessions. Based on the genetic diversity statistics, gene flow within Ukrainian accessions seems to be higher than in other accession groups. However, more data on the local distribution of wild and weed beet accessions in the Ukraine are necessary in order to support monitoring and conservation programmes.

United Kingdom

Brian Ford-Lloyd, who was unable to attend, provided a report before the meeting on "*Beta* genetic resources in the UK" focusing on activities carried out by the University of Birmingham School of Biosciences and the University of Bristol School of Biological Sciences.

USA

Lee Panella, also unable to attend the meeting, provided shortly afterwards a status report on "*Beta* genetic resources: North American activities" presenting a short history of the National Plant Germplasm System's (NPGS) *Beta* Collection at the United States Department of Agriculture (USDA)–Agricultural Research Service (ARS) Western Regional Plant Introduction Station (WRPIS).

The International Database for *Beta* (IDBB)

Passport modules—Identification of duplicates, rationalization of collections and implementation of a database concept for sharing of responsibilities

Christoph Germeier introduced the topic of the identification of duplicates as a pre-requisite for rationalization of collections and sharing of responsibilities, which needs to be based on a wealth of information including knowledge developed by the holding genebanks and international crop experts. In the new version of the IDBB, accession data have been collected in an ACCESSION table, listing accession-specific data such as "holding institute" and "accession number", along with original passport data provided by the holding genebanks. By manual or computer-assisted duplicate searches, accessions have been combined into duplicate groups. Duplicates are defined by their common origin, which may be known from data documenting transfer between genebanks or may be due to similarities

in the original passport data. Passport data describing the genotypic origin of a set of duplicate accessions (duplicate group) ideally should be identical. According to the normalizing concept in relational database theory, these common data should be extracted into a new table (GENOTYPE) with only one entry for each duplicate group. Nevertheless, inconsistencies in original data should remain unchanged in the ACCESSION table for documentation purpose, since the definition of duplicate groups and the harmonization of data sets would never be definitive, but would likely be subject to modification based on better knowledge.

A framework of concepts and definitions for recording the sharing of responsibilities for probable duplicate accessions within the IDBB was presented. Parts of the concept, such as management duties of the holders of primary responsibility and of the holders of safety-duplicates had already been defined in the 1999 meeting report.[4]

Recommendation

The IDBB original passport data (ACCESSION table) should be completely updated in order to fulfil the standards of the recently released EURISCO/MCPDv2 passport list.

Beta *germplasm curators are invited to assign responsibility, restriction and storage status to all their accessions on the basis of definitions outlined in Table 1, and register their decisions in the IDBB according to the procedure described in the workplan.*

Workplan

By no later than the **end of March 2003**, Working Group members and WBN participants will ensure that curators provide the IDBB manager with their passport accession data in the EURISCO/MCPDv2 format (the document containing the list of EURISCO descriptors was distributed during the meeting and is available from C. Germeier). Descriptors tracing the transfer of accessions between genebanks (DONORCODE, DONORDESCR, DONORNUMB and ACQDATE) or referring to the origin of an accession COLLCODE, COLLDESCR, COLLNUMB, COLLDATE, BREDCODE, BREDDESCR are especially important for duplicate tracing and should be given special attention. This also applies to stock numbers for breeding material (BREDNUMB), which are not yet included by MCPDv2, but should be added to the list when available.

After having provided their passport update, curators will receive from the IDBB manager a Windows application displaying duplicate groups and enabling them to fill in their agreements regarding responsibility, restrictions and resulting storage status for their accessions. Definitions are given in Table 1.

The result of the first round of decisions on sharing responsibility will be made available online via the IDBB by the database manager. It will be possible for responsible curators to edit these data on-line.

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[4] Germeier, C.U. and L. Frese. 2000. International Database for *Beta* - state of the art. Pp. 55-64 *in* Report of a Working Group on *Beta.* First meeting, 9-10 September 1999, Broom's Barn, Higham, Bury St. Edmunds, United Kingdom (L. Maggioni, L. Frese, C. Germeier and E. Lipman, compilers). International Plant Genetic Resources Institute, Rome, Italy.

Table 1. Definitions of "Duplication" and "Responsibility" as a basis for a differential storage management concept

A) Duplication (van Hintum and Knüpffer 1995[5], Knüpffer *et al.* 1997[6])	
MOS	Most original sample
IDD	Identical duplication: genetically identical (e.g. clones)
COD	Common duplicates: derived from the same original population
PAD	Partial duplicates: selected from the same original population
CPD	Compound duplication: one accession is a selection from the other
PRD	Probable duplicate: Duplication indicated by identical or similar passport data

B) Responsibility (modified after Bücken and Frese 1999[7])

Responsibility		**Restriction**		**Storage Status**	
PGR	Primary genetic resource	PUB	Public	ACO	Active collection
REF	Reference sample	RES	Restricted	BAS	Base collection
SDS	Safety-duplicate sample of other institutions	EMB	Embargoed	BAS	Base collection
PEN	Pending responsibility	TOC	Temporarily out of collection	NEW	Newly acquired accession
REJ	Responsibility rejected	EXE	Lost or discarded	DAT	Sample lost or withdrawn, only information available
DMS	Demonstration sample	PUB	Public	ACO	Active collection
PRO	Project / working sample	RES	Restricted		

Characterization and evaluation data

C. Germeier reported that users of central crop databases increasingly demand to have access to characterization and evaluation data. Documentation and presentation have to fulfil practical (breeding) as well as scientific purposes. Within the framework of the GENRES projects a wealth of characterization and evaluation data has been accumulated. Concepts and recommendations for documentation of characterization and evaluation data have been presented and database applications newly available for the IDBB on-line and off-line have been demonstrated.

Recommendation

The scientific community and beet researchers are invited to send their characterization and evaluation data to the IDBB manager, according to the procedure described in the workplan.

Workplan

Working Group members and WBN participants will encourage the scientific community and beet researchers to provide the IDBB manager with additional characterization and evaluation data, following the guidelines indicated below.

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5 Hintum, T.J.L. van and H. Knüpffer. 1995. Duplication within and between germplasm collections. I. Identifying duplication on the basis of passport data. Genetic Resources and Crop Evolution 42(2):127–133.

6 Knüpffer H., L. Frese and M.W.M. Jongen. 1997. Using central crop databases: searching for duplicates and gaps. Pp. 59-68 *in* Central Crop Databases: Tools for Plant Genetic Resources Management (E. Lipman, M.W.M. Jongen, Th.J.L. van Hintum, T. Gass and L. Maggioni, compilers). International Plant Genetic Resources Institute, Rome, Italy/CGN, Wageningen, The Netherlands.

7 Bücken, S. and L. Frese. 1999. Differential and hierarchical seed stock management – a new alternative for the management of large-sized genebank holdings. Pp. 96-101 *in* Implementation of the Global Plan of Action in Europe – Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture. Proceedings of the European Symposium, 30 June–3 July 1998, Braunschweig, Germany (T. Gass, L. Frese, F. Begemann and E. Lipman, compilers). International Plant Genetic Resources Institute, Rome, Italy.

Guidelines for inclusion of characterization and evaluation data into the IDBB

Data should be delivered to the IDBB in a state as original as available but in columns with clearly defined data format (numeric or text). Acceptable file formats are DBase or Excel. Implementation of XML is under consideration. Measurement data in SI units are generally preferred. They should not be transformed into scores. The database will have algorithms converting original data into universal scores (ranges from 0 to 9 as indicated) and will provide these to the user, together with the original data and descriptive statistics. Suggestions to improve these algorithms are welcome.

It is preferable to send raw data rather than already aggregated data. The database is able to extract and present simple descriptive statistics from the raw data and to import a wide range of statistical parameters for aggregated data. Raw data should be accessible for more advanced biometric analysis. It is considered important to indicate the date of evaluation and the development stage of the evaluated plants for all delivered observations.

Transforming qualitative observations (colours, habit descriptions, site descriptors, etc.) into numbers only makes sense if this is intended as a step to quantification, e.g. along scales from bright to dark, low to high, sparse to intense soil cover or on a scale of economic value. The definition of the scores should be consistent with these rankings. Thus the figures would be amenable to meaningful algebraic and sorting procedures. In any other case use of short words instead of scores avoids confusion and unintended quantification.

Scores should be restricted to figures (preferably 0-9) and not contain characters or special signs (0, 1 instead of +, - etc.).

All data provided to the IDBB should be delivered on an experiment-by-experiment basis especially if they refer to field observations. An experiment is defined by its dates (usually the growth period of the crop) and its location and the data should be accompanied by a detailed description of experimental site, design, descriptors and methods used for data acquisition.

Recommendation

The Chair also mentioned the need for updating the existing "Descriptor list for Beta*" which is incomplete, e.g. regarding viruses. Possibilities for the elaboration of an updated version should be discussed with IPGRI.*

Development of a quality concept

Definition and implementation of specific quality standards for the conservation of *Beta* genetic resources is considered a pre-requisite to establish a reliable mechanism for responsibility sharing. The meeting split into two working sessions. A sub-group chaired by Loek van Soest addressed the task of elaborating elements of a quality concept for *Beta* conservation. The second sub-group, chaired by Lothar Frese, focused on regeneration guidelines.

Summary of the discussion on quality concept

Loek van Soest reported that the Dutch genebank is trying to obtain an ISO 9001 quality certification for what is called at CGN "the genebank quality management system", as requested by the government as a pre-requisite to obtain public funds. This is a lengthy process that requires the preparation of a handbook describing in detail all the genebank operations and the obtention of the official certification is not expected before end 2003. This is considered a useful exercise to ensure that new staff would know how to continue to run the genebank after older staff retired. The whole process is also useful for improving

genebank operation as a result of the necessary reconsideration of all internal procedures. A similar experience was said to also be under way at the Nordic Gene Bank.

On the basis of the Dutch experience, the sub-group listed a number of operations that should be considered for a quality concept, with distinctions made for cultivated or wild materials, monogerm or multigerm seed, modern or old varieties. These are:

• ***Germplasm acquisition***	The number of plants from which seed is obtained should take into consideration basic concepts of sampling strategies discussed by Jain (1975) and Marshall and Brown (1975).[8] The actual number of sampled plants should be documented.
• ***Status of acquired material***	Acquired material should be assigned a specific status (such as "accepted for conservation" or "rejected"). This could be reflected by the assignment of specific coding, such as preliminary numbers to all material and acquisition numbers only to accepted material.
• ***Regeneration***	(see below, discussion on seed regeneration guidelines)
• ***Postharvest***	Operations affecting quality are drying, seed cleaning and the quantity of seed to be harvested.
• ***Pre-storage***	Germination testing should be described, with specific details for the various wild *Beta* species.
• ***Germination capacity***	To be defined for wild and cultivated material.
• ***Storage conditions***	These usually differ in the active and base collections.

Recommendation

It is recommended that expertise present in the Group for the development of a quality concept be channelled to L. Frese. Collection holders in Europe are recommended to follow the quality concept once agreed by the Group and/or to publish the details of the procedures adopted.

Workplan

The Group will develop a specific quality concept for *Beta* genetic resources conservation, following the scheme outlined above. By **the end of November 2002**, L. Frese will send a draft document to all WG members for comments and revisions, to be sent back to him by **the end of December 2002**. A revised document will then be circulated to the Group by L. Frese for final endorsement.

Summary of the discussion on seed regeneration guidelines

L. Frese introduced the session by referring the members to the background document on "Seed increase protocol" prepared for the GENRES project and suggested using it as a basis for comments and revisions.

It was felt that since local conditions and available facilities differ between genebanks, curators should not be forced to adopt standardized seed multiplication procedures. As seed production procedures largely determine the genetic integrity of accessions and the quality

[8] Jain, S.K. 1975. Population structure and the effects of breeding system. Pp. 15-36 *in* Crop genetic resources for today and tomorrow (O. Frankel and J.G. Hawkes, eds). Cambridge Univ. Press, New York.
Marshall, D.R. and A.H.D. Brown. 1975. Optimum sampling strategies in genetic conservation. Pp. 53-80 *in* Crop genetic resources for today and tomorrow (O. Frankel and J.G. Hawkes, eds). Cambridge Univ. Press, New York.

and longevity of seeds in long-term storage, the Working Group agreed that each *Beta* curator should produce a description of his/her seed production procedures. The following aspects should be considered: methods for breaking seed dormancy (physiological as well as physical); sowing and planting; effective population size; isolation methods; seed harvest (aliquots, bulk); seed threshing, cleaning, drying and storage. The descriptions should consider the different requirements of the various species.

It was agreed that publication of the protocols would enhance transparency and mutual trust in the collection management work. It would also allow curators to crosscheck and critically revise and improve their own standard procedure. It was stressed that a publication of the seed production protocols would facilitate the implementation of the concept of sharing of maintenance responsibilities. In particular, *Beta* section *Corollinae* species are difficult to regenerate outside of their natural distribution area. This problem was mentioned by the Turkish and German curators. A solution could be to increase these accessions in a region with ecological conditions similar to the original collecting sites.

A description of basic elements for successful plant and seed production is not only of interest to curators. As wild species require quite different growing conditions compared to sugar beet, a publication of seed multiplication procedures would also be very useful for researchers in charge of screening exotic material. For that specific purpose, a publication should be made available on the Internet and/or included into the International Data Base for *Beta*.

Workplan

Using the seed multiplication manual drafted by the BAZ Gene Bank as an example, curators should document their own seed production procedures. To facilitate a standardized documentation L. Frese will provide curators and/or WG members with a base document that can be completed by the *Beta* curators in accordance with specific local conditions. The base document will be circulated **by 15 November 2002.** Curators and/or WG members will be requested to return their contributions to the BAZ Gene Bank **by 30 November 2002**. Individual reports will be compiled and published on the Web page of the ECP/GR *Beta* Working Group.[9]

Priorities for Phase VII of ECP/GR

L. Frese informed the Group that a reply was sent on its behalf to the questionnaire prepared by the Steering Committee task force for Phase VII of ECP/GR. He mentioned that the reply reflected the few comments received from WG members, but encouraged the Group to continue to express opinions on priorities for the WG and the expectations from the future Phase of ECP/GR.

L. Frese reported the recommendation made by the Industrial Crops and Potato Network Coordinating Group on 22 October to the ECP/GR Steering Committee (see Appendix I): "*Maintain in existence the WG on* Beta *to facilitate the formalization of responsibilities on a decentralized basis, as well as to address specific issues such as the complementary conservation strategy for* Beta *genetic resources in Europe, with special attention to the conservation of the wild populations.*"

He specified that the WG on *Beta* would be competing for ECP/GR funds with the other WGs.

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[9] See http://www.ecpgr.cgiar.org/Workgroups/beta/beta.htm

Among the possible options for future funding he mentioned the WG meetings, *ad hoc* thematic meetings, small projects (such as to close collecting gaps, recommended in 1993 but never implemented due to lack of funds).

Discussion

A. Tan commented that the WG should become proactive and coordinate work so as to propose collaborative international projects. She also recommended that news and information from the national programmes be provided to the Secretariat for uploading onto the ECP/GR *Beta* WG Web page. This would ensure timely exchange of information among the members, thereby reducing the need to use meetings for this purpose.

G. Poulsen said that the Group ought rather to hold more frequent meetings since the preparations for the meetings are useful to renew and reconfirm each member's cohesion and commitment.

M. Asher asked about the prospects for EU funding in the field of plant genetic resources. L. Maggioni reported that a new EU regulation, as a continuation of the former 1467/94, was expected to be launched very soon, although its finalization by the EU Commission suffered a long delay as a result of the process of negotiation with the member countries.

Recommendation

*The Group recommends that during Phase VII of ECP/GR (which is expected to span the years 2004-2008) funds be assured to hold one meeting of the WG, as well as additional funds to be managed with considerable flexibility as a "*Beta *fund" for small technical meetings and* ad hoc *actions.*

Task-sharing within the WBN Steering Committee (BBC and ECP/GR)

L. Frese introduced the discussion by expressing concern that the role and function of the Chair has been too centralized in the past and therefore too dependent on the initiative and health of one individual. He therefore suggested that it would be appropriate to define areas of activity for which the initiative would be delegated to "thematic moderators " as new driving forces. Proposed areas such as evaluation and pre-breeding, *in situ* and on-farm conservation, international core collection and molecular techniques should be encouraged. The names and designations of the future sub-working groups should allow sufficient flexibility to cope with future developments.

Role and function of the sub-working groups

- Experts from very different research disciplines are attending *Beta* meetings, representing only a fraction of the interested fellow scientists
- Subgroup chairs would function as theme specialists
- Their role would be to disseminate information on *Beta* Working Group meetings through mailing lists and to collect the information required to plan the next *Beta* Working Group meetings from their fellow colleagues
- This would facilitate more communication between the *Beta* Working Group and the much larger user community of *Beta* genetic resources as well as assisting in taking high-priority actions
- It would also allow work to be done within the group to speed up implementation of *Beta* Working Group recommendations
- Subgroup chairs would contribute to the mid-term report of the WG to be delivered to the ECP/GR before ECP/GR Steering Committee meetings.

Recommendation
The Group approved the role and functions defined above and recommended that L. Frese should contact potential "thematic moderators" who could initiate and lead several group activities.[10]

Scientific presentations

Scientific basis for in situ *management of* Beta

Taxonomy and distribution of the genus *Beta*—Achievements, criticism, research needs

Lothar Frese demonstrated the "Taxonomic guide for wild and cultivated *Beta*" available on-line at <http://www.fal.de/bgrc/eu9542/default.htm>. The guide contains information on the distribution area of wild beets as well as a key to the taxa. A. Tan and L. Frese discussed problems related to the existing taxonomic keys. There are indications that *B. webbiana* and *B. procumbens* are not really distinct. In addition, the genetic distance between the section *Procumbentes* and the rest of the genus is very large. The decision to include or exclude this section from the genus *Beta* is pending. It was noted that research is required on the taxon "*B. foliosa*". A. Tan explained that because of the apomictic behaviour *B. trigyna, B. intermedia* and *B. lomatogona* could be considered to be part of a wide continuous variation of the *B. lomatogona* complex. L. Frese noted that he had not added the hybrid species *B. trigyna* and *B. intermedia* to the key as there is no way of determining these taxa correctly. He said that there is no formal taxonomic link between the wild form of section *Beta* and the cultivated types. The description of the cultivated types is therefore presented in the guide without a determination key. He explained that we first have to develop a reliable key to the taxa that enables field botanists not familiar with the genus to determine the correct taxon, on the basis of what they see in nature. The on-line key should be considered as a working document. Experts are invited to review and improve the guide.

Christoph Germeier remarked that the taxonomic system for cultivated types used by the Vavilov Institute is very informative. As this key is not consistent the WBN decided in 1996 to apply the biological species concept for *Beta*. C. Germeier suggested that users of a central crop database (CCDB) should be enabled by the database manager to use any taxonomic key they are used to. A CCDB should therefore document different taxonomic systems.

The guide was developed within the framework of the GENRES CT95-42 project on *Beta* after the *ad hoc* meeting of the International *Beta* Core Collection working group. The *ad hoc* group had recommended promoting *in situ* management of *Beta*. L. Frese explained that he had tried to provide a first assessment of the risk of genetic erosion for some of the species on-line so as to encourage local authorities responsible for nature preservation in the

[10] The following sub-working group names and chairpersons were suggested. Dr Brian Ford-Lloyd, Dr Eric Ober and Dr Ayfer Tan agreed to chair the groups during the next three years.

Sub-working group title	Chairperson	Subjects covered
1. Genetic resources management	A. Tan	Assessment of genetic erosion, *ex situ* management, *in situ* and on-farm management, core collection, data documentation
2. Genetic diversity	B.V. Ford-Lloyd	Taxonomy and nomenclature, ecogeographic patterns of genetic diversity, gene flow, trait and gene diversity
3. Evaluation and breeding	E. Ober	Evaluation methodology, pre-breeding and breeding, genetics and genomics

distribution area of wild *Beta* species to check the current situation and to take the initiative if action appears necessary.

Prospects for *in situ* conservation of beets in Turkey

Ayfer Tan (Aegean Agricultural Research Institute, Menemen, Izmir, Turkey) presented the *in situ* programme of Turkey, based on the notion that *in situ* conservation is a complementary strategy to *ex situ* conservation. This strategy involves the preservation of genetic variation of plant taxa at the site/location, either in traditional farming systems or in the wild. The programme started in 1993 with a project called "*In situ* conservation of genetic diversity". Two additional projects were initiated in 1999 on "Conservation of land/local races on-farm" and "Ecosystem conservation and management for threatened plant species".

The project on "*In situ* conservation of genetic diversity" aims to conserve *in situ* the progenitors and wild relatives of cereals, legumes, wild fruit and forest species. Several gene management zones (GMZs) were identified for each target species in different ecosystems and the associated species, including wild beet species (e.g. *Beta lomatogona*) were defined and listed for each GMZ, and GMZ management plans were prepared.

The *in situ* on-farm conservation project involves conservation of common and coccineus bean, lentil, chickpea, and hulled wheat land races grown in the northwestern transitional zone. During the project implementation phase, an inventory of other landraces, including vegetable beets (leaf beet and beetroot) has been created from the ecogeographical and socioeconomic survey.

The objective of the third project ("Ecosystem conservation and management for threatened plant species") is to conserve some of the threatened species which are listed in the Appendix of the Bern Convention for Turkey. Twenty-three species from the list are found in the wetland ecosystem under study. The endemic and endangered beet species *B. adanensis* is one of the target species of this project. For each species the important plant areas (IPAs) will be identified and management plans prepared.

The presentation discussed the components of the *in situ* conservation programme (both wild and on-farm), selection criteria of target species, factors influencing conservation value, factors of environmental threats, criteria for selecting the GMZs and IPAs, with emphasis on the beet species.

The sea beet of the Po delta as source of resistance for sugar beet

Piergiorgio Stevanato (ISCI-Rovigo, Italy) presented a historical review of the studies carried out in Italy on resistance to cercospora leaf spot (CLS) and rhizomania obtained from sea beet. Sea beet populations are arousing ever greater interest as sources of resistance from which to improve the cultivated species. In 1909, Munerati had already begun crossing the sea beet of the Po delta with sugar beet. After several years this led to the production of the first varieties resistant to cercospora leaf spot. Recent work supports the speculation about the common origin of both cercospora and the different types of rhizomania resistance. More recently, genes from sea beet have been used for conferring resistance to cyst nematodes. Because of the importance of this genetic resource, wild populations of sea beet should be catalogued and conserved to safeguard them from genetic erosion and from the risks of gene flow.

Introduction of GRACE: "Genetic Resources and Changing Ecosystems"

L. Frese informed the Group about the funding opportunity offered by the imminent launch by the European Commission of the Sixth Framework Programme for Research (www.cordis.lu/fp6). He also outlined the details of the "Expression of Interest" for the preparation of an integrated project, which was recently submitted by N. Maxted and

B. Ford Lloyd, University of Birmingham, UK. The project is called "Understanding and managing change in European Genetic Resource Conservation and Use" (with the short title "GRACE", standing for "Genetic Resources and Changing Ecosystems") and is expected to involve 80-120 partners, including all relevant stakeholders in the EU and other countries. With a funding request of Euro 30-35 million, it aims at contributing to the assessment and prediction of change in European animal and plant genetic resources within ecosystems, and to enhancing their conservation and sustainable use. The intention is to bring together the European animal and plant genetic resource conservationists and their user communities with socioeconomists, policy-makers and environmental legislative experts. The project would be implemented through a series of interrelated "work packages" and case studies.

L. Frese had sent to the project coordinators a specific expression of interest for the involvement of the *Beta* WG in the project, since research on wild *Beta* species could cover one of the proposed case studies. He thought that the Group could get involved in two work packages, WP1 and WP6. WP1 consists of "Diversity and economic assessment", which includes taxonomic, ecogeographic and genetic assessment, current conservation assessment, and identification of the economic drivers of genetic resource loss. WP6 is concerned with "Implementing conservation and use" with gap analysis, establishment of *in situ* methodologies, targeted *in situ* and *ex situ* conservation, production of European animal and plant genetic resources key taxon conservation and use action plans, and public education of the need for diversity in European domesticated species and their wild relatives.

Recommendation

The Group recommended that L. Frese follows the events leading to the launching of the Sixth Framework Programme (expected for November 2002) and keeps interested partners of the Group informed about the necessary steps to prepare a Beta *component for the GRACE project (first call for proposals expected for the end of 2002/beginning of 2003).*[11]

Genetic resources for beet breeding

Deployment of *Beta* genetic resources

Mitchell McGrath (USDA-ARS, Michigan State University, East Lansing, Michigan, USA) gave an insight on the likely future impact of genomic technologies on germplasm conservation and the incorporation of novel *Beta* germplasm into improved crop types. The amount of allelic diversity present in wild beets may exceed that in sugar beet 10-fold or more and if only 1% of the allelic variation in the wild species would enhance the agronomic performance of cultivated beets, then efforts to introgress this diversity should be attempted. Over 2500 Plant Introduction accessions in the US National Plant Germplasm System and over 10 000 accessions stored in the decentralized *Beta* collections, both *ex situ* and *in situ*, are held in trust for the preservation of genetic diversity. Current applications of these technologies have allowed massive scaling to look at hundreds and thousands of genetic elements simultaneously or over a short time period, leading to massive amounts of data being collected about individual biological processes. However, the tools have not been sufficiently developed in sugar beet and related species to make these applications become obvious or routine. One of the tasks ahead is to identify molecular processes in beets that are similar and those that have diversified between plant lineages and within *Beta* populations. For *Beta* species, the entire genome sequence is unlikely to be obtained soon, but progress in developing other genomic tools for beet may accelerate this process.

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[11] By the time of printing of this report, calls for proposals launched by the Sixth Framework Programme did not result suitable to the submission of a project like GRACE.

Exploiting disease resistance in wild *Beta* species

Mike Asher (Broom's Barn Research Station, Bury St Edmunds, UK) reported on the results of the evaluation of ca. 600 *Beta* accessions from the BAZ Gene Bank for resistance to eight diseases of major economic importance in the European sugar beet crop, carried out under GENRES CT95-42. Results obtained from the 11 collaborating institutes showed that highly resistant (category 1: no detectable infection) accessions occurred at a frequency of between 0.2 and 5.0% depending on the disease. If category 2 (trace of infection) accessions were included, the proportion of resistant accessions increased to between 2.0 and 21.0%.

Published information on the identity and location of disease resistance genes in *Beta vulgaris* is extremely sparse, compared to most other major crop species. Only six major genes, governing resistance to curly top virus, cyst nematode and rhizomania (BNYVV), and located on three chromosomes, have been mapped to date. To improve our understanding of the distribution and inter-relationships of major disease resistance genes in the sugar beet genome, mapping populations have been developed from resistant *B. vulgaris* sources identified in the GENRES programme.

For the diseases caused by beet mild yellowing virus (BMYV), beet yellows virus (BYV), *Erysiphe betae* and *Aphanomyces cochlioides*, individual plants from each resistant accession were selected following evaluation. Resistant plants (mainly *B. vulgaris* subsp. *maritima)* were crossed with a common genetic male-sterile sugar beet line to develop F_1 hybrid populations for analysis.

Twenty-five individuals from each F_1 generation were screened for resistance using established artificial inoculation techniques under controlled environmental conditions. Segregation was observed in many of these test populations, indicating that the parent had been heterozygous for resistance, and that the F_1 generation was suitable for mapping. In cases where no segregation was observed, indicative of a homozygous resistant parent, highly resistant F_1 individuals were selected for selfing and simultaneous backcrossing to the male-sterile line to produce the segregating F_2 and BC_1 generations required for mapping.

To date, approximately 450 F_1 or F_2 mapping populations have been produced, covering sources of resistance to seven diseases. Preliminary screens are being carried out on all of these populations to identify resistance that appears to be under relatively simple genetic control. Future work will involve the genetic analysis of mapping populations, where single genes of large effect have been implicated in the resistance, utilising AFLP and microsatellite markers to locate genes to chromosomes.

Evaluation of sugar beet germplasm for improvement of drought tolerance

Eric Ober (Broom's Barn Research Station, Bury St Edmunds, UK) presented the work done in the UK on the screening of 46 genotypes to identify drought tolerance among *Beta* germplasm obtained from genebanks and plant breeders. Field and controlled environment screens were developed for this purpose. Controlled environment screens may be more useful for phenotyping mapping populations than for pre-breeding in a crop improvement programme. There are possibilities for improving the drought tolerance of crop plants through transgenic manipulation. However, for *Beta vulgaris*, in the short and medium term, the resources for genetic improvement exist within germplasm collections. There is now progress toward identifying those materials.

Discussion

E. Ober offered to coordinate exchange of information between researchers working on drought stress and the Group welcomed this initiative.

Conclusion

The section *Discussion and Recommendations* of the report was presented to the participants and was approved with minor modifications.

Organizational aspects and election of the Coordinating Committee of the ECP/GR Working Group on Beta */ World* Beta *Network*

L. Frese reminded the Group that he was both the Chair of the *Beta* WG and member of the BCC. The BCC of the World *Beta* Network had been defined in 1999 as consisting of the IDBB manager and representatives of the major sugar beet production areas and the distribution area of the genus. L. Frese noted that participation in the meeting was mostly from Europe and discussion was mainly focusing on European interests and there was a risk of losing contact with experts outside Europe. He suggested establishing a Coordinating Committee consisting of the Chair and Vice-Chair of the ECP/GR Working Group and two members from American and Asian countries. This committee would help organize meetings and look for funds.

The Group agreed with the suggestion and elected the representatives of the Coordinating Committee. M.N. Arjmand, recently retired from SBSI, declined the offer to stand as Asian countries representative but proposed Dr Mahmoud Mesbah to replace him, indicating that he would however remain as WBN member to help Dr Mesbah and other members as needed. The composition of the Coordinating Committee was therefore agreed upon as follows:

ECP/GR WG on *Beta* - Chair	Lothar Frese
ECP/GR WG on *Beta* – Vice-Chair	Bruno Desprez
America Member	Mitchell McGrath
Asia Member	Mahmoud Mesbah

Closing remarks

L. Frese thanked the local organizers for the excellent organization of the meeting and the ECP/GR Secretariat and hoped to meet again at the next occasion. He indicated some opportunities for the venue of the next meeting that can be expected to be held in 3 years, to be confirmed by the ECP/GR Steering Committee. Córdoba (Spain) and Quedlinburg (Germany) were suggested as possible options.

The participants thanked L. Frese for his efficient chairing of the sessions and the meeting was officially closed.

PART II. PRESENTATIONS AND PAPERS

National Collections

Beta *genetic resources in Belarus*

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Introduction

Beet (*Beta vulgaris* L.) has been cultivated in the Republic of Belarus for many decades as a traditional crop for sugar production and as a fodder and vegetable crop. Cultivation and breeding activities in our country are mainly carried out in the public sector – collective and state farms – and in households. The sugar beet producing area covers 50 000 ha, fodder beet 80 000 ha, table beet more than 10 000 ha. There are five sugar-producing factories in the country. Seed production and local breeding are developed at the following institutions: Belarusan Regional Experimental Breeding Station for Sugar beet near Nesvizh (BREBSS); Institute of Genetics and Cytology in Minsk (IGC); Belarusan Research Institute of Farming and Fodders in Zhodino (BRIFFC); and Belarusan Research Institute of Greengrocery (BRIG) in Samohvalovichi. Thus, there are few working collections of beets with sub-collections for sugar beet (BREBSS and IGC), fodder beet and table beet.

Germplasm holdings

Activities on *Beta* genetic resources in Belarus include germplasm collection, characterization and evaluation, *ex situ* management and some safety-duplication. Different organizations are involved in the management of beet genetic resources: state organizations (Ministry of Agriculture and Food, State Committee for Science and Technologies) and professional organizations (Institutes of the Belarus National Academy of Sciences).

Beet germplasm collections are divided between three institutes (BRIFFC, BRIG and IGC) of the Belarus National Academy of Sciences and the Breeding Station and include:

- populations and some old cultivars originating from former USSR (mainly from the Ukraine, Russian Federation and Latvia) cultivated in recent decades on the territory of our Republic;
- commercial cultivars and components for commercial hybrids arising from local breeding activities in Belarus;
- germplasm of wild species (mainly sources of genes for disease resistance) from the N.I. Vavilov Institute for Plant Industry (VIR, St. Petersburg, Russian Federation);
- material arising from existing breeding programmes;
- germplasm produced by biotechnological methods: doubled haploid (DH) and dihaploid lines.

According to the catalogue of *Varieties included in the State Compendium for 1998-2001* (Starovojtov 2001), the following cultivated varieties are currently distributed in Belarus:

- sugar beet: 14 triploid monogerm hybrids, including three of joint production – 'Beldan' and 'Danibel' of IGC and Danisco Seed (Germany); 'Kavebel' of IGC and KWS (Germany). The other 11 triploid, as well as 4 diploid monogerm hybrids, are of foreign origin;
- fodder beet: 13 varieties in total, mono- and multigerm, triploid, diploid and polyploid of foreign origin (German KWS, Danisco Seed and Polish HBP) and one diploid variety 'Darinka' of Belarusan origin;
- table beet (all red): 5 multigerm varieties, including four introduced and one local, 'Pryhazhunja'.

The IGC working collection of sugar beet DHs consists of 30 lines. Seeds are available for six of them.

National Programme

The Belarus National Programme entitled "Creation of the National Genetic Fund for economically-important plants" started in 2000 with funding for six years. Ten research and educational institutions joined the programme. The following tasks regarding beet genetic resources management were assigned:

- creation of the National Genetic Centre for plant genetic resources (cereals, industrial, fodder and grain crops), with the subtask for 2000-2001 to perform a complete national inventory of the genepool of cultivated crops and their wild relatives within each crop group, and to guarantee reproduction of the collection and its short-term conservation (this Centre was created on the basis of the Belarusan Research Institute of Farming and Fodders);
- creation of a genebank of sugar beet germplasm with the subtask to develop the system of identification and passporting of sugar beet genetic material, and to carry out the inventory of sugar beet germplasm collection (responsibility of BREBSS);
- development by genetic methods and biotechnologies of a new germplasm bank of economically important plants to be used in breeding work, with the subtask to develop the system of identification and passporting of new genetic material of economically important plants (responsibility of IGC, Belarus National Academy of Sciences).

Germplasm characterization and evaluation

The responsibilities for evaluating, utilizing and storing genetic resources of sugar beet are concentrated mainly at the Belarusan Regional Experimental Breeding Station for Sugar beet, where working collections include monogerm and multigerm diploid and tetraploid fertile populations, diploids with CMS, and corresponding O types. Tetraploid lines pollinators and a collection of haploid and doubled haploid lines of gynogenetic origin are maintained at the IGC, with the best accessions to be safety-duplicated at the Breeding Station. The Belarusan Institute of Farming and Fodders is responsible for characterization and evaluation of fodder beet germplasm and the Belarusan Institute of Greengrocery for that of table beet.

The evaluation of the collection is carried out according to the descriptors recommended by the State Committee for Trials and Conservation of Plant Varieties. For cultivars/hybrids they are as follows:

1. Name, producer
2. Botanical traits: family, species, subspecies, cultivar
3. Breeding method (technology)
4. Biological traits: M trait (form of seeds), ploidy level, percent of ploidy, 1000-seed weight
5. Morphological traits: hypocotyl colour
6. Root traits: form, position (depth) in soil, colour of overground part, colour of underground part
7. Leaves' traits: distribution, percent of total weight, colour, petiole colour
8. Agronomical traits: yield, sugar content, K/Na content, amino-N content, growth period duration, resistance to bolting
9. Disease resistance to *Cercospora*, *Ramularia*, powdery mildew, *Rhizomania*
10. Possible agricultural application of a cultivar.

Seed processing and storage

Biennial material is vernalized in cold stores and chilling chambers at 4°C. To multiply beet accessions, isolation in greenhouses, spatial isolation in the fields and isolation with cereals

(rye) are used at the Breeding Station and in experimental fields of the institutes. Seed stalks are dried in isolated parts of greenhouses for a few weeks. The seeds are threshed in threshing machines, sieved and sorted in sorting machines. At the IGC a polishing machine has been used for seed processing. Seeds of biennial accessions are sown in May. One hundred seeds are commonly taken for the germination tests. Seeds are put into moist sand at 28°C in the dark (thermostatic chambers) and the number of germinated seeds is recorded twice: on the third day ("energy of germination") and on the tenth day ("germination rate"). Seeds are stored at low temperature (4-10°C) without moisture content control.

Research

Research activities include investigation of genetic problems related to the utilization of germplasm in breeding, study of the *Beta* genome and relationships between species. Project proposals can be submitted to a number of national or international funding agencies. The group of researchers from the Institute of Genetics and Cytology was given two grants by the Belarusan National Fundamental Foundation (1994-1996, 2002-2004), and in order to initiate molecular biology research (Svirshchevskaya and Dolezel 2000) it received two more grants from the International Atomic Energy Agency (1999, 2002). In the coming years we plan to evaluate newly arisen haploid and doubled haploid sugar beet lines for disease resistance, quantitative traits and molecular genome studies (AFLP markers).

International cooperation

The Belarusan Regional Experimental Breeding Station for Sugar beet maintains contacts with German, Polish and Swedish breeding companies (KWS, Strube-Dickman, Danisco Seed, HBP, PNOS, Novartis AB) which provide its working collections with material for obtaining hybrids. Since 2000 the IGC has cooperated with the USDA-ARS Research Unit in Fort Collins, Colorado in the testing of gynogenetic lines for resistance to cercospora and rhizoctonia diseases and in relevant germplasm exchange (susceptible and resistant checks for the above-mentioned diseases).

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Beta *genetic resources in Bulgaria*

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The Bulgarian *Beta* genetic resources include 680 accessions, mainly from the following two species: *Beta vulgaris* subsp. *vulgaris* and *B. trigyna*. There are also a small number of accessions belonging to the wild species *B. lomatogona* and *B. corolliflora*.

A small part of the material is kept in long–term storage in the genebank of the Institute for Plant Genetic Resources (IPGR) in Sadovo, but most of the accessions obtained through exchange are in medium-term storage (+4-5°C). Working collections are located only in the Agriculture Research Institute (ARI) in Shumen, where breeding activities are also carried out (Table 1).

Table 1. Status of the Bulgarian *Beta* collections

Institute	No. of accessions							
	Origin			Type of material				Total
	Bulgarian	Foreign	Unknown	Cultivars	Breeding lines	Populations	Wild relatives	
ARI-Shumen	420	6	24	10	150	284	6	450
IPGR- Sadovo	20	200	10	11	18	194	7	230
Total	**440**	**206**	**34**	**21**	**168**	**478**	**13**	**680**

Owing to difficulties in the maintenance and evaluation of *Beta* collections, together with a lack of funds, the regeneration and conservation of all accessions was not possible. The main activities on B*eta* were restricted to the creation of collections of valuable breeding materials and cultivars, suitable for the climatic conditions of Bulgaria.

Organized breeding activities with sugar beet started in 1921-1922 in Bulgaria, based on cultivars of foreign origin. The first Bulgarian cultivar 'Endje' was registered in 1934; it has a high sugar content and comparatively good resistance to cercospora leaf spot. 'Endje' was grown for more than 25 years in Bulgaria.

During the period 1959-1980, the available sugar beet cultivars were exchanged. The cultivar 'Endje' was replaced by more productive polygerm diploids such as 'Beta C–242/53' and 'Beta K–91' introduced from Hungary. Very soon these were also replaced by more productive polyploid foreign cultivars: 'Beta poli 3' (Hungary), 'Maribo PA' (Denmark), 'Janash poli 2' and 'Janash Polikama' (Poland).

The Bulgarian polygerm polyploid cultivar '22x10 poli' was created in 1964. Its cultivation started in 1969 and owing to its productivity and excellent technological characteristics, the cultivar covered more than 70% of the crop cultivated area.

The second polygerm polyploid cultivar 'Hybrid 9 poli' was introduced in 1973, intended for irrigated areas; it is characterized by increased sugar content and resistance to cercospora leaf spot.

Breeding activities with sugar beet monogerms started in 1958 in Bulgaria. The first monogerm male-sterile hybrid, 'Hybrid poliE-1', was created in 1973.

Bulgarian polyploid cultivars are characterized by intensive root growth and a favourable combination of yield and sugar content. Cultivar 'Ticha' was introduced after 1980, the year of registration of cultivar 'Hemus'.

Since 1990, the following sugar beet cultivar groups have been created and registered:

- Group I = cultivars tolerant to rhizomania virus disease*:* 'Radnevo' (1990) and 'Peshtera' (1994);

- Group II = cultivars with high productivity and high sugar content: 'Shumen' (1994), 'Elit' (1995), 'Hybrid 917' (1996), 'KI-1216' (1997) and 'KI–1239' (2000).

During the following decade (1990-2000), 10 sugar and fodder beet cultivars, including 2 cultivars tolerant to rhizomania, were registered and cultivated in Bulgaria.

Presently about 157 accessions are maintained in *ex situ* breeding collections in Shumen, grouped as follows:

- **Monogerm fertile diploids – 29 accessions**

This material can be used as sources of new "O" types. Some of them are included in backcrosses with polygerm diploids for enrichment of their genetic heredity, others have a high sugar content and are resistant to cercospora leaf spot.

- **Monogerm fertile tetraploids – 8 accessions**

In spite of their rather limited utilization, they are used mainly for enrichment of the *Beta* germplasm, included in different breeding programmes to develop sustainable monogerm materials through the high ploidy levels.

- **Monogerm diploid male-sterile lines and their "O" types – 33 accessions**

From a total of 80 currently available accessions, only 33 are included in breeding programmes. Work on CMS started in the 1970s in Bulgaria. The sterility of most of the materials is over 93-95%. They have good agronomic characters such as root yield, sugar content, and high resistance to disease (cercospora leaf spot, powdery mildew and rhizomania).

- **Monogerm tetraploid male-sterile lines – 6 accessions**

The sterility of these lines is about 70-90 % and they are used to obtain tetraploids (MS 4x x 2x MM). The cultivar 'Endje–316' was created this way. A great number of crosses with dihaploids were carried out.

- **Polygerm fertile diploids – 36 accessions**

This group contains 123 accessions, kept at the Agriculture Research Institute-Shumen, but only 36 are included in collections. Some have a good productivity and high resistance to cercospora leaf spot and powdery mildew; others are very tolerant or entirely resistant to rhizomania and other diseases. Breeding lines with very high sugar content were identified.

- **Polygerm fertile tetraploids – 45 accessions**

This is the main group of sugar beet accessions, distinguished by a great genetic diversity. The 4 x MM accessions are used as male parents. They are maintained through different breeding schemes and permanent cytological control.

The pollinators, tolerant to rhizomania, are maintained through permanent selection in the experimental fields of the village Draganovo (Veliko Tarnovo region). There are two cultivars tolerant to rhizomania cultivated in Bulgaria. They are no worse than the common cultivars in terms of yield and disease resistance.

Wild species

A detailed study conducted by IPGR-Sadovo on the current distribution of wild *Beta* species in Bulgaria indicated that *B. trigyna* is still widely distributed, as described in the *Flora of Bulgaria* (Stojanov *et al.* 1966). The species *B. vulgaris* subsp. *maritima* was not found at the sites referred to.

The species *B. trigyna* Wadst. & Kit. is a Mediterranean plant, widely distributed in Bulgaria. First records about its distribution mention only a few sites in the country (Velenovsky 1891, 1898).

During the period 1924-1966, the Bulgarian botanists Stojanov, Stefanov and Kitanov recorded the distribution of the species: *"almost all over Bulgaria"* or *"mostly in southern and eastern Bulgaria"*. A detailed distribution by floristic regions was presented in 1966. Later the species was found in all parts of the country (Bondev 1991; Dimitrov 2002).

Through expeditions carried out during the period 1995–2001 in the Thracian Plain, southern and northern Black Sea Coast, Rhodope Mountain and Dobrudja region, a considerable number of sites of subsp. *trigyna* were identified and marked. Later on, reproductive material was collected from some of the sites mentioned. The next stage of IPGR's activities is the creation of *ex situ* collections in the Botanic Garden, which are to include the whole plant genetic diversity in Bulgaria.

The species *Beta vulgaris* L. subsp. *maritima* (L) Arcang. is a submediterranean plant, rarely occurring in Bulgaria. There are only herbarium specimens from two locations – the Bourgas and Sofia regions. It is reported in the town of Sozopol, but plant samples are not available. A collaborative programme, aiming at investigating species habitats reported in the *Flora of Bulgaria* or other published sources, is planned with the Institute of Botany in Sofia.

Long-term storage contains 11 accessions of Bulgarian cultivars. About 230 accessions are kept in medium-term storage in the genebank of IPGR-Sadovo. The main part of the collection (90%) consists of foreign cultivars and hybrids. Plants of local origin represent only 10%, consisting of old seed materials collected during expeditions (Table 2).

The rest of the accessions are kept at the Agriculture Research Institute-Shumen. They include breeding lines, hybrids, populations and all Bulgarian cultivars (11). One of these is used in pre-breeding and breeding, the others are stored as seeds. Three cultivars which are currently cultivated in Bulgaria are used as standards: 'Endje 316', 'Elit-Radnevo' and 'Radnevo'.

An integrated collaborative programme between the ARI-Shumen and IPGR-Sadovo is ongoing, but, owing to lack of significant funds, the maintenance and enlargement of the beet collection are limited. The establishment of contacts with international and national partners is of utmost importance for the elaboration of cooperative projects to protect and conserve the available sugar beet plant genetic resources.

Table 2. Number of accessions conserved and evaluated in the Bulgarian *Beta* collections

Institute	No. of accessions conserved				No. of accessions evaluated
	Long-term	Medium-term	Working collection	Others(*)	
ARI-Shumen			157	293	217
IPGR-Sadovo	11	219			230 (**)
Total	**11**	**219**	**157**	**293**	**447**

(*) seed storage
(**) passport data only

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The Beta *collection in the Czech Republic in the period 2000–2002*

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Current status of the Czech *Beta* collection

The collection of *Beta* genetic resources in the Czech Republic is included in the National Programme of Plant Genetic Resources Conservation and Utilization. During the last three years, the number of accessions in the collection has not increased much because of the orientation of breeding systems towards hybrid production.

Attention has been paid to increasing seed availability, characterization and evaluation. Seed has been regenerated in the sub-collection of garden beets. A few accessions of *Beta vulgaris* var. *altissima* were multiplied in the framework of GENRES CT95-42.

Table 1. *Beta vulgaris* genetic resources – seed samples availability in the Czech collection

Subspecies	1999	2002
Beta vulgaris L. subsp. *maritima* (L.) Thell.	3	3
Beta vulgaris L. subsp. *vulgaris* var. a*ltissima* Doell	29	32
Beta vulgaris L. subsp.. *vulgaris* var. *cicla* L.	17	27
Beta vulgaris L. subsp. *vulgaris* var. *rapacea* Koch	28	28
Beta vulgaris L. subsp. *vulgaris* var. *vulgaris*	113	118
***Beta vulgaris* L – total**	**190**	**208**

During preparation of seed samples for their storage in the genebank, their moisture content is reduced to 6–7% at a temperature not higher than 25°C. The samples are maintained in glass jars with vapour-proof lids. The active collection is maintained at a constant temperature of –5°C.

Evaluation of the *Beta vulgaris* var. *vulgaris* and *B. vulgaris* var. *cicla* sub-collections

Within the *Beta* collection, salad beet (*Beta vulgaris* var. *vulgaris*) is represented by 118 accessions and Swiss chard (*B. vulgaris* var. *cicla*) by 27 accessions. In the past, mixed pollination occurred between cultivars owing to poor isolation. Using repeated regenerations and perfect isolation in isolation cages covered with glass or with a thick net, we succeeded in gradually cleaning these cultivars and stabilizing their respective characteristic traits.

- **Salad beet**

The group of salad beets (118 accessions) shows a great variability in the shape and colour of the beetroot (Fig. 1).

The following root shapes are observed: flat (cv. ´Egyptska plocha´), circular (cv. ´Detroit´), cylindrical (cv. ´Cylindra´), conic (cv. ´Dobbie's Purple´) and also various intermediate types.

Various intensities of anthocyanin coloration of the skin and root flesh can also be found; some cultivars have an orange skin colour (e.g. ´Severnaja oranzevaja´).

Cultivar ´Nutting's´ is interesting because of its nut flavour when eaten fresh.

Fig. 1. Different root shapes of *Beta vulgaris* var. *vulgaris*

a. Variety 'Detroit' – circular root

b. Variety 'Dobbie's Purple' – conic root

c. Variety 'Cylindra' – cylindrical root

d. Variety 'Egyptská plochá' – flat root

- **Swiss chard**

The group of Swiss chards (27 accessions) comprises cultivars with various leaf colorations, ranging from yellow-green (´Gelber Krauser´) to light green (´Lyoner´), dark green (´Poise Verte A Carde Blanche´) and red colour (´Rhubarb Chard´).

The leaf blade surface also shows great variability according to the cultivar: smooth, moderately wavy or very curly.

The petiole of the Swiss chard is a very interesting part of this plant. It sometimes reaches 40 cm-length and 5.5 cm-width (e.g. in the big cultivar ´Blonde d'Hiver de Genève´). The petiole colour can be white, light green, yellow, orange or red.

Report on Beta *genetic resources activities in Germany*

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Introduction

The acreage of arable land in Germany is 11 805 ha of which 3.8% is used for sugar beet production, equalling 451 410 ha in the period 2000-2001. The production of fodder beets has dramatically dropped from 152 000 ha in 1980 to only 9000 ha in 2001. Garden beets were produced on 602 ha in 2000, an increase of almost 100% compared to the period 1994-1999. Leaf beets are not mentioned in easily accessible statistics; however, this vegetable has been described as a winner in the group of neglected vegetable crops. Leaf beets are produced by hobby gardeners but can also be purchased on local markets and small, mostly Italian or Turkish, vegetable shops. Breeding research on *Beta* genetic resources and the development of improved commercial varieties focuses therefore on the sugar beet crop.

Fundamental research and breeding research on sugar beet is conducted by universities (Kiel, Halle), the Max-Planck-Institute at Köln, the Institute of Plant Genetics and Crop Plant Research (IPK, Gatersleben) and the Institute of Sugar Beet Research (Göttingen) in close cooperation with breeding companies. Research projects are often co-funded through the Association for the Promotion of the German Private Plant Breeding (GFP). Aspects of management of native *Beta* genetic resources are investigated by the Rheinisch-Westfälische Technische Hochschule Aachen (RWTH).

Genebank holdings

Beta genetic resources collections are maintained by two public institutions:

- The BAZ Gene Bank, as part of the research sector of the Ministry of Consumer Protection, Food and Agriculture (BMVEL) currently manages 1887 accessions (1999: 1837 accessions) of the German-Dutch *Beta* collection within the framework of an agreement signed by the German and Dutch Ministries for Agriculture in 1984. The BAZ holding consists of both cultivated types and wild species of all four sections. No *Beta* collecting missions have been implemented by the BAZ Gene Bank since 2000. The increase in the number of accessions held by the BAZ Gene Bank is due to the integration of new material into the publicly accessible collection after successful seed increase.
- The IPK, with its genebank, operates under the Ministry of Education, Science, Research and Technology (BMBF). The IPK genebank holds 406 accessions (1999: 365) of the genus *Beta*,. almost exclusively belonging to section *Beta* (Table 1). Forty-one new IPK accessions originate from plant explorations. Today, the total national *Beta* germplasm holding consists of 2293 accessions (Table 1 and Fig. 1). The four sections of the genus *Beta* are represented in a well-balanced way if the size of their distribution areas is taken as a criterion.

The BAZ Gene Bank is the successor of the Braunschweig Genetic Resources Collection (BGRC) also known as "FAL genebank" which was founded by the former Ministry of Food, Agriculture and Forestry (BML) in 1970. The genebank was established by the Federal Agricultural Research Centre (FAL). In 1996 the responsibility for the genebank was assigned

to the BAZ. As a result of difficult negotiations between the responsible Ministries, the BAZ Gene Bank will be closed and the germplasm as well as data linked with the accessions will be transferred to the IPK in 2003-2004. The total *ex situ* collection will be managed by the IPK genebank from next year onwards.

From October 2002, users of the German *Beta* holding are requested to send their seed orders to the IPK genebank. The seed transfer from the location Braunschweig to Gatersleben has commenced and the BAZ Gene Bank can no longer provide users with germplasm.

Table 1. German *Beta* holdings by taxon

Botanical name	BAZ holding	IPK holding
Beta sp.	19	26
B. macrocarpa	39	4
B. patula	5	
B. vulgaris subsp. *adanensis*	37	
B. vulgaris subsp. *maritima*	386	83
B. vulgaris	119	51
B. vulgaris subsp. *vulgaris*	51	2
B. vulgaris subsp. *vulgaris* Leaf Beet group	142	72
B. vulgaris subsp. *vulgaris* Garden Beet group	202	73
B. vulgaris subsp. *vulgaris* Fodder Beet group	141	73
B. vulgaris subsp. *vulgaris* Sugar Beet group	218	17
B. corolliflora	84	1
B. macrorhiza	32	
B. lomatogona	106	1
B. intermedia	222	
B. trigyna	26	1
B. nana	14	
B. procumbens	6	
B. webbiana	3	
B. patellaris	35	2
Total	**1887**	**406**

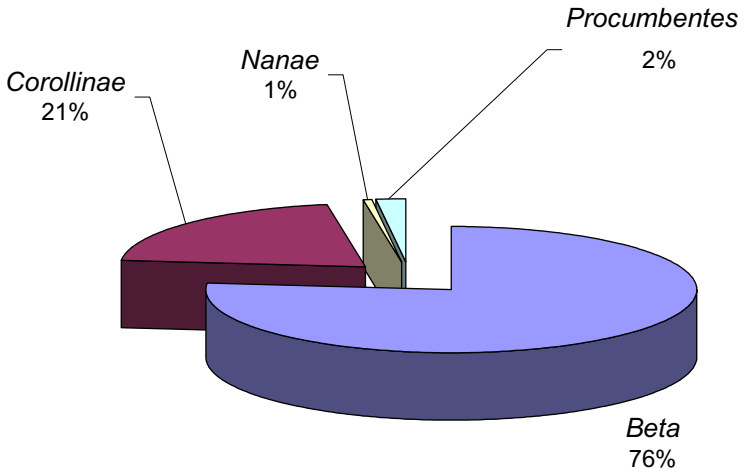

Fig. 1. German *Beta* holding by sections

- **Seed increase procedures and seed stock management**

The species-specific seed production methods are described in a BAZ manual which is considered an element of a genebank quality management manual. The BAZ Gene Bank mainly uses small greenhouses and hemp strokes for controlled pollination. The IPK genebank uses almost exclusively isolation greenhouses. Table 2 compares the seed production methods used by the BAZ and IPK for section *Beta* species.

Table 2. Seed increase production procedures

Measure	IPK	BAZ
Wild forms		
Sowing and transplanting	October, heated greenhouse	October, heated greenhouse. Annual types in batches from January to March depending on bolting behaviour
Vernalization	Cold greenhouse	Cold greenhouse or climate chamber, then at + 4 to 6°C and artificial light 10 hours, 12 weeks
Planting	Unheated greenhouse in February until transfer into isolation greenhouses, cultivation in large pots	Unheated greenhouse until mid-March until transfer into isolation greenhouse, cultivation in large pots
Number of plants	Up to 25 plants	Up to 50 plants
Pollination	By wind and insects *Osmia rufa* and *Eristalis tenax*. Beets share isolation greenhouse with other species	By wind
Cultivated forms		
Sowing and transplanting	July, production of stecklings, harvest in November, recording of observations during plant production	October, greenhouse or climate chamber, then at +4 to 6°C and artificial light 10 hours, 12 weeks
Vernalization	35 beets overwinter in a shelter, covered with glass and straw	Cold greenhouse
Planting	Stecklings are planted in isolation greenhouse	Unheated greenhouse until mid-March until transfer into isolation greenhouse, cultivation in large pots
Number of plants	Up to 35 plants	Up to 50 plants
Pollination	By wind and insects *Osmia rufa* and *Eristalis tenax*. Beets share isolation greenhouse with other species	By wind
General conditions and measures		
Growing conditions during seed ripening	Temperature below 30°C	During sunny periods temperatures reach more than 35°C, plants then often drought stressed
Seed harvest	At once	Starts when seed skin colour of fruits of the upper third of the stem turns from white/yellow to dark brown. Single plants are harvested depending on maturity. If seed shattering of green fruits is observed the harvest starts earlier
Pre-processing	Plants are dried at 25°C	Plants are dried at 25°.
Threshing	Threshing machine	Threshing machine
Final processing	Mechanical sieving, then final cleaning by hand	Sieving by hand, air separator, belt sorting machine, polishing
Drying before storage	At room conditions approx. 22°C for several weeks	Three weeks at 25°C in an air current of 3% relative humidity
Storage	In air-tight glass jars at –15°C, silica gel is added	Air-tied tin cans at –10°C
Germination test	Filter paper, count after 4 and 14 days	8 x 25 fruits on round filter paper, count after 5 days, 20°C, 8 h light, 16 h dark, no test for hard-seeded species

- **Characterization and evaluation**

The BAZ Gene Bank uses the "Descriptors for *Beta*" (IPGRI 1996) for characterization of accessions. In general, observations are recorded during seed increase on a limited number of traits (male sterility, multigermicity, seed maturity, seed shattering, seed yield, stem betacyanin coloration, stem colour, stem number, growth habit, growth height, leaf hairiness, leaf thickness, bolting, flowering start, flowering end, annuality). The IPK genebank uses its own descriptors to record shape, colour, flesh colour, ring formation, leaf shape and colour, petiole colour, and beet position in soil. The growth habit of wild beets is also recorded. All cultivated forms are photographed by the IPK genebank and photos are kept as slides (old ones) in an archive or as files (new ones) on a PC.

- **Data documentation**

Evaluation and characterization data on *Beta* received by the BAZ Gene Bank since 1987 have been documented in the International Data Base for *Beta* (IDBB) directly. During 1996 and 2001, 16397 new characterization and 5248 evaluation data have been added to the International Data Base for *Beta*. These data result from the EU-funded *Beta* project GENRES CT95-42. The IDBB architecture and functions (as well as that of the European *Avena* Database) have been improved considerably during the past three years (see paper by C. Germeier and L. Frese, pp. 84-102, this report). The BAZ will continue to manage these central crop databases. Priority now needs to be given to the improvement of the database content and data quality and reliability.

Inventory and monitoring of *in situ* populations

The decision to establish a central national collection of plant genetic resources for food and agriculture (PGRFA) at IPK by merging the BAZ Gene Bank collection with the IPK collection was facilitated by the a priori agreement to share tasks between the BMVEL and BMBF genebanks. Except for the *Vitis* and fruit genetic resources collection, IPK will be responsible for the national PGRFA holding while BAZ will investigate and develop genetic resources management procedures that complement *ex situ* activities. Complementary germplasm management concepts cover a whole range of possible measures, activities and crop species.

A basis for the *in situ* management of native *B. vulgaris* subsp. *maritima* populations has actually been created in the framework of GMO risk assessment studies conducted by the University of Aachen. The Institute of Ecology, Ecotoxicology and Ecochemistry has conducted biosafety research since 1993. Before the onset of these studies a single *B. vulgaris* subsp. *maritima* population was known to exist in Germany on the North Sea island Helgoland. A search for further populations along the Baltic Sea coast has shown that additional populations exist south of the Danish distribution area of this wild beet. Monitoring of the population is currently done by the RWTH Aachen. However, as to date there are no management plans to protect the sites and to preserve the populations. The need for a nationwide agreed concept and plan for *in situ* management of native wild PGRFA has been recognized only recently. First a framework programme and principles for *in situ* management of wild PGRFA needs to be developed. Then detailed measures can be derived from the programme for species like the sea beet.

Studies on *in situ* management of PGRFA and GMO risk assessment studies have interests in common as they are dealing with the same populations. The common interests are the inventory of populations, data documentation and the aim of safeguarding the genetic integrity of natural populations. The Institute of Ecology, Ecotoxicology and Ecochemistry currently runs two projects:

- **Biosafety of genetically modified *Beta vulgaris* L. and biodiversity of beet genetic resources 1993-2004**

In 1993, genetically modified sugar beet with resistance against infection by the BNYVV (beet necrotic yellow vein virus) were released for field tests. Monitoring the spreading of transgenic traits is a point of emphasis in ecological research. It can be subdivided into two types: specific and general monitoring. Specific monitoring comprises the direct evidence of cause-effect relations, in this case investigations about hibernation, potential advantages in succession, etc., using direct comparison of transgenic and non-transgenic plants. For general monitoring, analyses of population dynamics and gene flow between wild, weed and sugar beet populations will elucidate potential ways of distribution and help evaluate the danger of outcrossing of transgenic traits into wild beet populations or closely related cultivated plants like Swiss chard (*B. vulgaris* subsp. *vulgaris,* Leaf Beet group) or garden beet (*B. vulgaris* subsp. *vulgaris,* Garden Beet group). The investigations focus on the potential influence of transgenic sugar beet on wild beet populations located in Italy, where the main proportion of seed for the European market is being produced.

Focal points of investigation are as follows:

- **Outcrossing potential**
  The likelihood of outcrossing of transgenic traits into wild and cultivated subspecies has been proved by several crossing experiments (Bartsch and Pohl-Orf 1996).
- **Pollen dispersal**
  The range of pollen has been examined by Saeglitz (2000)
- **Competitiveness**
  The competitiveness against arable weeds was evaluated in field experiments in 1993-1999 (Bartsch *et al.* 1996; Pohl-Orf *et al.* 2000).
- **Hibernation**
  Tests for the hibernation of non-transgenic and transgenic sugar beet have been conducted. General survival in relation to weather has been tested (Pohl-Orf *et al.* 1999).
- **Succession**
  The succession of conventional sugar beet in a typical fallow as well as succession of wild beet/sugar beet hybrids and weed beet as modelling organisms for potential degeneration have been investigated in 1993-1996 with non-transgenic plants. Experiments have been extended to transgenic individuals.
- **Population dynamics**
  Population structures and dynamics of wild beet populations of the Po delta and the Adriatic coast were examined during three collection trips in the years 1993-1996 (Bartsch and Schmidt 1996). The collected material will now be subjected to molecular analysis.
- **BNYVV infestation**
  The BNYVV infestation in wild mesohaline habitats has been compared within and between different wild beet populations using the ELISA test (Bartsch and Brand 1996).
- **Molecular analysis of population genetic and phylogenetic relationships**
  For general monitoring, molecular methods are applied to reveal diversity within wild beet populations and mechanisms of genetic interaction between wild and sugar beet and their hybrids (weed beet). First results are published in Mücher *et al.* (2000).

- **Ecological role of plant disease in natural habitats of wild beet populations**

Transgenic resistance traits against fungi or nematodes would offer a better performance to cultivars, but at the same time wild beet would profit by gene flow in natural habitats where a disease has a significant influence on population fitness. Gene flow from conventional

sugar beet to wild sea beet can hardly be avoided and has been documented for several areas in Europe and USA. Whether resistance traits offer an ecological advantage to sea beet populations depends both on the distribution of the pathogen and natural tolerance alleles. The first preliminary data of German and Danish sea beet that have been screened in 1999 for fungi infestation symptoms suggest that diseases are common, but found only in a low frequency in coastal habitats. Data from beet germplasm collections screened for resistance alleles revealed that strong pathogen resistance is rare. Future biosafety research has to deliver data on the demographic co-occurrence of pathogen and resistance, as well as the ecological performance of transgenic and isogenic sugar beets hybridized with wild beets.

EU project VRTP IMPACT (2001-2004) Framework 5: Virus-resistant transgenic plants: ecological impact of gene flow

The objective of this project is to provide detailed evaluation of the two sources of potential genotypic impact that could result from large-scale cultivation of virus-resistant transgenic plants, and particularly those expressing viral sequences. Genotypic impact could result from two types of gene flow: one involving recombination between viral sequences transcribed from the transgene and the genome of an infecting virus, and another due to the potential for sexual outcrossing between the transgenic plant and a compatible wild species. In both cases, this requires not only close examination of the interaction of the transgenic plants, on the one hand with the genome of other viruses, and on the other hand with related plant species, but also requires establishment of baselines on the role of these same processes in a non-transgenic context. Thus, the idea of impact as used here only concerns additional, i.e. above borderline, novel effects that could be caused by interaction of the transgenic plants with their biological environment. In order to address these interlocking concerns, the VRTP IMPACT project has been divided into four work packages. Each of these will involve collaboration among several participants, and as a result, most of the participants are involved in more than one work package. The first two work packages (WPs I & II) are organized in a parallel fashion to evaluate the impact of recombination between transgene sequences and those of the genome of two particularly important groups of plant viruses, the potyviruses and the cucumoviruses, which are extremely different in both their biological and molecular properties, and thus may have different aptitudes for recombination in transgenic plants. WPs I & II will focus on comparisons of the outcome of recombination in transgenic plants with that in non-transgenic ones. Since our knowledge of the prevalence in nature of recombinant virus genomes is extremely sparse, this question will be addressed in a separate work project (WP III) that will involve molecular epidemiology studies of virus populations in Spain and France. In WP IV, we will examine the impact of plant-to-plant gene flow from two major crop species where this is known to occur, canola seed and beet. In both cases, this will involve field and glasshouse studies to evaluate if a virus resistance gene could confer a fitness advantage on the receptor wild or weedy species.

On-farm management

Around 1900 a large diversity of fodder, garden and leaf beet landraces existed in Europe (Vilmorin 1923; Dahl 2000). These local varieties were selected and managed by individual farmers or so-called breeding associations of local farmers. The selection of local fodder beet varieties ceased in the 1960s. By chance a unique example of a farmer-selected fodder beet variety was detected at the Vogelsberg, an area close to Frankfurt. The example has been described by Frese and Efken (2002) mainly to provide a historical record. Since the management of fodder beet germplasm is not at all done for economic reasons but for tradition only, we expect that the locally used germplasm will become extinct soon. Especially in sugar and fodder beet there are little or no economic incentives that would persuade German farmers to manage germplasm on the farm.

The situation with garden beet and leaf beet differs from that of sugar and fodder beet. Garden beet plays a role in organic farming. Members of associations such as the "Kultursaat e.V." select garden beet varieties for organic farming and by doing so they contribute to the broadening of genetic diversity in the agricultural system.

The use of traditional germplasm by consumers plays an essential role in on-farm management of PGRFA. The consumption of genetic resources is promoted by the "Slow Food" association as a method that assists the marketing of underutilized crops and traditional varieties. By developing and disseminating specific cooking recipes the consumer's demand for old varieties is stimulated. This in turn can result in a larger production of specific varieties and hence to an enlargement of genetic diversity in agricultural production. The Slow Food organization has repeatedly demonstrated that the consumer's interest in new products (often in the high price sector) can be used to change consumption behaviour. The Slow Food branch at Hamburg has succeeded in stimulating interest in white and yellow garden beets. Slow food has screened parts of the BAZ garden beet holding and has chosen two garden beet types with white and yellow flesh, respectively, to develop specific recipes. The white fleshed garden beet, previously unknown in the German cuisine, is now produced for a restaurant on a limited scale. The use of specific garden beets has little impact on agriculture on the whole. Yet it is an interesting case, showing how genetic diversity could be increased in the agricultural system.

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The National Beta *Collection of the Institute for Agrobotany (Hungary) as part of the National Gene Bank Programme*

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Introduction

The Institute for Agrobotany was founded by the Ministry of Agriculture in 1958 with the following responsibilities: *"...collection, maintenance and taxonomic, botanical, physiological, biochemical as well as plant pathological examination of domesticated plants and world collections of cultivated crops"*. After several reorganizations, the Institute for Agrobotany was re-established on 1 January 1993.

Overview of activities

The Institute for Agrobotany (ABI) is responsible for the development and maintenance of field crop and vegetable genetic resources collections. It performs overall genebank activities, including the following "classical genebank activities":

- Exploration and collection of genetic resources of field and vegetable crops with special emphasis on local, Hungarian material
- Medium- and long-term conservation of seed samples in cold stores and with the use of meristem cultures in the case of vegetatively propagated crops
- Multiplication and regeneration of accessions aimed at obtaining sufficient quantities of high quality seeds for medium- and long-term conservation, evaluation and distribution
- Isoclimatic regeneration of Hungarian landraces, ecotypes and populations on the site of their places of origin (*in situ*, on-farm and backyard garden multiplication)
- Characterization and evaluation of plant genetic resources (PGR) collections according to internationally accepted descriptor lists
- Development and maintenance of the National Base Collection for seed-propagated crops
- Documentation of passport and evaluation data for the PGR maintained by ABI and other partners in Hungary (National Database)
- Distribution of seed samples together with relevant information to users
- Nationwide responsibility for the technical coordination of Hungarian PGR activities
- Participation in the ECP/GR and other international and national programmes.

The Ministry of Agriculture and Rural Development also provides funds for the maintenance of collections. This support is available for all institutes carrying out genebank activities if they meet the following requirements:

- The applicants should possess unique germplasm, not duplicated in existing germplasm collections;
- The material should be made freely available;
- A basic set of passport and/or collecting information should be supplied to the NGBAB (Hungarian National Gene Bank Database);
- After multiplication of the accessions, the applicants should arrange for long-term preservation of the material in the National Base Collection;
- Supported genetic resources activities should be conducted in accordance with international standards (FAO/IPGRI *Genebank standards*, IBPGR/IPGRI descriptor lists).

This year (2002) 94 institutes, universities etc. submitted applications for funding, but there was only one application including accessions of *Beta* (nine accessions of fodder beet).

The National *Beta* Collection

More than 59 000 accessions are available to Hungarian and foreign breeders and other users in the collection of Institute for Agrobotany, which represents more than 800 species of 250 genera. The more than 25-year-old National *Beta* Collection with its 301 accessions, of which 96% belong to *Beta vulgaris* L., is part of that collection.

The *Beta* collection of the Institute for Agrobotany shows a wide range of diversity where sugar beet (47%), garden beet (24%), fodder beet (17%) and mangel (13%) represent the highest percentage, but also contains accessions of mangold, sea beet and other wild beet (Table 1).

Table 1. Composition of the Hungarian *Beta* collection by subtaxon

Cultivar group	Species	Subtaxon	No. of acc.
Beet (1%)	*B. vulgaris* L.	var. *alba* DC.	1
		var. *rapa* Dumort.	2
Fodder beet (17%)	*B. vulgaris* L.	subsp. *vulgaris* convar. *vulgaris*	48
		subsp. *vulgaris* convar. *vulgaris* f. alba DC.	1
		subsp. *vulgaris* var. *flavescens* DC.	1
Garden beet (24%)	*B. vulgaris* L.	subsp. *vulgaris* convar. *vulgaris* var. *vulgaris*	71
Mangel (13%)	*B. vulgaris* L.	subsp. *vulgaris* convar. *vulgaris* var. *rapacea* Koch	2
		subsp. *vulgaris* convar. *vulgaris* var. *rapacea* Koch f. *crassa* (Alef.) Helm	4
		subsp. *vulgaris* convar. *vulgaris* var. *rapacea* Koch f. *longorubra* (Alef.) Helm	2
		subsp. *vulgaris* convar. *vulgaris* var. *rapacea* Koch f. *xanthina* Aellen	5
Mangold (foliage beet) (2%)	*B. vulgaris* L.	subsp. *vulgaris* convar. *cicla* (L.) Alef.	4
		subsp. *vulgaris* convar. *cicla* (L.) Alef. var. *cicla* L. s.l.	1
		subsp. *vulgaris* convar. *cicla* (L.) Alef. var. *flavescens* DC. f. *rhodopleura* (Alef.) Voss.	1
Sugar beet (47%)	*B. vulgaris* L.	subsp. *vulgaris* convar. *vulgaris* var. *altissima* Döll	142
Sea beet (4%)	*B. vulgaris* L.	subsp. *maritima* (L.) Arcang.	12
Other wild beet (4%)	*B. patellaris* Moq.	---	1
	B. trigyna Waldst. et Kit.	---	3
Total			**301**

Following the recommendations of the first UN Conference on the Environment (Stockholm, 1972), cooled seed storage rooms were built and seed samples are stored in the active and base collection chambers at the Institute. All the *Beta* accessions are stored in the active collection at 0ºC. The chambers of the base collection (-20ºC) hold 21% of the samples (63 accessions) (Table 2). The total number of accessions of *Beta* landraces is 88, of which 34% are maintained in the base collection (Table 3). The proportion is much higher for *Beta* accessions of Hungarian origin (44%): 45% of fodder beet, 29% of garden beet and 62% of sugar beet accessions are maintained in the base collection chambers (Table 4).

Table 2. Number of *Beta* accessions in the active and base collections

Cultivar group	No. of accessions in	
	Active collection	Active and base collections
Beet	3	
Fodder beet	50	18
Garden beet	71	18
Mangel	13	1
Mangold (foliage beet)	6	
Sea beet	12	
Sugar beet	142	26
Other wild beet	4	
Total	**301**	**63**
%	100%	21%

Table 3. Number of landraces collected by the Institute for Agrobotany in active and base collections

Cultivar group	No. of accessions in		% in base collections
	Active collection	Active and base collections	
Fodder beet	30	11	37%
Garden beet	48	16	33%
Sugar beet	10	3	30%
Total	**58**	**30**	
%	100%	34%	

Table 4. Number of *Beta* accessions of Hungarian origin in active and base collections

Cultivar group	No. of accessions in		% in base collections
	Active	Active and base	
Fodder beet	40	18	45%
Garden beet	51	15	29%
Sugar beet	42	26	62%
Total	**133**	**59**	
%	100%	44%	

The *Beta* collection is increased through seed exchange with Hungarian and foreign institutes and collecting.

Most of the accessions are of Hungarian origin (133), but information about origin is lacking for 27% of the collection (Table 5). Several accessions are of German (27), Dutch (14), Danish (10), Swedish (8) and Russian (8) origin. The total number of accessions of Hungarian origin is 133, including 30% fodder beet, 38% garden beet, and 32% sugar beet.

The 301 *Beta* accessions were received from 15 countries; only one accession lacks information about its donor country (Table 6). The largest part of the collection was obtained from Hungarian institutes (219), but the contribution of formal Soviet (29) and German (23) institutes to the development of our *Beta* collection is also considerable.

A valuable part of the *Beta* National Collection is represented by the 88 accessions collected by the Institute (30 fodder beet, 48 garden beet, and 10 sugar beet) (Table 7). Collecting was most intensive in the period 1981-1985, when 48% of the landraces (13 fodder beet, 25 garden beet and 4 sugar beet) were collected.

Table 5. Composition of the *Beta* collection by country of origin

Country of origin	No. of accessions
Austria	1
Belgium	3
China	1
Czechoslovakia	5
Denmark	10
Former Soviet Union	8
France	2
Germany (DEU + DDR)	25+2
Hungary	133
Italy	1
Netherlands	14
Poland	1
Portugal	1
Romania	2
Sweden	8
Unknown	81
Yugoslavia	3
Total	**301**

Table 6. Composition of the *Beta* collection by donor countries

Donor	Beet	Fodder beet	Garden beet	Mangel	Mangold	Sea beet	Sugar beet	Wild beet	No. of accessions
Algeria			1						**1**
Belgium							1		**1**
Czechoslovakia		1	3				1		**5**
Former Soviet Union		6	6			2	14	1	**29**
France		1		1		2			**4**
Germany (DEU)	1	2						1	**4**
Germany (DDR)			2	11	2	2	1	1	**19**
Hungary		40	57		2	1	119		**219**
Italy						1			**1**
Japan	2			1					**3**
Netherlands							4		**4**
Poland					1				**1**
Portugal					1	3			**4**
Romania			2					1	**3**
United Kingdom						1	1		**2**
Unknown							1		**1**
Total	**3**	**50**	**71**	**13**	**6**	**12**	**142**	**4**	**301**

Table 7. Collecting of landraces in 5-year periods

Cultivated groups	No. of accessions					
	<1980	**1981-1985**	**1986-1990**	**1991-1995**	**1996-2000**	**Total**
Fodder beet	6	13	10	0	1	30
Garden beet	7	25	12	4		48
Sugar beet	2	4	3	0	1	10
Total	**15**	**42**	**25**	**4**	**2**	**88**
%	17%	48%	28%	5%	2%	

Documentation

The documentation of the passport, evaluation and genebank management data of the PGR maintained by the Institute is computerized and the hardware facilities and software systems have been updated regularly. The database structure is based on genebank standards and takes into account the recommendations of FAO/IPGRI (1994). It has some specific features essential for the effective daily database management. The central passport database of the Institute (Table 8) shows considerable similarity with the structure of

FAO/IPGRI multicrop passport descriptors, which facilitates conversion into that format (Table 9). The software used for passport and genebank data management is dBase.

Table 8. Structure of the central passport database maintained at the Institute for Agrobotany

1	ACCESSION ID NUMBER
2	GENUS (ARRIVAL)
3	SPECIES (ARRIVAL)
4	SUBSP (ARRIVAL)
5	GENUS (ACCEPTED)
6	SPECIES (ACCEPTED)
7	SUBSP (ACCEPTED)
8	GENUS (CHECKED)
9	SPECIES (CHECKED)
10	SUBSP (CHECKED)
11	CROP NAME
12	CULTIVAR NAME
13	COUNTRY OF ORIGIN
14	DONOR COUNTRY
15	DONOR INSTITUTE
16	DONOR ID NUMBER
17	OTHER ID NUMBER
18	PLOIDY LEVEL
19	GENERATION
20	DATE OF STORAGE
21	STORAGE TYPE
22	STORED QUANTITY
23	ACQUISITION TYPE
24	YEAR OF ACQUISITION
25	COLLECTING INSTITUTE
26	COLLECTING NUMBER
27	SITE OF COLLECTING
28	ALTITUDE
29	LATITUDE
30	LONGITUDE
31	DATE OF LAST REGENERATION
32	PLACE OF REGENERATION
33	GERMINATION DATE
34	GERMINATION %
35	1000 SEED WEIGHT
36	SAMPLE TYPE
37	DATE OF COLLECTING
38	COLLECTING SOURCE
39	REMARKS

Table 9. The multicrop passport structure of the *Beta* database and the completeness of fields

Field	Field name	Completeness
1	INSTCODE	100%
2	ACCENUMB	100%
3	COLLNUMB	29%
4	COLLCODE	29%
5	GENUS	100%
6	SPECIES	100%
7	SUBTAXA	99%
8	CROPNAME	100%
9	ACCNAME	89%
10	ACQDATE	99%
11	ORIGCTY	73%
12	COLLSITE	27%
13	LATITUDE	27%
14	LONGITUDE	27%
15	ELEVATION	0%
16	COLLDATE	29%
17	SAMPSTAT	94%
18	COLLSRC	100%
19	DONORCTY	99%
20	RCATDONCOD	99%
21	DONORCODE	99%
22	DONORNUMB	1%
23	OTHERNUMB	100%
24	STORAGE	100%
25	AVAIL	100%
26	CHARAVAIL	100%

Multiplication and regeneration

For multiplication and regeneration of accessions the Institute has nearly 145 ha of arable land, of which 15-20 ha are used for genebank nurseries and other field trials each year. The general volume of *Beta* field multiplication and regeneration varies from year to year according to the changes due to introduction or collecting, and is basically defined by the needs of genebank regenerations in the given period. During multiplications special attention is paid to isolation; in the case of beet space-isolated nurseries are used for this purpose. Besides *ex situ* conservation, in case of landraces the multiplication is carried out according to a "backyard multiplication system", where the locally adapted populations are multiplied in selected districts where the ecological conditions (soil type, climatic conditions etc.) are similar to those of their places of origin.

On-farm conservation is also carried out: the Institute participates in the project "Strengthening the Scientific Basis of *In situ* Conservation of Agricultural Biodiversity Conserved On-farm". The on-farm project is currently targeted only on bean and maize

landraces and only three environmentally sensitive but ecologically different agricultural regions are involved in this project. In the future we would like to expand this programme to other parts of the country and to as many genera as possible (including *Beta*).

Characterization and evaluation

The characterization and evaluation of PGR collections are carried out using internationally accepted descriptor lists. The basis for the characterization and evaluation is the "Descriptors for *Beta*" (IBPGR/CGN 1991), complemented by a few additional traits. The evaluated characters are listed in Table 10.

Table 10. Descriptor list for evaluation and characterization of *Beta* at the Institute for Agrobotany

1. Accession Data	1	4.2 Beet traits	
		4.2.1 Hypocotyl colour	*2*
2. Collecting Data	1	4.2.2 Beet shape in longitudinal section	1
		4.2.3 Beet shape in transverse section	*2*
3. Site Data	1	4.2.4 Beet length (cm)	1
3.4 Sowing date	1	4.2.5 Beet diameter (cm)	1
3.5 Harvested date	1	4.2.6 Beet position in soil	3
3.6 Evaluation environment	1	4.2.9 Root groove depth	3
3.8 Number of days to 50% field emergence	1	*4.2.10 Skin roughness*	*2*
3.9 Sowing site in field	1	4.2.11 Skin colour	1
3.10 Field spacing	1	4.2.12 Flesh colour	1
3.12 Watering	1	*4.2.13 Flesh coarseness*	*2*
		4.2.14 Ring formation	*2*
4. PLANT DATA	1	*4.2.15 Ring colour*	*2*
4.1 Leaf traits	1	Beet ring number (pc)	1
4.1.1 Leaf rosette erectness	*2*	Beet head length (cm)	1
4.1.2 Leaf rosette diameter (cm)	*2*	Beet head shape	1
4.1.3 Leaf rosette height (cm)	*2*		
4.1.4 Leaf attitude in autumn	*2*	4.3 Inflorescence	1
4.1.5 Leaf number	1	4.3.1 Annuality	1
4.1.6 Leaf blade length (cm)	*2*	4.3.2 Growth habit	1
4.1.7. Leaf blade width (cm)	*2*	4.3.6 Flowering start	1
4.1.8 Leaf thickness (mm)	*2*	4.3.7 Flowering end	1
4.1.9 Petiole length (cm)	*2*	Starting date of tepal	1
4.1.10 Petiole width (cm)	*2*	4.3.10 Tepal shape	1
4.1.11 Leaf colour	1	4.3.12 Tepal border	1
4.1.12 Leaf pigmentation	1	4.3.15 Male sterility	1
4.1.13 Petiole colour	1	4.3.20 Stem pigmentation	1
4.1.14 Leaf curliness	*2*		
4.1.15 Leaf hairiness	1	6. Plant	1
4.1.16 Cuticle thickness	2	6.1 Yield and quality attributes	1
Leaf shape	3	6.1.11 Root dry matter content (%)	1
Leaf blade peak	3		
Leaf blade shoulder	3		
Leaf margin	3		
Leaf graininess colour	3		

1 = for all cultivar groups
2 = for garden beet only
3 = for all except garden beet
N.B. Descriptors with no numbering do not belong to the internationally accepted descriptors published by IBPGR/CGN in 1991 (Descriptors for *Beta*); they have been added by the genebank curators.

Almost half of the *Beta* collection has been characterized. Garden beet, with 59% characterization data, is outstanding among the other cultivar groups, but all cultivar groups have a high level of characterization, except for "other wild beets" (Table 11). The Hungarian accessions give a favourable picture: 85 accessions (64%) are characterized (Table 12). Most of the landraces (57%) have also been characterized: 40% of the fodder beet, 69% of the garden beet and 50% of the sugar beet accessions collected by the Institute have already been characterized (Table 13).

Table 11. Characterized accessions in the *Beta* collection by cultivar group

Cultivar group	No. of accessions	Characterization			
		No		Yes	
		No. of accessions	%	No. of accessions	%
Beet	3	3	100		0
Fodder beet	50	28	56	22	44
Garden beet	71	29	41	42	59
Mangel	13	10	77	3	23
Mangold (foliage beet)	6	3	50	3	50
Sea beet	12	7	58	5	42
Sugar beet	142	80	56	62	44
Other wild beet	4	4	100		0
Total	**301**	**164**	**54**	**137**	**46**

Table 12. Characterization level of Hungarian accessions

Cultivar group	No. of accessions	Characterization			
		No		Yes	
		No. of accessions	%	No. of accessions	%
Fodder beet	50	21	53	19	48
Garden beet	51	17	33	34	67
Sugar beet	42	10	24	32	76
Total	**133**	**48**	**36**	**85**	**64**

Table 13. Characterization level of landraces

Cultivar group	No. of accessions	Characterization			
		No		Yes	
		No. of accessions	%	No. of accessions	%
Fodder beet	30	18	60	12	40
Garden beet	48	15	31	33	69
Sugar beet	10	5	50	5	50
Total	**88**	**38**	**43**	**50**	**57**

References

FAO/IPGRI. 1994. Genebank Standards. Food and Agriculture Organization of the United Nations, Rome/International Plant Genetic Resources Institute, Rome.

IBPGR/CGN. 1991. Descriptors for *Beta*. International Board for Plant Genetic Resources, Rome, Italy.

Report on collection and characterization of beet landraces and in situ *conservation of* Beta lomatogona *in Iran*

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Introduction

The collection and evaluation of *Beta* germplasm has recently received increased attention in Iran due to the need for resistant/tolerant genes to biotic and abiotic stresses and concern about loss of germplasm due to gradual elimination of natural habitats.

Factors threatening or causing extinction of local populations included overgrazing, industrialization, war, natural disasters and land management changes. Therefore it is essential that such germplasm be conserved for future use.

Due to severe drought, our agriculture (farming and pastures) suffered very badly in the past few years. Fortunately we had an abundant rainfall this year (2002).

The Sugar Beet Seed Institute (SBSI) holding the *Beta* Gene Bank in Iran carried out a national project in 1998-2001 with the main aims of collecting, characterizing and regenerating *Beta* germplasm.

Collecting

Expeditions were conducted each year to collect the existing *Beta* genetic resources, especially landraces in different provinces.

Beside sugar beet germplasm, the SBSI *Beta* Gene Bank holds a total of 342 accessions, including 274 fodder and table beets (*B. vulgaris* subsp. *vulgaris*), 41 sea beets (*B. vulgaris* subsp. *maritima*) and 13 *B. lomatogona.* The remainder is constituted by other species received from the BAZ Gene Bank.

Characterization of landraces

The evaluation of morphological and agronomic characters was carried out on the field plots after the cold weather occurring in early May each year in Karadj. During the growing season, characters such as hypocotyl colour, morphological foliage characters and annuality of the genetic material were recorded. Root shape, skin and flesh colour of roots, yield and technological characteristics of the collected landraces were recorded (Tables 1-3). Much variation was found both between and within the populations (Fig. 1). All accessions were a mixture of different root shapes and colour. Cytological analyses revealed that all accessions studied were diploid.

Table 1. Root and seed characteristics of 18 beet landraces

Accession no.	Skin colour			Flesh colour				Ring colour				Germination (%)	Monogermity (%)	1000-seed weight (g)	Red petiole (%)
	Red	Yellow	White	Red	Yellow	White	Pink	Red	Yellow	White	Pink				
7003	+	+	+	+	-	+	+	+	-	+	-	71	71	10.20	90
7004	+	+	-	+	-	+	-	+	-	+	-	59	50.25	11	94
7107	+	+	-	+	+	+	-	+	+	+	+	89	26.75	14	91
7109	+	+	+	+	+	+	+	+	+	+	+	93	28	13.4	79
7111	+	+	+	+	-	+	+	+	+	+	+	89	46.25	10	93
7115	+	-	+	+	-	+	-	+	-	+	-	77	21.50	22.6	98
7122	+	-	+	+	-	-	-	+	-	+	-	85	42.50	11.40	95
7123	+	-	-	+	-	-	-	+	-	+	-	93	49.50	8.6	93
7124	+	-	-	+	-	+	+	+	-	+	+	86	52.25	10.6	95
7129	+	-	+	+	-	+	-	+	-	+	-	95	32.5	12.8	16
7211	+	+	+	-	+	+	+	-	-	+	+	84	38.50	20.40	84
7212	+	+	-	+	-	+	+	+	-	+	+	85	58.75	14.8	92
7214	+	+	+	+	-	+	+	+	-	+	-	81	50.50	9.6	99
7223	+	+	-	+	-	+	-	+	-	+	+	85	39.75	12.40	99
7225	+	-	-	+	-	+	-	+	-	+	-	66	63.25	9.6	100
7227	+	-	-	+	-	+	-	+	-	+	-	60	56.5	10.20	98
7310	+	+	+	+	+	+	+	+	+	+	+	71.50	23.75	14.8	16
7312	+	+	+	+	+	+	+	+	+	+	+	63	45	13	74

+ = Existence of different colours in each evaluated accession. Evaluation was carried out according to the “Descriptors for *Beta*” (IBPGR/CGN 1991)

Table 2. Morphological characteristics of 18 beet landraces

Accession no.	Growth habit	Blade length (cm)	Mean blade length (cm)	Blade width (cm)	Mean blade width (cm)	Petiole length (cm)	Mean petiole length (cm)	Petiole colour	Leaf thickness	Hypocotyl pigmentation	Root shape	Collection site
7003	Erect & prostrate	10-19	12.8	6-10	7.8	7-21	12.6	Green, red	Medium	Green	Circular	Sardastan
7004	Erect	14-21	18	7-17	12	9-21	14.5	Green, red	Medium, thick	Green, red	Elliptic, circular	Dastjerde Fasa
7107	Erect & prostrate	15-23	18.2	9-17	12.5	7-21	11.5	Green, red	Medium, thick	Green, red	Elliptic	Torbate heydariye
7109	Erect & prostrate	11-17	14	7-16	10.6	8-21	15.2	Green, red	Medium	Green, red	Elliptic	Chenaran
7111	Erect & prostrate	11-17	11.8	7-16	7.5	8-21	16.5	Green, red	Medium	Green, red	Elliptic	Nayshaboor
7115	Erect & procumbent	13-25	17.5	10-22	15.2	19-32	25.6	Green, red	Medium, thick	Green, red	Elliptic, circular	Semnan
7122	Erect	21-29	24.5	10-19	15	30-45	40.5	Red, green	Medium	Red, green	Elliptic	Varamin
7123	Erect	22-28	24.6	10-15	12.5	18-37	29.3	Red, green	Medium, thick	Green, red	Elliptic	Shahre ray
7124	Erect	21-25	23.2	11-16	13.7	25-35	30.6	Green	Thick	Red, green	Elliptic	Shahriar
7129	Erect	20-34	24.6	8-12	10.8	10-22	16	Green	Medium, thick	Green	Circular, elliptic	Fasa
7211	Prostrate	13-22	15.6	9-18	11.3	15-27	22.3	Green, red	Medium, thick	Green, red	Elliptic	Darab
7212	Erect & procumbent	13-21	16.1	6-24	12	14-32	17.8	Red, mixed	Medium	Red, green	Elliptic	Garmsar
7214	Prostrate	12-17	13.6	8-12	9.6	8-17	11.2	Green, red	Thin, medium	Red	Elliptic	Esfahan
7223	Procumbent	13-15	14	8-12	10	21-32	26.5	Green	Medium	Red	Elliptic	Bojnord
7225	Erect	14-26	18.8	7-17	10.5	16-30	25.1	Green, red	Thin, medium	Red, green	Elliptic	Nayshaboor
7227	Erect	12-21	16.8	3-13	9.2	13-24	19.1	Red, mixed	Medium	Red, green	Elliptic	Torbate heydariye
7310	Erect	13-22	18.5	8-14	10.5	11-30	22.5	Green, red	Medium, thick	Green	Elliptic	Hamedan
7312	Erect & procumbent	15-27	20.1	8-17	11.8	15-27	19.6	Green	Medium	Green	Elliptic	Malayer

Table 3. Yield and technological characters of 18 beet landraces

Accession no.	Root yield (t/ha)	SC (%)	K (Meq/100g beet)	Na (Meq/100g beet)	N (Meq/100g beet)	ALC[(1)]	Sugar (t/ha)	Yield (%)[(2)]	MS (% per beet)[(3)]
7003	40.2	10.53	7.65	2.52	2.08	4.89	7.14	67.77	3.39
7004	45.8	10.39	7.36	2.51	2.91	3.39	7.52	69.06	3.37
7107	51.3	10.62	7.47	3.01	1.89	5.54	7.14	67.21	3.48
7109	69.4	12.06	6.73	1.80	1.25	6.82	9.31	77.77	2.75
7111	62.5	9.89	7.07	3.20	1.86	5.52	6.48	65.55	3.41
7115	38.8	12.74	6.96	1.65	2.52	3.42	9.84	77.24	2.90
7122	40.2	11.25	7.38	2.01	2.00	4.70	8.13	72.28	3.12
7123	50	11.20	6.73	2.37	2.06	4.42	8.18	73.99	3.02
7124	87.5	11.78	7.17	2.48	3.58	2.70	8.42	71.51	3.36
7129	50	11.82	6.36	1.70	2.44	3.30	9.12	77.12	2.70
7211	66.6	11.59	7.21	2.19	1.71	5.50	8.50	73.30	3.09
7212	69.4	9.90	8.20	3.53	3.42	3.43	5.85	59.04	4.05
7214	81.9	12.60	6.54	1.99	2.10	4.06	9.77	77.51	2.83
7223	48.6	10.25	7.32	2.81	3.26	3.11	6.76	65.94	3.49
7225	55	9.66	7.22	3.65	2.69	2.15	5.98	61.86	3.68
7227	72.2	6.82	6.95	3.84	4.43	2.44	4.99	56.61	3.83
7310	63	15.71	6.80	1.60	3.56	2.36	12.18	80.64	2.93
7312	52.7	11.28	6.94	2.69	2.56	3.76	8.03	71.15	3.25

(1) ALC = coefficient of alcalinity
(2) Yield = extraction sugar.
(3) MS = molasses was measured according to Reinefeld *et al.*1974.
Technological characters are measured by Betalyser.

Fig. 1. Root variability in landraces 7215 and 7217

Multiplication

Each accession is planted in a 10 m-long plot of 3 rows and thinned to 18-20 cm in the row in early May. This provides between 150-200 roots per accession. Originally, collections do not have sufficient seed for the next evaluations, therefore seed increase is essential to maintain the genetic variability of the parent population. For this reason the harvested roots are overwintered in suitable silos according to the traditional two-year cycle system. In spring the damaged roots were discarded and the healthy roots were transplanted in the isolation plots, separated by screens of tightly woven fabric before flowering, with proper distances apart to prevent pollen contamination. There was a wide variation in the quality of the seed produced, maybe due to the wide genetic variability of the germplasm multiplied.

Each year multiplication was conducted for about 25 accessions depending on facilities and possibilities. The multiplied accessions are available for evaluation of resistance/tolerance to biotic and abiotic stresses. It is strongly recommended that this programme be continued, as it not only provides seed for evaluation purposes but also replenishes seed as it is used.

In situ conservation of *Beta lomatogona*

The wild beet species *Beta lomatogona* Fisher & Meyer (*Beta* section *Corollinae*) is native to Ardabil (Iran). Hobenacker (1838) detected the species in the Talysch Mountains at Tatuni. Buttler (1977) considered *B. lomatogona* as a model plant for the Irano-Turanian flora because the limits of distribution of this wild beet species are almost congruent with the oriental Turanian geobotanical area. This species has its main distribution area in Turkey. Its abundance decreases from eastern Turkey to northwestern Iran and Azerbaijan.

B. lomatogona used to grow among different field crops, in pastures and alongside streams and orchards in Ardabil. Due to severe drought, land management changes and overgrazing, populations of this species have suffered badly, so that the collecting mission could not find any plant of this species in 1999. In fact, the population size of *B. lomatogona,* surveyed several times in the past few years, is apparently decreasing in a number of localities, suggesting the need for protection of this natural reservoir of potentially useful traits. The collecting mission drew attention to this and strongly suggested establishing *in situ* conservation to rescue this wild beet (Frese *et al.* 2001). SBSI agreed to establish *in situ* conservation in Ardabil Research Station.

The pericarp caps of fruit balls of *B. lomatogona,* collected in Gardeh, were removed manually and sown in April 2000 in the greenhouse in Karadj in one-litre pots filled with sterile soil. Some seeds did not germinate due to damage during cap removal. Seedlings were maintained in the greenhouse until reaching a well-developed stage. 150 plants were transported to the research station of Ardabil in 2001 and transplanted to the prepared plot. These plants survived the winter conditions of Ardabil. Seed stalks appeared in late May and seeds were harvested in bulk in August 2002. The plants are kept in the research station of Ardabil.

Reference

IBPGR/CGN. 1991. Descriptors for *Beta*. International Board for Plant Genetic Resources, Rome/Centre for Genetic Resources, The Netherlands.

Reinefeld, E., A. Emmerich, G. Baumgarten, C. Winner and U. Beiss. 1974. Zur Voraussage des Melassezuckers aus Rübenanalysen [Prediction of molasses sugar from beet analysis]. Zucker 27:2-15.

Current status of Beta *genetic resources in Lithuania* [12]

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Four institutions are responsible for the national *Beta* collection in Lithuania:

- Lithuanian Institute of Agriculture (LIA, Akademija) (long-term storage),
- Lithuanian Institute of Horticulture (LIH, Babtai),
- UAB Agrofirma "Sėklos" (headquarters in Vilnius, breeding laboratory in Akademija), and
- UAB "NATURlitA" (headquarters in Babtai).

The long-term storage collection currently contains 9 accessions of red beet (all Lithuanian varieties and 3 new stable breeders' lines) and 7 accessions of fodder beet (Bartkaitė 2000).

The working collection of red beet (*Beta vulgaris* var. *conditiva* Alef.) is maintained at LIH. Since 1999 it has been enriched with more than 40 accessions. The red beet accessions maintained in the working collections include breeders' lines (characterized by high yield, earliness and bigermity) and foreign varieties (as donors of earliness, root type, monogermity, etc). The accession of a red beet landrace collected in 1996 near Vilnius in the village of 40 Totoriu was found to be a valuable donor of bolting and disease resistance (Petronienė 1998).

Since 2001 the collection, evaluation and utilization of genetic resources of sugar and fodder beets are based at the UAB Agrofirma "Sėklos" (Breeding Laboratory in Akademija). This company is also responsible for pre-breeding work, breeding activities and primary seed production of the registered Lithuanian fodder beet varieties and landraces.

In 2000 the working collection of fodder and sugar beets included 30 accessions. In 2001 the collection contained the same number of accessions. 17 accessions were obtained from VIR. In 2002 the collection consisted of 26 accessions (including 5 of sugar beet with CMS) for further selection and use in the breeding process.

Since 2004 evaluation and utilization of genetic resources of sugar and fodder beets are based at the UAB "NATURlitA".

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[12] (updated November 2004)

The Beta *Collection in the Nordic Gene Bank*

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The Nordic Gene Bank (NGB) was established in 1979 as a joint effort to conserve the germplasm from the five participating countries on a regional basis rather than five parallel collections. This must be seen in the light of Nordic collaboration that has existed for centuries. Particularly during the last 150 years, during which commercial seed production and plant breeding developed, much exchange took place. The material in the NGB is only "Nordic" material.

NGB is organized as an institute under the auspices of the Nordic Council of Ministers, which is an intergovernmental organization between Denmark, Finland, Iceland, Norway and Sweden. The NGB is located in Alnarp in Scania, in the southern part of Sweden, on a campus of the Swedish Agricultural University. The Scandinavian region is the home for two important sugar beet breeding companies: Danisco in Denmark and Syngenta in Sweden.

The NGB mandate species of *Beta vulgaris* L. (Chenopodiaceae) material include

Beta vulgaris subsp. *cicla*	Swiss chard
Beta vulgaris subsp. *maritima*	wild beet
Beta vulgaris var. *alba*	fodder beet
Beta vulgaris var. *altissima*	sugar beet
Beta vulgaris var. *conditiva*	Beetroot

The work with the germplasm is organized in inter-Nordic working groups (WG). The responsible groups for *Beta* are the WG for Root crops and the WG for Vegetables.

Sugar beet is a mandate crop of NGB. However, for historical reasons, the sugar beet breeders have preferred to submit their material to the Genebank of the Federal Centre for Breeding Research on Cultivated Plants (BAZ collection). The International *Beta* Database (IDBB) contains 272 accessions of Nordic origin of which only 29 entries come from NGB. Here we may find accessions to be repatriated.

The NGB collection comprises 60 accessions accepted for long-term conservation. Table 1 shows that beet material has only been collected from Denmark and Sweden because in these two countries the cultivation has been established.

Table 1. Country of origin of *Beta* material in the Nordic Gene Bank

	Denmark	Sweden	Norway	Iceland	Finland
Beta vulgaris subsp. *cicla*	2	-	-	-	-
Beta vulgaris subsp. *maritime*	-	-	-	-	-
Beta vulgaris var. *alba*	28	8	-	-	-
Beta vulgaris var. *altissima*	-	-	-	-	-
Beta vulgaris var. *conditiva*	14	8	-	-	-
Total	**44**	**16**	**0**	**0**	**0**

Table 2 shows that the NGB collection also contains some wild beets from Denmark and some from southern Sweden will be collected this season. The region is located on the northern limit of the extension of wild beets. Presently, a diversity study among these populations is carried out to identify key populations for *in situ* conservation. This study is

carried out in collaboration with the Risø Research Centre in Denmark. Table 2 also shows the responsibility for the accessions in storage.

Table 2. Conservation status of *Beta* material in the Nordic Gene Bank

	Accept	Pending	Temporary	Reject
Beta vulgaris subsp. *cicla*	2	-	-	-
Beta vulgaris subsp. *maritima*	-	11	-	8
Beta vulgaris var. *alba*	36	1	5	-
Beta vulgaris var. *altissima*	-	-	-	-
Beta vulgaris var. *conditiva*	22	-	20	-
Total	**60**	**12**	**25**	**8**

Table 3 shows the distribution of the material according to the accession type.

Table 3. Accession types of *Beta* material in the Nordic Gene Bank

	Cultivars	Landraces	Breeding material	Wild relatives
Beta vulgaris subsp. *cicla* var. *cicla*	4	-	-	-
Beta vulgaris subsp. *maritima*	-	-	-	11
Beta vulgaris var. *alba*	41	-	-	-
Beta vulgaris var. *altissima*	4	-	-	-
Beta vulgaris var. *conditiva*	42	-	6	-
Total	91	0	6	11

Storage

The NGB accessions are stored in the base collection and the active collection at -20°C after drying to 5-7% moisture content (FAO/IPGRI 1994). The safety storage is subject to natural conditions at -4°C. Generally, we store 4000 viable seeds in the base collection, 10 000 in the active collection and 500 in the safety store. After 15 years' storage seed germination in the safety storage ranges between 75% and 94%. Viability tests are performed after 10 years and regeneration is initiated when germination drops below 70%.

Characterization

The official descriptions of the material are available for most of our material and 40 accessions of fodder beets have been characterized using isozymes.

Documentation and availability

All our material can be found on the NGB homepage (www.ngb.se). The characterization data have not been fully published yet. The material in the NGB is presently available without any restrictions to *bona fida* users. In the future we will adapt to international legislation.

Reference

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The Beta *collection in Poland*

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The *Beta* collection in Poland is located in the Research Division Bydgoszcz of the Plant Breeding and Acclimatization Institute (headquarters in Radzików). This collection is a unit of the National Centre for Plant Genetic Resources (NCPGR), based in Radzików, which coordinates, finances and provides storage facilities for crop genetic resources in Poland.

The *Beta* collection consists of wild species, old varieties, breeding material and cultivated beets from Poland and from abroad. The material received from international expeditions and local populations is also of great interest.

The collection contains 300 accessions: 112 of sugar beet, 156 of fodder beet and 32 wild forms belonging to sections *Beta*, *Corollinae* and *Procumbentes.* Species of the *Corollinae* section (perennial species) grow in the field. Male-sterile ecotypes of subsp. *maritima* are kept and regenerated in *in vitro* cultures.

The main aim of the conserved beet materials is to save the genepool from old multigerm cultivars because of the use of hybridization methods based on CMS lines which led to the narrowing of the genetic background in the new cultivars. Wild species of the genus *Beta* and local populations are also important as a source of resistance to diseases, pests and abiotic factors.

Evaluation is conducted according to the "Descriptors for *Beta*" (IPGRI 1996). Evaluation for agricultural characters is carried out at the Experimental Station in Konczewice, on 10 m^2-plots in two replications with standard check varieties, over a 2-year cycle. Evaluation for morphological and cytological characters, seed quality and seed germination tests are carried out in Bydgoszcz.

Passport characterization and evaluation data are documented and stored in our collection and sent to the NCPGR in Radzików. Part of the data is sent to the International Database for *Beta*. Each year about 25 accessions are evaluated and statistical data analyzed and documented.

For several years some of the accessions have been evaluated for two economically important beet diseases: *Aphanomyces cochlioides* Drechsler and *Cercospora beticola* Sacc. in *in vitro* tests, using a modified version of the method of Stähle-Csech and Gisi (1991).

There are no wild beets, local populations or landraces in natural habitats in Poland.

Seed is multiplied when the seed amount available from expeditions or other sources is insufficient. Seed multiplication is carried out in field conditions under strict isolation.

Our *Beta* collection is conserved in the Long-Term Storage Laboratory in Radzików as seed samples kept in glass jars at -15°C and 5-8% moisture content. Some of the accessions are stored in Bydgoszcz in medium-term storage (0-4°C) as a working collection.

Last year some of the beet accessions stored during the period 1981-1991 were evaluated for seed viability (germination test according to ISTA rules). All tested materials revealed good germination and therefore need no multiplication.

Information and seed samples are distributed freely. A quarantine certificate is necessary to send samples abroad.

The collected and evaluated germplasm is used in sugar and fodder beet breeding and in several research programmes.

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Beta *genetic resources in Romania*

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The Romanian *Beta* germplasm collection is held by the breeding departments of the four research institutions that carry out sugar beet and fodder beet breeding: the Research Institute for Potato and Sugar Beet in Braşov, Sugar Beet Research Station in Roman, Beet Breeding Laboratory in Fundulea and Agricultural Research Station in Lovrin. Most of the germplasm is conserved in working collections while a small part is kept as safety-duplicates at the Suceava Gene Bank, under medium- and long-term storage conditions.

The *Beta* germplasm collection consists of:

- indigenous and foreign sugar beet (monogerm and multigerm varieties)
- breeding materials (diploid and tetraploid monogerms and multigerms)
- indigenous and foreign fodder beet varieties
- breeding material of fodder beet
- indigenous and foreign varieties of garden beet
- wild species.

Only two wild species are found *in situ*: *Beta vulgaris* subsp. *maritima* L. (annual) and *Beta trigyna* Wald (perennial). There are also landraces of garden beet and fodder beet in farmers' gardens in the hills.

Table 1 gives the composition of the collection, currently containing 858 accessions.

Table 1. Composition of the *Beta* collection maintained in Romania

Taxa		No. of accessions
Beta vulgaris subsp. *maritime*		1
Beta vulgaris subsp. *rapacea*		2
Beta vulgaris subsp. *vulgaris* var. *cycea*		1
Beta vulgaris subsp. *vulgaris* var. *altissima*		1
Beta vulgaris subsp. *vulgaris* var. *saccharifera*		
Indigenous multigerm sugar beet varieties		7
Indigenous monogerm sugar beet varieties		6
Foreign monogerm sugar beet varieties		30
Breeding sugar beet material:	2x multigerm	123
	4x multigerm	132
	2x monogerm	246
	4x monogerm	88
Landraces		36
Indigenous fodder beet varieties		4
Foreign fodder beet varieties		23
Breeding fodder beet material:	2x multigerm	87
	4x multigerm	68
Garden beet varieties		3
Total		**858**

The "short-term" collection is conserved as seeds in breeding centres where morphological, physiological and biochemical studies and evaluations are conducted.

The characterization descriptors (morphological and physiological) are based on measurements and observations made on 10 plants per accession, from which the average is calculated (for instance the length of the leaf or of the petiole).

Biochemical descriptors are used for the secondary evaluation and are determined by the specialists of the breeding centres. For instance, the sugar content is determined polarimetrically in laboratories; a minimum of 10 roots per accession is analyzed and the average is calculated.

The seeds of each accession in the collection are processed, shelled and dried before being stored. Each accession contains a minimum of 1000 seeds.

The existing germplasm sources are used for:

- maintenance of the gene stocks;
- creation of resistant genitors, especially to *Cercospora beticola* and *Rhizomania*;
- creation of new highly productive varieties, with high sugar content and high juice purity.

Because the germplasm collection holders do not have appropriate conditions for long-term seed storage, after the accessions have been stored for 4-5 years, the germination is reduced and there is a need for regenerating 20% of the collection each year. In practice 60-70 accessions are multiplied each year, but this number is not sufficient.

For the moment, we do not have the necessary financial support for the *Beta* germplasm resources programme and it is very difficult to evaluate and characterize these resources, because the research institute and station owning this germplasm do not have adequate resources.

There is no standardized national database on *Beta* because each holder has evaluated its own breeding material according to its own priority objectives and the descriptors used differ according to these objectives.

We have not used isoenzymes or AFLP markers to identify different accessions of sugar beet, fodder beet, garden beet or wild beet.

Breeding for disease resistance is one of the major objectives, especially for *Cercospora beticola* and *Rhizomania*. Breeding lines and hybrids combining tolerance to *Cercospora* and *Rhizomania* have been selected through screening in heavily infested fields.

We try to select germplasm that is tolerant to drought and scorching heat, because in the south of Romania summers are very hot and dry.

The planned expansion of the *Beta* germplasm collection has the following objectives:

- acquisition of newly registered varieties;
- evaluation of the germplasm collection and conservation of a duplicate collection in medium- or long-term conditions in the Suceava Gene Bank;
- collecting of leaf beet and garden beet germplasm from the farmers' vegetable gardens;
- collecting of fodder beet germplasm from the farmers' fields and gardens in the hilly part of the country;
- collecting of wild species in the southern part of the country.

The purpose of the collection is to preserve valuable gene stocks and making valuable germplasm sources available to breeders to achieve their specific aims.

Current status of the Beta *collection in Russia*

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The collection

Beta genetic resources activities in Russia started in 1924 with N.I.. Vavilov's collecting missions. At present, the VIR *Beta* collection contains 2882 accessions, including 1602 accessions in the basic catalogue and 1380 accessions in the temporary catalogue. The material includes 10 groups of accession types collected all over the world, except tropical countries (Table 1).

Table 1. Structure of the VIR *Beta* collection (2002)

Type of accessions	No. of accessions
Wild species (accessions)	13 (51)
Primitive forms	136
Landraces	911
Breeding cultivars	1444
Hybrids	272
Mutant forms	2
Self-pollinated lines	11
Accessions with marker character	3
Genetic sources with identified genes	134
Donors	5
Total	**2882**

Basic research trends include enrichment of the collection, evaluation, multiplication and utilization of the accessions in breeding.

Characterization and evaluation

Most of the accessions have been characterized for 24 morphological characters according to the international *Beta* descriptor list and evaluated for main commercial traits. Characterization and evaluation of the collection have been carried out at three experiment stations, situated in different geographical zones of the country. Evaluation of the accessions is carried out for three years; the obtained data are then compared to estimate the accessions' ecogeographic variability and determine their genetic potential. The level of genetic evaluation of the *Beta* collection is presented in Table 2; the most important breeding characters are "growth type" (annual, biennial, etc.) and variations in the reproductive system (self-incompatibility, cytoplasmic male sterility, monogermicity, etc.). The genetic collection includes 200 accessions: 54 of table beet, 24 of fodder beet and 122 of sugar beet. Evaluation of the genepools has helped selecting and identifying four donors of the most important characters: monogermicity, bolting resistance and resistance to diseases. These experimental data are very important for effective and objective utilization of initial breeding materials.

Table 2. The *Beta* genetic collection of VIR

Gene	Character	No. of accessions	Country
RR	anthocyanin colour hypocotyls and root	3	The Netherlands, Denmark, Russia
Bl	black skin of root	1	France
Rg	white colour skin of root	5	Iran, Russia, Germany, Italy, Canada
Vi	green hypocotyls and leaf rosette	10	Russia, Georgia, USA, United Kingdom, Canada
nn	dwarfish leaf rosette	2	United Kingdom, USA
l_1l_2	flat root shape	3	France, Germany
Ll	rounded root shape	2	Russia, Byelorussia
L_1L_2	long root shape	14	France, The Netherlands, United Kingdom, Russia, Georgia, Australia, Yugoslavia
Mm	monogermicity	61	Russia, Ukraine, Finland, France, The Netherlands, United Kingdom, Denmark, Sweden, Canada, Poland, Belarus, Kyrgyzstan, Lithuania, Moldova
NbNb	bolting resistance	8	Russia, USA, The Netherlands, Tanzania, Denmark
Sxxzz	CMS type	17	Russia, Germany, United Kingdom, USA, Italy, Japan
Nxxzz	O type	16	Russia, Germany, United Kingdom, Italy, Japan
a_1a_1	GMS	1	Ukraine
Sf	self-fertility	6	USA, Sweden, Italy
C	curly leaf resistance	2	Canada, Germany
4n(4x)	tetraploid	42	Russia, Lithuania, Ukraine, Belarus, Hungary, Denmark, The Netherlands, Germany, Austria, Hungary, Moldova

Documentation

At present, VIR's *Beta* databases consist of the passport and conservation data. Characterization and evaluation data are recorded in workbooks and special cards, and need to be computerized. The results of tests for resistance to black root (258 accessions) and bolting resistance (535 acc.) are published in special catalogues.

Utilization and availability

Utilization of the collection materials is determined by the main trends of breeding. Every year about 200 accessions are distributed to Russian research institutes, national breeding centres, foreign genebanks and breeders. Requests of the foreign users are fulfilled according to the availability of accessions. Availability of the materials depends on the seed quantity and the type of accessions. Small seed samples, new breeding lines, donors of most important commercial traits are limited for distribution.

Regeneration and multiplication

Regeneration of the beet accessions is carried out when seed viability decreases to 50-60%, and multiplication when the seed stock is below 1000 seeds.

The collection materials are regenerated at five experiment stations situated in different ecogeographical zones within the country. They regenerate 585 accessions every year.

Isolation cabins and houses, spatial isolation and individual isolation are used for the multiplication of *Beta* accessions.

Storage

At present, the base collection is preserved in medium-term storage at +4°C in the National Seed Storage at the Kuban experiment station (Krasnodar region) and for long-term storage at –10°C in the VIR genebank.

The active collection is stored at room temperature in St. Petersburg at the Department of Vegetable and Cucurbits crops. The duplicate active collection is placed for storage at +4°C in a special room.

Seed samples for long-term storage are dried until seed moisture content of 2-6% is reached and packed in laminated aluminium bags.

Seed viability monitoring of the working and active collection is carried out when necessary; for the base collection, after 10 years of storage.

Collecting activities

Three collecting missions were organized in Russia in 1996-2002: Altai region (southwestern Siberia), Mordovia, Voronezh, Tambov and Lipetsk provinces (Central Chernozem zone). A total of 28 samples of beet accessions were collected, including 17 samples of sugar beet, 10 of table beet, and 1 of fodder beet.

Activities planned for the future

- Multiplication of collected accessions for long-term storage at -10°C;
- Screening of the collection and identification of genetic sources of the most important characters;
- Creation of evaluation databases;
- Collecting and exchange.

The Beta *collection in Slovenia*

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Introduction

Slovenia belongs to the Mediterranean and European centres of diversity. Slovenia can be considered as a gene centre for some Brassicaceae (cabbage, turnip), Alliaceae (onion, garlic), Asteraceae (lettuce, chicory), Valerianaceae (corn lettuce) and some fruit and grapevine species, grasses, clovers, medicinal and aromatic plants. In the wild we can find relatives of crop plants like *Mycelis muralis, Lactuca serriola* and *Cichorium intybus* that are species of the Asteraceae. Due to extensive grassland area in Slovenia, many different ecotypes of grasses and clovers are found. In addition many landraces appear in crops which were introduced more than a century ago from other parts of the world. From America, maize, beans and potato were spread at the time of the Austro-Hungarian Monarchy. In different ecological conditions of Slovenia, farmers selected many different populations adapted to less favourable growing conditions.

Early projects to collect Slovenian autochthonous populations, ecotypes and landraces of agricultural species with the goal of breeding new and improved cultivars were initiated about 40 years ago. In the former Yugoslavia during the late 1980s a programme was started to collect plant genetic resources for the Yugoslav genebank. After the independence of Slovenia, the Slovenian Ministry of Science and Technology financed the genebank of vegetables, potato, fodder plants, grasses, clovers, small fruits and grapevine from 1992-1994. In 1996 the Ministry of Agriculture, Forestry and Food started financing the Slovene Plant Gene Bank Programme with the goal to maintain, evaluate, regenerate and preserve Slovenian autochthonous species, ecotypes, populations and landraces of agricultural, medicinal and aromatic plants, forest trees and other woody plants from Slovenian forests. They include Slovenian cultivars, old cultivars, landraces, various populations, clones and lines bred from autochthonous plants and ecotypes from the natural habitat important for food, agriculture and forestry (Černe *et al.* 1998).

The *Beta* collection

The germplasm collection at the Agricultural Institute of Slovenia is one of the three working collections within the Slovene genebank system. It maintains a fairly large *ex situ* collection of vegetables, winter wheat, grasses and clovers, fodder crops, small fruit, grapevine and grain legumes. The *Beta* collection is part of the fodder and vegetable crops and consists of 46 accessions (Table 1).

Table 1. The *Beta* collection at the Agricultural Institute of Slovenia

Species	No. of accessions
Beta *maritima*	2
Beta *vulgaris var. rapacea* (fodder beet)	9
Beta vulgaris var. *altissima* (sugar beet)	18
Beta vulgaris var. *conditiva* (red beet)	12
Beta vulgaris var. *cicla* (mangold)	5
Total	**46**

Seed samples and passport data were obtained with the help of local elementary and agricultural schools, the Agricultural Advisory Service, newspaper ads, seed companies and farmers. Most of the people who sent us samples filled out a questionnaire which provided

necessary data and some additional information on local names and growing practices. All accessions were inspected, sorted and numbered. Efforts are being continued for the broadening of the *Beta* collection with fodder and wild species.

Documentation

The Agronomy Department of the Biotechnical Faculty, University of Ljubljana, the Agricultural Institute of Slovenia, the Institute of Hop Research and Brewing and the Slovenian Forestry Institute form the Slovenian Plant Gene Bank (SPGB) and work with species used in agriculture, forestry and for food. These institutions are responsible for *ex situ* germplasm collections stored in the form of seeds, *in vitro* and *in vivo* collections. Recently an initiative was taken up to establish an information and database management system for the Slovenian Gene Bank. Each institution holds a database for its working collection. With a need for a uniform and centralized documentation and information system, a computer program was used (Žitnik *et al.* 2000) to unite the four separate databases. This will enable easier and faster access to the complete information for all users, better management of germplasm resources in the Central Plant Gene Bank and exchange of information with other ECP/GR and EUFORGEN genebank databases. *Beta* accessions are documented for IPGRI minimum passport descriptors.

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Beta *genetic resources activities in Turkey*

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Introduction

Turkey is one of the centres of origin for beet (*Beta*). Species of section *Beta* and section *Corollinae* are widely distributed in Turkey (Tan 1992).

Species of section *Beta* are *B. vulgaris* subsp. *adanensis, B. vulgaris* subsp. *maritima, B. vulgaris* subsp. *maritima* var. *trojona, B. vulgaris* subsp. *provulgaris.* They are found from sea level to 700 m asl, mainly in coastal areas and some inland habitats influenced from littoral regions. They can be found on field borders and roadsides as secondary habitat and seashores as primary habitat.

Species of section *Corollinae* are *B. macrorhiza*, *B. lomatogona*, *B. intermedia*, *B. trigyna*, and *B. corolliflora.* They are found inland from 550 to 2300 m asl. Their habitats are mountainous areas, vegetation of woody perennials (mainly *Quercus* woodlands), field borders and roadsides.

Leaf beet and beet root landraces are also grown by farmers and in vegetable gardens.

Beta species in Turkey show continuous variation in most of the characteristics resulting from the gene flows between wild and cultivated forms (Ford-Lloyd and Williams 1975; Buttler 1977; Tan 1982; Ford-Lloyd 1991; Letschert 1993; Tan 1993; Doney *et al*. 1995). Different races for different uses are found. The diverse forms and landraces of vegetable, table and fodder beets have been grown and used locally for generations in Anatolia.

Beta genetic resources activities

Beta genetic resources activities are conducted within the framework of the National Plant Genetic Resources Conservation Programme (NPGRRP) of Turkey. The objective of NPGRRP is the exploration, collecting, conservation (both *ex situ* and *in situ*) and evaluation of existing plant genetic resources and plant diversity of Turkey for today and the future. The Aegean Agricultural Research Institute (AARI) has been designated as Coordination Centre for the National Programme (Tan 1992, 1998; Firat and Tan 1995).

Survey and collecting

Surveying and collecting of Beet (*Beta*) species were systematically initiated in the late 1960s in various parts of Turkey. The first step in beet genetic resources activities is collecting - sampling the maximum variation and determination of the interspecific, agroecological and phytogeographical distribution of *Beta* species. While planning the collecting missions, data of former surveys and expeditions are compiled and priorities regarding locations and *Beta* species are considered to avoid duplication of efforts. The missions are programmed each year to collect the existing *Beta* genetic resources within the framework of the Industrial Crops Genetic Resources Group. The collections of landraces, wild relatives, weedy and cultivated forms, landraces, old cultivars, local primitive varieties are considered in the group for *ex situ* conservation. The distribution and habitats of the species found in Turkey were revised (Tan 1992). Herbarium samples are also collected during the survey to maintain the specimens at AARI herbarium as the reference of the beet collection and for further identification.

Since the 1960s 445 beet samples have been collected and stored at the AARI National Genebank. These are listed in Table 1.

Table 1. The AARI *Beta* collection

Species	No. of accessions
B. adanensis	16
B. corolliflora	26
B. intermedia	58
B. lomatogona	91
B. macrorhiza	6
B. maritime	37
B. trigyna	11
B. trojona	17
B. vulgaris	123
B. vulgaris altissima	7
B. vulgaris cicla	52
B. vulgaris crassa	1
Total	**445**

Ex situ conservation

Ex situ conservation activities have been undertaken since 1964 and are still continuing within the framework of NPGRRP. *Ex situ* conservation is implemented in seed genebanks and field genebanks. The national collection consists of landraces and wild and weedy relatives (both as seed and vegetative collections). The main users of the material are the plant breeders and researchers from both Turkey and abroad. The storage facilities of the AARI Gene Bank have been designed for the needs of long-term (-18°C) and medium-term storage (0°C) for both base and active collections, respectively (Tan 1992). For temporary storage aluminium laminated foils are used. All the conditions in the genebank comply with internationally recommended standards. For the safety-duplicates of the base collection other storage facilities are available in Ankara at the Central Research Institute for Field Crops (CRIFC).

The beet collections are part of the National Plant Genetic Resources Collection. Therefore all beet accessions are maintained according to the same procedure as other materials.

In situ conservation

Three projects were initiated to conserve the priority species *in situ*. These projects are directly or indirectly related to *in situ* conservation of beet species. They are summarized below:

- ***In situ* conservation of wild species:** *in situ* conservation activities began in 1993. The "*In Situ* Conservation of Genetic Project" of Turkey aims to maintain the wild crop genetic resources in their natural habitats. This project considers both woody and non-woody crop relatives with an integrated multi-species and multi-site approach (Firat and Tan 1995). This has been done through conducting ecogeographical surveys and inventories to provide a basis for establishment of *in situ* Gene Management Zones (GMZs) in selected pilot areas that are rich in target crop wild relatives. The project has initiated and developed a mechanism to foster the ongoing National Plant Genetic Resources Research Programme for identifying, designating and managing the areas specifically for *in situ* conservation of nationally and globally significant wild crop relatives which originated in Turkey (Tan 1998). The project also aims at integrating *in situ* conservation complementary with the existing *ex situ* conservation programme of Turkey. The highest priorities have been given to globally significant non-woody crop species, which are in the first genepool of cereals as well as important woody species and selected forest species. Although priority has not been given to *Beta* species, some of the *Beta* species which have been found in the GMZs as associated species of target plants will be

conserved *in situ*. Beets have also been included in the priority list of the National Plan for *in situ* conservation.

- ***In situ* (on-farm) conservation of landraces:** Turkey has initiated a project on "*In Situ* on-farm conservation of landraces from the transitional zone in Turkey" in 1999. This project is involved in the *in situ* (on-farm) conservation of local crops, cultivars (or landraces) with active participation of farmers. Socioeconomic and ecogeographical surveys were conducted in the northwestern transitional zone adjacent to northwestern Black Sea, northeastern Aegean and central Anatolian Regions to determine the distribution of landraces and the socioeconomic status of landraces cultivation. A database of the information compiled from the surveys has been established. During the surveys, existing landraces have been collected and maintained *ex situ* which will be complementary to *in situ* (on-farm) conservation. Landrace(s) of hulled wheat, bean, chickpea and lentil were selected as target species and agromorphological variation analyses were conducted. The candidate Gene Management Zones (GMZs) were determined for the possibility of *in situ* (on-farm) conservation of target species. Data compiled from surveys and genetic analysis has been analyzed using Geographical Information Systems (GIS); maps are prepared to better understand ecogeographic and agromorphological variation of targeted landraces throughout the region. Since beet landraces are cultivated in the region where the project was conducted, the inventory of beet landraces was also identified within the framework of the project.

- **Ecosystem conservation and management for threatened plant species:** the overall objective of this project is the conservation and management of wetlands of steppe ecosystems, which are important plant areas (IPAs) for endangered herbaceous plant species listed in Appendix I of the Bern Convention. *Beta adanensis* is one of the listed species. Therefore this endemic wild beet species is one of the target species for conservation and management for sustainable protection. This project started in 2000 to initiate a collaborative work between the Ministry of Environment (MOE) and Ministry of Agriculture and Rural Affairs (MARA) and the Turkish NGO "Association for the Conservation of Nature" (member of the World Conservation Union, IUCN) for conservation and management of wetlands of steppe ecosystems. Goals to achieve the overall objectives mentioned above are: a) identification of IPAs in the project area, b) data management, c) raising awareness and public participation, d) managing the designated IPAs for sustainable use by management plan, d) monitoring the selected areas.

Multiplication and/or regeneration

The multiplication and regeneration procedures are similar for all Turkish collections. The regeneration of beet genetic resources collections is undertaken when the viability has dropped below 80%. Multiplication of the accessions is carried out when the quantity of the accessions decreases to a certain level. The multiplication or regeneration sites are chosen, wherever possible, according to similarity of ecology to those of the sites from which the accessions were originally collected. To avoid contamination (gene flow) the breeding system and reproductive biology of the species are taken into account during the multiplication/regeneration of accessions. Eighty percent of total *Beta* accessions have already been multiplied/regenerated.

Evaluation and characterization

Characterization/evaluation programmes are conducted within the framework of NPGRRP. The data resulting from evaluation carried out by users of the samples are returned if the evaluation and/or characterization work are planned in cooperation within the NPGRRP. An annual report of the characterization/evaluation project provides the results. If the material is distributed to external users, they are requested to provide feedback information to AARI when the research is completed. For the effective and intensive use of genetic resources collections by the breeding programmes, NPGRRP usually cooperate with evaluation/characterization programmes aiming at using this valuable material for breeding.

Characterization and evaluation activities started in the late 1980s for beet species. The IBPGR/IPGRI descriptors (IBPGR/CGN 1991) are used with some modifications. The *Beta* and *Corollinae* sections' samples collected from Turkey were evaluated for 23 characters and were interpreted with Principal Component Analysis (PCA). Samples of the sections *Beta* and *Corollinae* were evaluated and grouped according to the observed characters. The research was supported with meiotic chromosomal behaviour studies on the broadly variable samples. Among section *Beta*, continuous variation was observed in pigmentation, hairiness, plant habit, flowering, flower and seed clusters, pollen fertility and leaf types, whereas the C*orollinae* section samples exhibited broad variation in flower and leaf characteristics. Two groups of wild and cultivated types were observed in section *Beta* samples by PCA analysis. The wild type group consisted of *B. maritima, B. trojona* and *B. adanensis*. The section *Corollinae* samples were grouped with the *Beta lomotogona* complex, which consists of *B. lomatogona*, *B. intermedia, B. trigyna*, *B. corolliflora* and *B. macrorhiza*. Both sections were grouped as species complex, not at species level (Tan *et al*. 2000).

Another project, started in 2001, deals with the "Determination of isozyme variation of beet collection". Its goal is to identify the isozyme variation, compare the isozyme and morphological variation and interpret this comparison in order to establish a core collection of beet accessions.

Documentation

Documentation is one of the main functions of the NPGRRP for both *ex situ* and *in situ* activities. A Database Management System exists for documentation of both *ex situ* and *in situ* conservation information. Since the *in situ* conservation programme is complementary to *ex situ* conservation, the two databases are linked and complementary to each other. The Geographic Information System (GIS) is available to evaluate the quantitative and spatial data gathered especially from survey and inventory activities. *Beta* genetic resources data from survey, collecting and characterization activities are documented in the central NPGRRP Database Management System (Tan and Tan 1998a, 1998b).

Future activities

The Black Sea coast and Thrace (European part of Turkey) regions will be explored to collect the existing wild species and landraces. Multiplication/regeneration and documentation are the routine activities for beet collection, to be continued in the near future. Further evaluation will be conducted for old collections which were already characterized. Characterization of the new accessions will be undertaken.

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Beta *genetic resources in Ukraine – Genetic origin and diversity of Crimean wild beet*

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Introduction

Approximately 1 million ha of sugar beets are grown by farmers from year to year for sugar production in the Ukraine. In addition, about 9000 ha are seed production areas that are mainly concentrated in the Black Sea region using direct planting methods and some areas in the Central part using an indirect method of steckling cultivation. All research activities on beet, including a *Beta* germplasm collection, are managed by the Institute for Sugar Beet (ISB). Practical breeding work is carried out by six breeding stations located in different climate zones of Ukraine.

The ISB collection

Beta germplasm research activities in the Ukraine are maintained by the Ukrainian Academy of Agrarian Science (UAAS) as a part of the National Plant Genetic Resources programme. Currently there are more than 361 accessions in the ISB collection that represent 12 species of *Beta*. The largest part consists of 275 *Beta vulgaris* accessions that were added from breeding programmes. Some of them as well as wild *Beta* accessions are being obtained from the collections abroad and breeding companies worldwide. Seeds are packed in airtight foil bags and stored in separate rooms. All accessions are available for distribution. Moreover all Breeding Stations have their own *Beta* germplasm collections with a broad spectrum of accessions obtained from conventional breeding programmes.

Multiplication

The main task of the ISB collection is to provide breeders with a sufficient quality and quantity of seeds. Therefore accessions with low germination capacity or seed number must be multiplied. The work is usually carried out on the experimental plots or greenhouses of Breeding Stations linked to the ISB system. The process of multiplication includes two steps: 1) seed germination and steckling production on experimental plots or in a greenhouse; 2) seed beet cultivation from stecklings in isolation cages.

International cooperation

Until today, Ukraine seemed to be "unknown territory" as regards national *Beta* genetic resources. For example, only one accession of *Beta trigyna* from the Crimean Peninsula is present in the ISB collection and no detailed information is available from scientific literature. A new project started recently within the framework of the European Science Foundation programme "Assessment of the Impacts of Genetically Modified Plants". Both German and Ukrainian scientists examined the potential impact of gene flow from transgenic beet on wild and weed beet populations in Ukraine, a task that started in 2001. Germplasm collection and local wild beet habitat examination have been carried out in the Black Sea region. As a result, the ISB collection increased by new 7 *Beta maritima* and 10 *Beta trigyna* populations from the Crimean Peninsula. Some weed beet infestation has been identified, probably as a result of gene flow between cultivated and wild beet accessions. The

problem has increased during 20 years of conventional sugar beet seed production in Crimea and the Odessa region (Fig. 1).

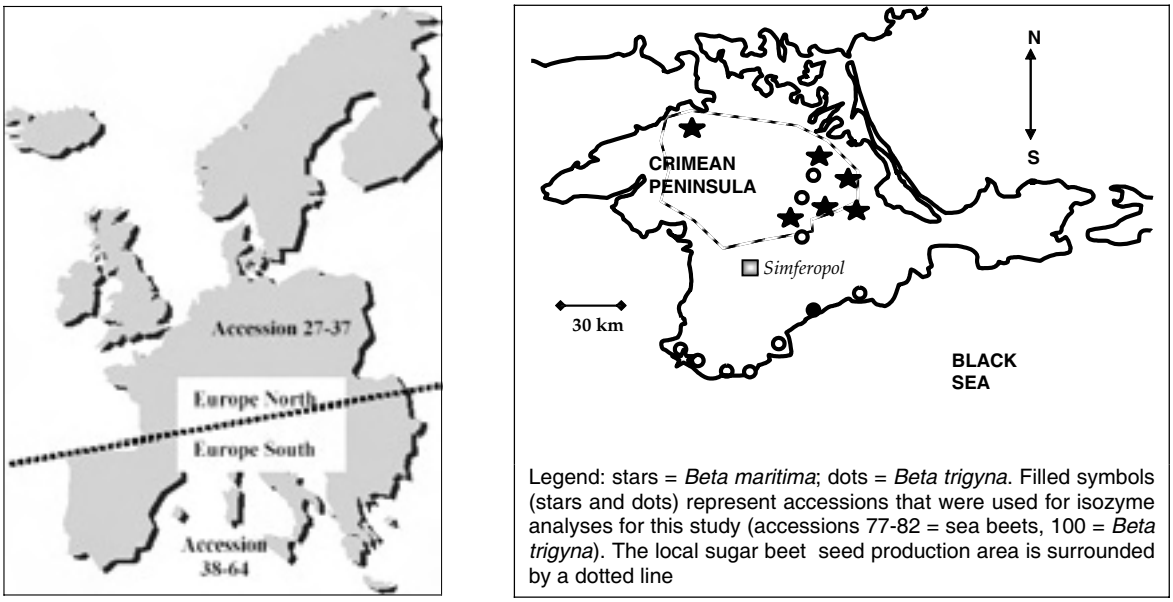

Fig. 1. Geographic origin of sea beet populations examined in this study.

Analyses of genetic origin

Beta vulgaris constitutes a highly variable group, in which it is often difficult to distinguish between cultivated and wild forms (Bartsch and Ellstrand 1999). This is mainly due to the extensive use of sea beet (*B. vulgaris* subsp. *maritima* Arcang.) gene resources in conventional breeding programmes. Sea beet is largely a coastal taxon, with a wide distribution from the Canary and Cape Verde Islands in the west, northward along Europe's Atlantic coast to the North and Baltic Seas. It also extends eastward through the Mediterranean region into Asia where it occurs in Asia Minor, in the central and outer Asiatic steppes, and desert areas as far as western India. Sea beet varies from self-compatible annuals to self-incompatible, iteroparous perennials with a life span between one and more than eight years (Desplanque *et al.* 1999). Cultivated *B. vulgaris*, including Swiss chard, red garden beet and sugar beet, are biennial. The latter is partially self-incompatible due to the extensive use of male sterility genes in sugar beet breeding. All cultivated and wild subspecies of *B. vulgaris* are mostly wind-pollinated, although some insect pollination has been noted.

In our latest study we examined wild beet accessions of Ukrainian origin. Allozyme diversity was assayed on 7 accessions collected in 2001 and compared with other beet accessions (Table 1) according to the methodology of Bartsch and Ellstrand (1999). We found that Crimean wild beets belong to two different taxa: *B. trigyna* and *B. vulgaris* subsp. *maritima* (Fig. 2). The results clearly revealed significantly greater genetic diversity of Ukrainian sea beet accessions in comparison with other European accessions (Fig. 3). Based on the genetic diversity statistics, gene flow measured as N_m within Ukrainian accessions seems to be higher than in other accession groups (Table 2). Gene flow between wild and cultivated accessions is difficult to control and must be minimized in seed production areas. The genetic distance of Ukrainian sea beets is relatively far from European sea beets (Fig. 2). As a first conclusion of our allozyme analysis, Ukrainian wild beet should be regarded as a valuable plant genetic resource. However, more data on the local distribution of wild and weed beet accessions in the Ukraine are necessary in order to support monitoring and conservation programmes.

Table 1. Species and accessions of beet surveyed for comparison of Ukrainian wild beets (**accessions 77 to 82 and 100**) in this study. N_i = number of individuals examined. Underlined accessions are recommended by for standard use (Dr Lee Panella, Fort Collins)

No.	Species	Subspecies	Variety/type	Accession	Origin	Location	N_i
1	*B. vulgaris*	*vulgaris*	Sugar beet	FC172	USA	(Reg. by Hecker and Ruppel, 1986)	15
2				KWS-2N1009	Germany		30
3				KWS-Kavetina	Germany		49
4				KWS-Rizor	Germany		48
5				KWS-246	Italy		39
6				KWS-247	Italy		41
7				Betaseed-4035	California		25
8				Betaseed-4581	California		24
9				Betaseed-4776	California		31
10				Spreckels-HH103	California		29
11				Spreckels-IV2R	California		30
12				Spreckels-NB2	California		34
13				Spreckels-SS781	California		85
14				Spreckels-VB7R	California		26
15				UCR-NB	California	Imperial County, Brawley, field site	70
16				UCR-BB	California	Imperial County, Brawley, field site	61
17	*B. vulgaris*	*vulgaris*	Swiss chard	Dark Green	USA		70
18				Chard Fordhook	USA		21
19				Chard Lucullus	USA		21
20				Chard Rhubarb	USA		39
21	*B. vulgaris*	*vulgaris*	Red beet	GB W300C	USA	(USDA Ft Collins Standard)	32
22				Burpee	USA		78
23				Detroit Dark Red	USA		16
24				Red Ball	USA		25
25				Tall Top	USA		29
26	*B. vulgaris*	*maritima x vulgaris*	Weed beet	RWTH - 7	Germany	Cologne County, Warden	30
27	*B. vulgaris*	*maritima*	Sea beet	PI518310	UK	East Sussex County	48
28			Europe North	PI518398	Ireland	Kerry County, Dingle	37
29				BGRC 54228	Ireland	(Standard)	26
30				RWTH-31	France	Seine-Marit. County, Fecamp	15
32				RWTH-32	France	Cotentin County, Utah Beach	15
32				PI 540575	France	Gironde County, Andernons Bains	21
33				PI 540588	France	Charante Marit. County, Brouage	30
34				HHU	Germany	Oldenburg, Botanical Garden	85
35				RWTH - 5	Germany	Hamburg County, Helgoland	30
36				RWTH - 6	Germany	Lübeck County, Fehmarn	30
37				RWTH - 8	Denmark	Storstrom County, Rodbyhavn	30
38	*B. vulgaris*	*maritima*	Sea beet	RWTH - 9	Portugal	Aveiro County, Aveiro	30
39			Europe South	RWTH – 1	Greece	Chalkidiki	7
40				RWTH – 2	Greece	Crete	21
41				RWTH – 3	Greece	Peleponnes	20
42				RWTH – 011	Italy (NE)	Gorizia County, Grado	10
43				RWTH – 012	Italy (NE)	Udine County, Auso Corno	5
44				RWTH – 013	Italy (NE)	Venice County, Bibione	5
45				RWTH – 014	Italy (NE)	Venice County, Torcello	15
46				RWTH – 015	Italy (NE)	Venice County, San Erasmo	21
47				RWTH – 016	Italy (NE)	Venice County, St. Michele	28
48				RWTH – 017	Italy (NE)	Venice County, Fusina	28
49				RWTH – 018	Italy (NE)	Venice County, Alberoni	9
50				RWTH – 019	Italy (NE)	Venice County, Porto Malamocco	23
51				RWTH – 020	Italy (NE)	Venice County, Pellestrina	42
52				RWTH – 021	Italy (NE)	Venice County, Chioggia	33
53				RWTH – 022	Italy (NE)	Rovigo County, Albarella 5	33
54				RWTH – 023	Italy (NE)	Rovigo County, Albarella 6	9
55				RWTH – 024	Italy (NE)	Rovigo County, Albarella 7	9
56				RWTH – 025	Italy (NE)	Rovigo County, Albarella 9	16
57				RWTH – 026	Italy (NE)	Rovigo County, Porto Levante	27
58				RWTH – 027	Italy (NE)	Rovigo County, Boccasette	23
59				RWTH – 028a	Italy (NE)	Ravenna County, Cervia 1997	57
60				RWTH – 028b	Italy (NE)	Ravenna County, Cervia 1998	92
61				RWTH – 029	Italy (NE)	Ancona County, Numana	27
62				Zayed collection	Egypt	Alexandria	21
63				PI 504266	France	Corsica, Ajaccio	26
64				PI 504172	Italy	Reggio di Calabria County, Palmi	20

Table 1 (cont.). Species and accessions of beet surveyed for comparison of Ukrainian wild beets (**accessions 77 to 82 and 100**) in this study. N_i = number of individuals examined. Underlined accessions are recommended by for standard use (Dr Lee Panella, Fort Collins)

No.	Species	Subspecies	Variety/type	Accession	Origin	Location	N_i
65	*B. vulgaris*	*maritima*	Sea beet	UCR – 01	California	Contra Costa County, Martinez	15
66			USA	UCR – 02	California	Alameda County, Fremont	20
67				UCR – 03	California	S. Clara County 1, Mountain High	20
68				UCR – 04	California	Santa Clara County 2, San Jose	17
69				UCR – 05	California	San Benito County, Hollister	17
70				UCR – 06	California	Los Angeles County, Pomona	25
71				UCR – 07	California	Riverside County, Wildomar	40
72				UCR – 08	California	San Diego County, Chula Vista	25
73				UCR – 09	California	Santa Barbara County, S. Barbara	40
74				UCR –14	California	Marina del Rey	17
75				UCR –15	California	Carpinteria	21
76				UCR –16	California	Irvine	8
77	***B. vulgaris***	***maritima***	**Sea beet**	**RWTH –30**	**Ukraine**	**Chkalovovo Crimean Peninsula**	**18**
78			**Ukraine**	**RWTH –31**	**Ukraine**	**Chapaevka Crimean Peninsula**	**20**
79				**RWTH –32**	**Ukraine**	**Maliy Mayak Crimean Peninsula**	**20**
80				**RWTH –33**	**Ukraine**	**Stepne Crimean Peninsula**	**20**
81				**RWTH –34**	**Ukraine**	**Nekravovka Crimean Peninsula**	**20**
82				**RWTH –35**	**Ukraine**	**Urozhain, Crimean Peninsula**	**20**
83	*B. macrocarpa*		Wild	UCR – 10	California	Imperial County (Introgressed pop.)	158
84			Macrocarpa	UCR – 11	California	Ventura County, Santa Cruz Island	30
85			California	UCR – 12	California	L. Angeles County, Catalina Island	40
86				UCR – 13	California	Imperial County	348
87				PI 546448	California	Imperial County	38
88				PI 546449	California	Imperial County	35
89				PI 546450	California	Imperial County, Imperial	7
90				PI 546454	California	Imperial County, Imperial	13
91				PI 546455	California	Imperial County	35
92				UCR –14	Mexico	Baja California, Rosarito	10
93	*B. macrocarpa*		Wild Macrocarpa	BGRC 53034	Israel	Athlistean Plain	26
94			Mediterranean	BGRC 57644	Cyprus	Larnaca	13
95				BGRC 57664	Spain	Cartagena	70
96				BGRC 57676	Spain	Granada	15
97	*B. webbiana*		Wild Webbiana	PI 564064	unknown		11
98	*B. patellaris*		Wild Patellaris	PI 566900	unknown		10
99	*B. procumbens*		Wild Procumbens	PI 564059	unknown		2
100	***B. trigyna***		**Wild Trigyna**	**RWTH - 36**	**Ukraine**	**Nikita, Crimean Peninsula**	**7**

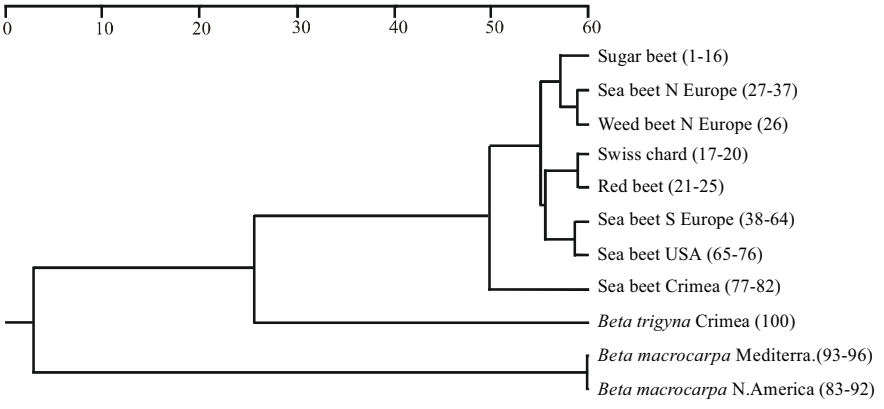

Fig. 2. UPGMA dendrogram of systematic relationships among 11 major groups (with accession number) of wild and cultivated beet based on Nei's (1978) genetic distances derived from allele frequencies at 13 polymorphic allozyme loci (see text for explanations of these designations).

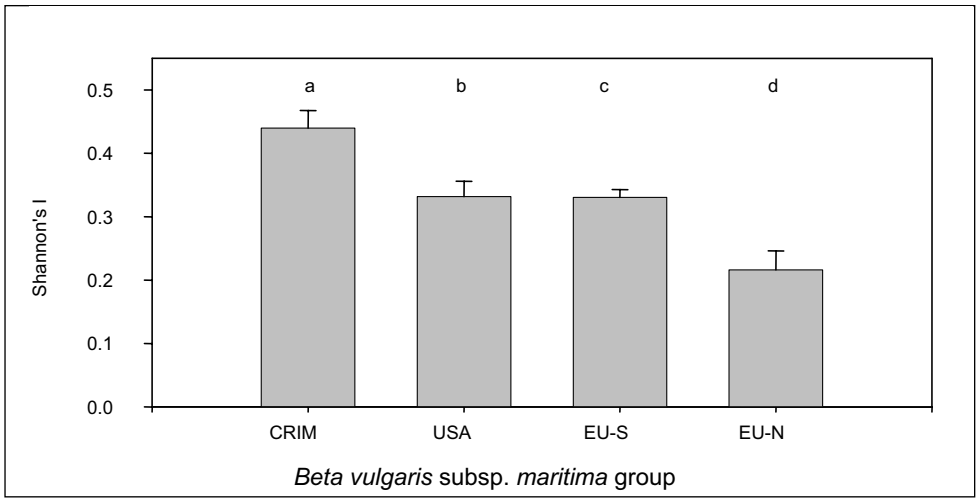

Fig. 3. Shannon's diversity index of a single population in comparison of different geographic origins.

Table 2. Genetic diversity statistics for seven major groups of genus *Beta*

	N^a	A	A_P	P	H	U	Fst	N_m
B. vulgaris (all)								
Sugar beet (1-16)	29.8	2.08	2.36	0.846	0.300	27	0.171	1.21
Swiss chard (17-20)	30.0	1.76	2.22	0.692	0.200	23	0.140	1.54
Red beet (21-25)	24.0	2.00	2.56	0.692	0.195	26	0.189	1.07
Weed beet (26)	30.0	2.00	2.40	0.769	0.260	26	-	-
Sea beet Europe North (27-37)	22.8	2.31	2.63	0.846	0.196	30	0.371	0.42
Sea beet Europe South (38-64)	21.7	2.85	3.18	0.846	0.294	37	0.309	0.56
Sea beet Ukraine (77-82)	20.0	2.23	2.45	0.846	0.320	29	0.091	2.51
Sea beet USA (65-76)	15.5	2.23	2.60	0.769	0.247	29	0.142	1.52
B. macrocarpa N. Americ. (83-92)	30.4	2.46	3.22	0.682	0.057	25	0.107	2.10
B. macrocarpa Mediterr. (93-96)	23.6	1.62	2.50	0.462	0.063	16	0.199	1.01
B. trigyna Crimea (100)	7.0	1.92	2.33	0.692	0.335	19	-	-
B. webbiana (97)	11.0	1.38	2.17	0.462	0.222	6	-	-
B. patellaris (98)	10.0	1.31	2.00	0.462	0.273	9	-	-
B. procumbens (99)	2.0	1.31	2.00	0.462	0.273	6	-	-

Abbreviations:
N = average number of plants sampled per accession
A = average number of alleles per locus
Ap = average number of alleles per polymorphic locus
P = proportion of polymorphic loci
H = estimated heterozygosity
U = number of unique alleles per group with the *B. vulgaris* alleles
Fst = Nei's (1978) summary F statistics for population differentiation between populations within *Beta vulgaris* and *B. macrocarpa*
Nm = estimated genetic migration from 0.25 (1-Fst)/Fst (Slatkin and Barton 1989)

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Beta *genetic resources in the United Kingdom – Current activities*

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School of Biosciences, University of Birmingham, Edgbaston, Birmingham, United Kingdom

Broom's Barn

Genetic resources activities at Broom's Barn are confined to the EU GENRES CT95-42 project and are reported in the paper by M. Asher and S.A. Francis, "Exploiting disease resistance in *Beta* germplasm" (this report, p. 111).

Centre for Ecology and Hydrology (formerly Institute of Terrestrial Ecology)

Dr Alan Raybould has now moved to Syngenta, and beet research appears to have ceased.

University of Birmingham, School of Biosciences *(Brian Ford-Lloyd, John Newbury, Nigel Maxted, Andy Cureton and Mark Raven)*

As part of a project funded by DEFRA (UK Government Department for Environment, Food and Rural Affairs), new wild beet germplasm has been collected. High throughput AFLPs are being used to study patterns of diversity in UK wild PGRFA, of which *B. vulgaris* subsp. *maritima* is just one of the target species. Preliminary results have not revealed substantial geographical patterns to the distribution of genetic diversity in sea beet in the UK, but clearly demonstrate the predominance of diversity within rather than amongst populations (Mark Raven).

A project studying gene flow amongst natural populations of *B. vulgaris* subsp. *maritima* in the UK (in collaboration with Dr Alan Raybould) is now nearing completion. New SSR markers were developed and used in a high throughput system employing the ABI 3700 DNA sequencer. A set of six microsatellite markers for sea beet (*Beta vulgaris* subsp. *maritima*) have been developed as well as three universal chloroplast CAPS markers to study gene flow between ten natural populations of sea beet around Poole Harbour, Dorset, UK. Four out of the six microsatellite markers were used in the study, all of which were highly polymorphic with between eight and 40 alleles being present across all of the populations. None of the universal chloroplast CAPS markers were found to be polymorphic. *Fis* estimates for each of the populations were significantly different from zero, which has been shown to be due to small allele dominance of the microsatellite markers and due to low levels of inbreeding. From sequencing data it was found that the microsatellite alleles did not differ in size simply by repeat number and so both *Rst* and *Fst* were estimated. *Fst* and *Rst* both showed isolation by distance although despite our markers not following a strict stepwise mutation model, *Rst* showed a much more significant correlation with distance than *Fst*. These new results will be used in a comparison with data obtained from the same populations ten years ago (Andy Cureton).

University of Bristol, School of Biological Sciences *(Keith Edwards and Livia Tommasini)*

Six microsatellite markers derived from sugar beet have been used to study the population structure of natural populations of sea beet (*Beta vulgaris* subsp. *maritima*) from polluted (Sand Bay, area 1) and unpolluted areas (Combe Martin Bay, area 2; Morte Bay, area 3) of the North Somerset coast. High levels of polymorphism were detected (on average 9.5 alleles per locus). Areas 1 and 3 showed the highest number of alleles. In area 2 a high level of homozygosity was detected. Cluster analysis and principal coordinates analysis based on percentage similarity matrix revealed a clear genetic differentiation between plants from Combe Martin Bay and plants from Sand Bay and Morte Bay. The analysis did not allow a

separation of the sea beet populations from Sand Bay and Morte Bay and it is therefore possible that gene flow might be occurring between areas 1 and 3. Area 2 appears to be genetically different from areas 1 and 3, which have a similar allele frequency. Interestingly, in the polluted area (Sand Bay) one specific allele was observed at an extremely high frequency when compared to the two unpolluted areas. Via undergraduate research projects there will be continued monitoring of both the spread of the various populations (via GPS) and their genetic makeup.

Beta *genetic resources: North American activities*

Lee Panella[1], Richard Hannan[2] and Alan Hodgdon[2]

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Introduction - *A short history of the National Plant Germplasm System's (NPGS) Beta Collection at the United States Department of Agriculture (USDA) - Agricultural Research Service (ARS) Western Regional Plant Introduction Station (WRPIS)*

In 1991-1992 Dr Richard Hannan, Horticultural Crops Curator at the USDA-ARS WRPIS, grew 10 accessions of *Beta vulgaris* L. for the beet curator, Peter Lundeen, at the North Central Regional Plant Introduction Station, Ames, IA. That Plant Introduction Station had been contracting beet increases in Utah, but the quantity and quality of the seed produced were suspect. Following successful seed increases at WRPIS in the 1992 and 1993 seasons in terms of seed quantity, discussions ensued for the transfer of the *Beta* collection to WRPIS. Contingent on funding, the entire *Beta* collection was transferred to WRPIS in 1994 and was assigned to Dr Alan Hodgdon to curate. In 1995 Hodgdon and Hannan designed and constructed new cloth pollination cages for field production.

Preliminary studies had shown that WRPIS could provide good pollen exclusion by using these new cages during the flowering and fruit set period of growth. However, from 1996 to 1999 there were mixed results at the Central Ferry, Washington location. In 1997, 1998, and 1999 a few lines were planted at the Pullman, Washington location as well, but there were significant amounts of roots frozen in the plots. While trying to get a reliable and reproducible field production programme going, Dr Hodgdon established a greenhouse programme that continued to produce seed from the accessions that were too vulnerable to put into field production.

Because of the increasing backlog of accessions needing increase, in 2000, Dr Hannan conducted a preliminary trial to modify the field increase programme fall planting and the use of simple cold frames to protect the plots through the winters. Results from the 2001 crop looked promising and a replicated trial was conducted at both the Central Ferry and Pullman locations. Seed yields from this study at the two locations differed significantly. There was excellent survival of the plants through the 2001-2002 winter, but the heat in the controlled pollination cages at Central Ferry reduced fruit set and seed yield significantly at that location. In contrast, seed yield at the Pullman location appears to have been excellent. At this time, the seed still has not been cleaned and weighed, but the differences between the two sites will not only be significant, it will be exponential. However, the results of seed germination tests will be critical. For the 2002-2003 season, caged beet field plots will only be planted at the Pullman location.

Seed increase issues (see Table 1)

- The backlog of seed needing increase exceeds our capacity to grow it all under greenhouse conditions. So, a high quality, reliable field increase programme needs to be developed.
- Most accessions of all of the wild species of *Beta* need increase. At Pullman, these must be done under greenhouse conditions.
- Almost 25% of the *Beta vulgaris* subsp. *maritima* need increase. These may or may not be able to be done in the field. This must be investigated.

- Only 67% of the collection is backed up at the National Center for Genetic Resources Preservation (NCGRP) – formerly the National Seed Storage Laboratory (NSSL). That leaves 33% of the *Beta* collection, which contains some of the most important materials, needing to be incorporated into the base collection at Fort Collins, CO.

Table 1. Status of the *Beta* collection at WRPIS

Taxon name	Accessions		Total PIs		Accessions at W6		Backed up	
	Total	Available	Total	Available	Total	Available	PIs	All *Beta*
Beta ALL	2440	1682	1910	1522	530	160	1625	1831
B. corolliflora	4	1	3	1	1		2	
B. lomatogona	29	1	5	1	24		2	
B. macrocarpa	16	12	15	12	1		13	
B. macrorhiza	20	1	5	1	15		2	
B. nana	1				1			
B. patellaris	29	14	10	9	19	5	7	
B. patula	3	2	3	2			2	
B. procumbens	15	9	3	3	12	6	3	
B. trigyna	47	5	8	2	39	3	4	
B. vulgaris	3		3					
B. vulgaris subsp. *maritima*	572	433	564	429	8	4	379	
B. vulgaris subsp. *vulgaris*	1667	1197	1286	1058	381	139	1206	
B. webbiana	8		1		7		1	
B. x *intermedia*	8	1			8	1		
B. hybrid	2	1	1	1	1		1	
B. sp.	16	5	3	3	13	2	3	

Based on Dr Hodgdon's seed increase priority system, there are 565 accessions that are top priority for increase (Table 2). That system is defined as follows: Priority 1#100 seed per accession; Priority 2 = 100 to 500 seed extant per accession; and Priority 3 = 500 to 1000 seed extant per accession. Of the number currently being increased, 33 Priority 1, and 32 of the Priority 2 lines are being grown in the greenhouse at Pullman. The remaining 43 Priority 2 and 38 Priority 3 accessions have been sent to Germany for increase and inclusion into the IDBB Core Collection and to be increased for the GENRES evaluation programme.

Table 2. Current status of Priority Increase Accessions at WRPIS

Priority code	No. of accessions	No. currently being increased
1	153	33
2	272	75
3	140	38
Total	**565**	**146**

Solutions to these seed increase problems are attainable.

- We can establish a field increase protocol for the backlog of sugar beet and table beet accessions that are adapted to this climate by using cold frames over the winter and cloth pollen proof cages for controlled pollination.
- Based on data from controlled pollination studies at the WRPIS site in Parlier, California by Dr M. Jenderek, we could successfully increase many of the difficult to grow Chenopodiaceous taxa in specially constructed, positive air flow, individually controlled environment chambers. The only thing we need is money for large scale construction.

Evaluation of the USDA-ARS *Beta* Collection

The GRIN system has 2447 *Beta* accessions, the majority of which are *Beta vulgaris* subsp. *vulgaris* (Table 3) and represent improved germplasm early open-pollinated varieties developed in the United States and throughout the world (Table 4). Some of the most interesting accessions are those in the taxon, *Beta vulgaris* subsp. *maritima*, which are a rich source of disease resistance genes and are being aggressively evaluated – 23 419 evaluations through 1999 (descriptors x accessions evaluated – see Table 5). The USDA-ARS NPGS *Beta* Core Collection (Hannan *et al.* 2000) consists of 110 accessions from *B. v.* subsp. *maritima* (68 accessions of the 572 in the collection) and *B. v.* subsp. *vulgaris* (42 accessions). The improved sugar beet germplasm, which makes up the bulk of the 1667 *B. v.* subsp. *vulgaris* accessions, has not been integrated into the core collection at this point.

Evaluations of selected germplasm accessions from the USDA-ARS *Beta* Collection have been coordinated by the U.S. Sugarbeet Crop Germplasm Committee since 1985 and, therefore, each year that the collection has been housed at WRPIS. In addition, starting in 2001, digital images have been acquired for each accession being increased at WRPIS and these images have been loaded onto GRIN. To date, images of 239 accessions have been loaded onto GRIN from WRPIS and by other evaluators. Dr Hodgdon at WRPIS has compiled descriptions of 584 accessions as they have been increased in the field and greenhouse. These data are being loaded into GRIN. This information can be found in GRIN at the NPGS Web home page (http://www.ars-grin.gov/npgs/) and the specific site of the *Beta* germplasm descriptors (http://www.ars-grin.gov/cgi-bin/npgs/html/desclist.pl?49) where rhizoctonia, cercospora, root maggot, curly top and rhizomania are accompanied in "code values" list by photographs that illustrate the values.

Reference

Hannan, R., L. Panella and A. Hodgdon. 2000. *Beta* genetic resources: North American activities. Pp. 49-54 *in* Report of a Working Group on *Beta*. First meeting, 9-10 September 1999, Broom's Barn, Highham, Bury St. Edmunds, United Kingdom (L. Maggioni, L. Frese, C. Germeier and E. Lipman, compilers). International Plant Genetic Resources Institute, Rome, Italy.

Table 3. *Beta* accessions maintained in the USDA-ARS NPGS

Taxon	Site	Total
Beta corolliflora	WRPIS	4
Beta hybrid	WRPIS	2
Beta lomatogona	WRPIS	29
Beta macrocarpa	WRPIS	16
Beta macrorhiza	WRPIS	19
Beta nana	WRPIS	1
Beta patellaris	WRPIS	29
Beta patula	WRPIS	3
Beta procumbens	WRPIS	15
Beta sp.	WRPIS	16
Beta trigyna	WRPIS	47
Beta vulgaris	WRPIS	3
Beta vulgaris subsp. *maritima*	WRPIS	572
Beta vulgaris subsp. *vulgaris (*)*	NSSL	8
Beta vulgaris subsp. *vulgaris*	WRPIS	1667
Beta webbiana	WRPIS	8
Beta x *intermedia*	WRPIS	8
Total		**2447**

(*) These 8 accessions are vouchers for a set of trisomics

Table 4. *Beta* accessions maintained in the NPGS by taxon and country

Country of origin	Taxon																Total
	Beta corolliflora	*Beta* hybrid	*Beta lomatogona*	*Beta macrocarpa*	*Beta macrorhiza*	*Beta nana*	*Beta patellaris*	*Beta patula*	*Beta procumbens*	*Beta* sp.	*Beta trigyna*	*Beta vulgaris*	*Beta vulgaris* subsp. *maritima*	*Beta vulgaris* subsp. *vulgaris*	*Beta webbiana*	*Beta* x *intermedia*	
Afghanistan														11			11
Albania										2							2
Argentina														1			1
Armenia	3				2						2			1			8
Asia Minor														1			1
Australia														1			1
Azerbaijan				1										1			2
Belgium													3				3
Brazil														1			1
Bulgaria							1			1	15			5			22
Canada														6			6
Chile														26			26
China													1	47			48
Cyprus													1				1
Denmark					1								24	7			32
Egypt													26	1			27
Ethiopia														2			2
Former Soviet Union			2		2						5			45			54
France				3							1		148	8			160
Germany							1						3	6			10
Greece										1			51	10			62
Hungary														24			24
India													2	54			56
Iran										1				43			44
Iraq														2			2
Ireland													46	2			48
Israel													1	1			2
Italy							1						100	11			112
Kazakhstan														3			3
Kyrgyzstan														1			1
Latvia														3			3
Lebanon														4			4
Macedonia														24			24
Mongolia										1							1
Myanmar														1			1
Nepal										1				1			2
Netherlands				1									2	12		2	17
Pakistan														7			7
Poland			1		2	1			2		1	3	1	53			64
Portugal								1					6	1			8
Russian Federation					2								1	35			38
South Africa														2			2
Spain				2			2			2			12	5			23
Sri Lanka														1			1
Sweden														6			6
Syria														6			6
Tunisia													1				1
Turkey	1		13		3						4		4	131		1	157
Ukraine											3			12			15
United Kingdom													115	29			144
United States		1	1	8	1		7	2	6	2	1		21	995	1	1	1047
Uzbekistan										1				1			2
Yugoslavia													1	9			10
No data available		1	12	1	6		17		7	4	15		2	16	7	4	92
Total	**4**	**2**	**29**	**16**	**19**	**1**	**29**	**3**	**15**	**16**	**47**	**3**	**572**	**1675**	**8**	**8**	**2447**

Table 5. USDA-ARS National Plant Germplasm System's *Beta* Collection – Summary of descriptors evaluated sorted by taxon

Descriptor name	Taxon															
	Beta corolliflora	***Beta* hybrid**	***Beta lomatogona***	***Beta macrocarpa***	***Beta macrorhiza***	***Beta nana***	***Beta patellaris***	***Beta patula***	***Beta procumbens***	***Beta* sp.**	***Beta trigyna***	***Beta vulgaris* subsp. *maritima***	***Beta vulgaris* subsp. *vulgaris***	***Beta webbiana***	***Beta* x intermedia**	**Total**
100 seed weight	4	2	25	15	10	1	29	3	13	15	40	502	1402	8	6	2075
A-amino-nitrogen check percent										1		4	74			79
Aphanomyces										2		87	299			388
Beet cyst nematode				6						2		182	202			392
Beet western yellows virus				3						2		48	207			260
Bolting tendency 1		1		9						2		230	352			594
Cercospora				2								121	396			519
Core subset												67	40			107
Crown height maximum													79			79
Crown height minimum													79			79
Crown width maximum													79			79
Crown width minimum													79			79
Curly top				7						2		158	184			351
Cuticle thickness												74	90			164
Diameter maximum													80			80
Diameter minimum													80			80
End use					1					2	3	34	423			463
Erwinia rot				8				1		1		38	113			161
Erysiphe				8				1		1		96	121			227
Flesh colour										1		31	245			277
Fusarium										2		22	56			80
Germination		2	6	14			12	2	5	5	1	438	1205	1	3	1694
Gross sugar												1	80			81
Growth habit										2		151	230			383
Height maximum													80			80
Height minimum													80			80
Hypocotyl colour				3								138	106			247
IPGRI core subset				1	2						1	62	84			150
Isolation												104	12			116
Leaf blade width maximum												80	124			204
Leaf hairiness												80	124			204
Leaf length maximum												80	124			204
Leaf length minimum												80	124			204
Leaf pigmentation											2	109	330			441
Leaf width minimum												80	124			204
Lifeform	3	1	29	15	17		23	3	13	2	30	521	887	9	7	1560
Male sterility												30	4			34
Multigermicity												39	82			121
Nitrogen										1		63	154			218
Nitrogen-sucrose												1	45			46
Number												104	132			236
Petiole colour										2	2	178	386			568
Petiole length - maximum												80	124			204
Petiole length - minimum												80	124			204
Petiole width - maximum												80	124			204
Petiole width - minimum												80	124			204
Picture/image	1			1	1		2				2	47	185			239

Table 5 (cont.). USDA-ARS National Plant Germplasm System's *Beta* Collection – Summary of descriptors evaluated sorted by taxon

Descriptor name	Taxon															
	Beta corolliflora	***Beta* hybrid**	***Beta lomatogona***	***Beta macrocarpa***	***Beta macrorhiza***	***Beta nana***	***Beta patellaris***	***Beta patula***	***Beta procumbens***	***Beta* sp.**	***Beta trigyna***	***Beta vulgaris* subsp. *maritima***	***Beta vulgaris* subsp. *vulgaris***	***Beta webbiana***	***Beta* x intermedia**	**Total**
Ploidy level		1		14			25	3	13	8		522	904	9		1499
Polymyxa												15	24			39
Potassium										1		63	154			218
Potassium check percent										1		4	74			79
Potassium-sucrose												1	45			46
Recoverable sugar												1	130			131
Rhizoctonia		1		7						3		136	384			531
Rhizomania				8				1		3		90	243			345
Ring colour										1		35	227			263
Root aphids				1						2		70	79			152
Root colour												51	351			402
Root division												34	213			247
Root length maximum													253			253
Root length minimum													259			259
Root maggot			2	3						2		65	165			237
Root position												10	211			221
Root shape												31	243			274
Root width maximum													227			227
Root width minimum													228			228
Rosette												14	198			212
Sample area												104	12			116
Sodium										1		63	154			218
Sodium check percent										1		4	74			79
Sodium-sucrose												1	45			46
Stem pigmentation												96	84			180
Sucrose										1		4	186			191
Sugar absolute												60				60
Sugar check percent												61	95			156
Suture													93			93
Tare check percent										1		3	51			55
Tare percent										1		3	51			55
Type of beet		2	27	14	13	1	27	3	13	6	24	523	420	9	8	1090
Uniformity												123	248			371
White sugar yield												1	24			25
Yield										1		2	75			78
Total	**8**	**10**	**89**	**139**	**44**	**2**	**118**	**17**	**57**	**78**	**105**	**6590**	**16102**	**36**	**24**	**23419**

The International Database for *Beta*

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A. Passport Modules - Identification of duplicates, rationalization of collections and implementation of a database concept for sharing of responsibilities

1. Data resources for identification of duplicates, rationalization of collections and sharing of responsibilities

The potential benefits, the requirements and the possible mechanisms for sharing of responsibilities have recently been described in a more general context by Frison *et al.* (2002). With rising costs and diminishing resources, especially working capacity, it became evident that rationalization of collections will be a prerequisite to maintain high standards of conservation. Within the European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR) this resulted in an upcoming discussion on rationalization of collections by searching for duplicates within the collections held at the multitude of European genebanks and sharing of responsibilities for duplicate groups. After many years of discussion of this issue, concrete actions have to be undertaken to obtain the potential benefits of the concept. Three basic approaches have been considered for rationalization of collections and sharing of responsibilities (Gass and Begemann 1999):

- Sharing of responsibilities on a crop-by-crop basis;
- Sharing of responsibilities on a regional or subregional basis; and
- Sharing of responsibilities on an accession basis.

Sharing of responsibilities on an accession basis is the current practice within the ECP/GR programme. Gass and Begemann (1999) outlined the pivotal role of central crop databases in the process of sharing of responsibilities, especially on an accession basis.

Savings resulting from sharing of responsibilities on an accession basis are based on the idea of a differential and hierarchical seed stock management as outlined by Bücken and Frese (1999). This is based on the following experiences and paradigms:

- In most cases requests are the main reason for the decrease in viable seeds in genebanks.
- Most seed requests are unspecified.
- "Just in time" delivery of germplasm availability has to be abandoned.
- The "one-to-one philosophy" of active to base collection has to be abandoned.
- Regarding regeneration of accessions, a priority system has to be established.

The conceptual framework has been further refined and a database design treating duplication, sharing of responsibilities and rationalization of plant genetic resources collections has been presented by Germeier *et al.* (2003). These concepts have been implemented in the International Database for *Beta* (IDBB) since 1999 (Germeier and Frese 2000).

Sharing of responsibilities on an accession basis and the search for duplication in collections which is its precondition have to be based on a wealth of information including knowledge of the holding genebanks and international crop experts. Fig. 1 gives an overview of basic modules necessary for a comprehensive documentation of plant genetic resources.

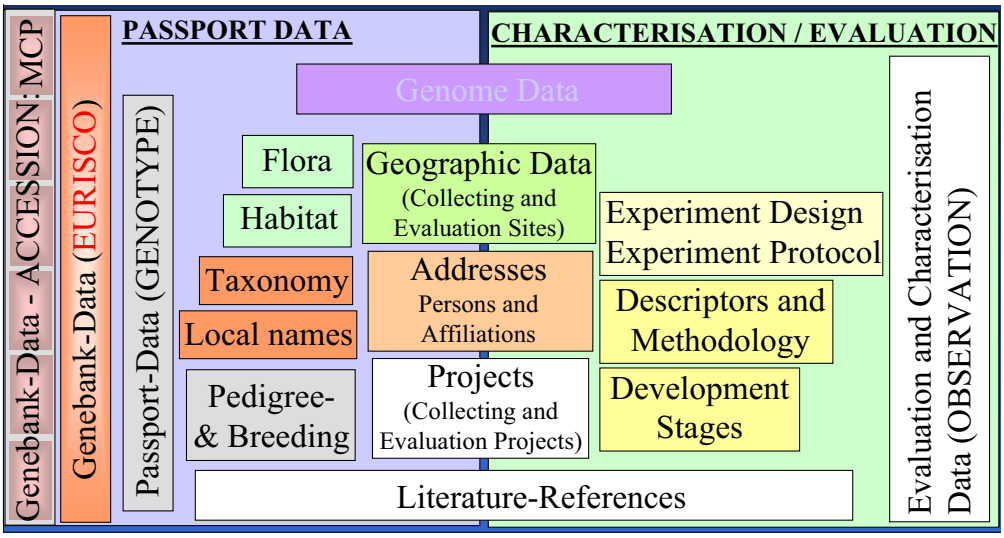

Fig. 1. Elements of a genetic resources documentation system.

The IDBB began with collection of passport data from 28 collections, including non-European ones, in 1989 (Frese and Hintum 1989). Since 1996 a standardized multicrop passport format (Hazekamp *et al.* 1997) has been agreed on for the transfer of accession data (accession passport data) from the various genebanks to the ECP/GR central crop databases. These "multicrop formatted passport data" are located in our current databases within an ACCESSION table listing accession data as accession number, donor, donor number and information on the status of an accession in the holding collection along with original accession data provided by the holding genebank.

By manual or computer-assisted duplicate search, accessions are collected into duplicate groups. Treating the problem of duplication within the genebank network in central crop databases has to take into account the following facts:

1. Passport data describing the origin for a set of duplicate accessions (duplicate group) should be identical. According to the normalizing concept in relational database theory, these common data should be extracted into a new table with only one entry for each duplicate group.
2. Compilation of duplicate groups is often highly hypothetical (Hintum and Visser 1995) and based only on similarities (not even identities) in passport data. Thus the database design has to allow for changing the classification into duplicate groups without loss or change of original information.

These items have been treated in the IDBB by dividing passport information into two major tables (Fig. 2): GENOTYPE, which describes the origin or genetic identity of a duplicate group, and ACCESSION, which describes individual accessions of a "genotype'" stored in different genebanks. Referring to a common origin – see table ORIGIN in Germeier and Frese (2000) – we now prefer GENOTYPE as the name for this table. It indicates that genetic entities are assumed to be represented by the duplicate groups. Yet the term "genotype" does not imply genetic homogeneity. Depending on the breeding system, sample status and scope of the collection, genotypes may be inbred lines, cultivars or wild material of self-pollinating or outcrossing species as in the case of the genus *Beta* or even heterogeneous populations as in the cases of landraces or multilines. Nevertheless they are

genotypic entities defined by their common genetic origin as indicated in their passport descriptors.

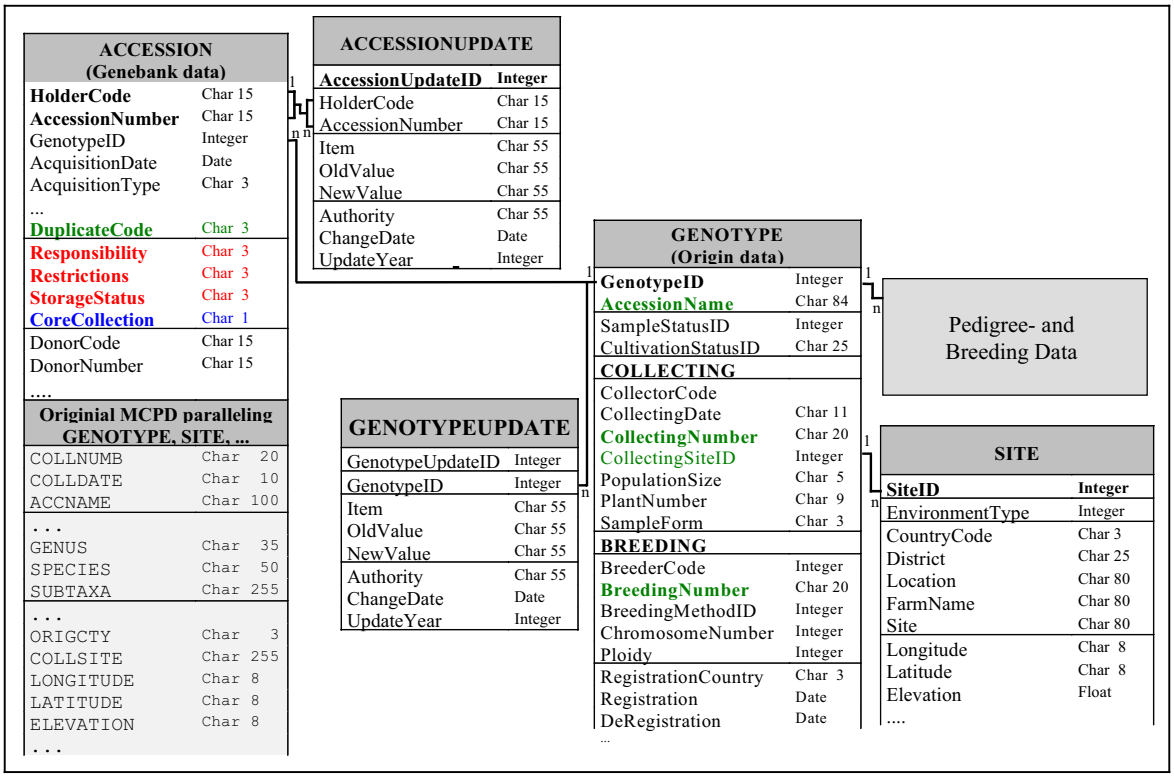

Fig. 2. Database design for passport data compiling corrected and harmonized information (GENOTYPE, SITE, pedigree and breeding data), original information (ACCESSION) and logs for alterations in repeated updated original data (ACCESSIONUPDATE, GENOTYPEUPDATE).

Further normalization of the data suggests additional modules for taxonomy and pedigree, each with its specific functionality. Modules for documenting eco- and ethnobotanic data such as habitats, geographic distribution, plant associations (flora), local names and utilization as crops have already been implemented as table structures into the IDBB, but not yet filled in with data. These modules will be of special interest for the *in situ* conservation of plant genetic resources. Central modules for managing addresses (donors, holders, collectors and breeders of accessions), geographic locations, and projects (collecting missions or evaluation projects) connect the two major parts of a genetic resources documentation system, passport and characterization/evaluation data. The latter will be discussed in a separate section below. A literature base refers to any kind of object in the database. In future, genome data will additionally span over passport, characterization and evaluation data.

A central European Internet Search Catalogue (EURISCO) will be implemented and hosted at IPGRI (http://www.ecpgr.cgiar.org/epgris/index.htm) within an EU-funded documentation project (EPGRIS). It will be based on a revised flat file FAO/IPGRI *Multicrop descriptors list* (EURISCO/MCPDv2). Centralizing the acquisition of original genebank data and providing regularly updated passport information on an accession level, it will be able to feed or replace the ACCESSION table in our current IDBB architecture (Fig. 1). Nevertheless the central crop databases will also play an important role in identification of duplicates and resulting activities such as rationalization of collections and sharing of responsibilities and fulfil additional important tasks in genetic resources documentation.

2. Additional functions within the IDBB passport module

- **Including additional passport data**

There is a strong wish in several crop networks and working groups to include non-European data, especially from the United States and Canada, into the central crop databases. Duplication is evident between European and American collections. The IDBB, since its initiation, has included 2255 accessions from the US collection (Beltsville Agricultural Research Centre, Plant Genetics and Germplasm Institute). We explored the possibility of including these accessions in a regular update procedure. We forwarded further data (evaluation and characterization data) to the IDBB in discussions with database managers in Beltsville in summer 2000. There are no general obstacles for doing so, but several major data warehousing problems have to be solved. The GRIN system used in the US and Canada is designed at a higher level of granularity than the IDBB. Especially in the field of passport data it deviates largely from the concepts implemented in European databases and the ECP/GR MCPD format. Identification of accessions, with the aim of searching for duplication, was not seen as a priority task when designing the GRIN system. Instead it has been optimized for easily finding any kind of identifiers irrespective of their types as accession numbers, donor numbers, collecting numbers, stock numbers, accession or cultivar names.

Table 1 gives an overview of MCPDv2 descriptors and their representation within normalized concepts of the IDBB and within the GRIN system.

Table 1. Database design for passport data in EURISCO, IDBB and GRIN

EURISCO: MCP	IDBB: ACCESSION	GRIN: ACC, AG, AN, IV, SRC	EURISCO: MCP	IDBB: GENOTYPE	GRIN: AN, ACC, SMBR, SRC
INSTCODE	HolderCode	ACC.site	ACCENAME	AccessionName	AN.plantid
ACCENUMB	AccessionNumber	ACC.acid	SAMPSTAT	SampleStatusID	ACC.acimpt
DONORCODE	DonorCode	SMBR.cno	BREDCODE	BreederCode	SMBR.cno
DONORNUMB	DonorNumber	AN.plantid	-	BreederNumber	AN.plantid
OTHERNUMB	AccessionNumber	AN.plantid	COLLCODE	CollectorCode	SMBR.cno
ACQDATE	AcquisitionDate	ACC.received	COLLNUMB	CollectingNumber	AN.plantid
ACQTYPE	AcquisitionType	SRC.srctype	COLLDATE	CollectingDate	SRC.srcdate
STORAGE	StorageType	IV.ivt	COLLSRC	EnvironmentType	-
DUPLSITE	HolderCode	ACC.site			
ACCEURL	AccessionURL	AG.URL			
EURISCO: MCP	IDBB: SITE	GRIN: GEO, HAB	EURISCO: MCP	IDBB: TAXONNAME	GRIN: TAX
ORIGCTY	CountryCode	GEO.Iso3	GENUS	Genus	GN.genus
COLLSITE	Location	HAB.locality	SPECIES	Species	TAX.species
LATITUDE	Latitude	HAB.Latd, latm, lats, lath	SPAUTHOR	SpeciesAuthor	TAX.sauthor
LONGITUDE	Longitude	HAB.Lond, lonm, lons, lonh	SUBTAXA	Subspecies || Varietas || etc.	TAX.subsp || TAX.var || etc.
ELEVATION	Elevation	HAB.elev	SUBTAUTHOR	TaxonNameAuthor	TAX.sspauthor || TAX.varauthor || etc.
EURISCO: MCP	IDBB: ANCESTOR	GRIN: PED	EURISCO MCP	IDBB LOCALNAME	GRIN: CROP
ANCEST	AncestorName	PED.pedigree	CROPNAME	LocalName	CROP.crop

It is evident that entities in the IDBB concept are often represented by multiple entities in GRIN. On the other hand, accession and donor numbers, breeding stock numbers and collecting numbers are all entered as plantid into the AN (annotate names) table. Donors, breeders and collectors are found as cno into the SMBR (source member) table. Qualifiers identifying types of both entities (idtype, srctype) are implemented but often not filled with data.

- **Providing a framework for storing corrected, harmonized and normalized data as well as original data provided by holding genebanks for their accessions within duplicate groups**

Update of passport data up to now has been achieved from Dbase files containing a list of accessions provided by each genebank in the MCPD format. Besides new entries, these update lists frequently contain alterations in data sets already present in the database. In a complex relational database system, a mere replacement of the old data with new ones is not possible due to violation of integrity constraints set up by foreign keys from other tables during the replacement process. Furthermore it is not even feasible to simply replace older information. Not all alterations really improve the correctness of the data set, and attributes relating e.g. to taxonomic systems undergo frequent modifications related to changing taxonomic concepts. Recourse to the most original information and the history of changes would be feasible in many of these cases. Fig. 2 shows a database design for passport data, providing corrected, harmonized and original information at various levels.

Passport information held in GENOTYPE and related tables (SITE for collecting sites and several tables for breeding and pedigree data) is compiled for a whole duplicate group in a standardized and corrected manner from all information provided by the genebanks holding the individual accessions (see above, section 1). Thus duplication can also be a chance for broadening the information base for a group of duplicate accessions. Normally these tables start out with taking over passport information from the best informant genebank for each duplicate group, whereby "best" means the most complete and correct passport data set. Further standardization, correction and completion are achieved gradually by the central crop database manager and compilation algorithms in the database.

The ACCESSION table gives information about duplicate status, responsibility of genebanks for accessions of a duplicate group, assignment of accessions to a core collection, number of user requests and similar information specific to a duplicate accession in a certain genebank. It also holds all original passport information contributed by the various genebanks holding the duplicate accessions in the original MCPD format. The apparent redundancy of information in GENOTYPE and related tables is necessary to provide original as well as standardized and corrected passport information. The latter is presented to the user, while original information should be provided on special request and in cases of doubt and disagreement.

Incoming database updates will be first checked against the original information in the ACCESSION table, which will be updated with changed original information. Alterations of original data provided by holding genebanks are automatically detected by the database application and logged, if considered important by the database managers, in a table named ACCESSIONUPDATE. This guarantees that information referred to in (older) scientific literature will not be lost by database updates.

In cases of alterations to already existing accession data, the database manager will be prompted to check whether the new information could also improve describing information in the tables representing the harmonized genotype information. Alterations to genotype entries are logged in a table GENOTYPEUPDATE (Fig. 2).

Updating and importing passport data should generally be accomplished with a duplicate search comparing the newly introduced or updated accessions with already existing entries in the database (Fig. 3). Scanning databases with several thousands of entries for duplicates

manually would be very time-consuming and ineffective. Nevertheless many duplicate groups in the IDBB have already been established this way by Frese and Hintum (1989). During future updates of passport data from information provided by EURISCO or the holding genebanks, additional duplicates may be detected with the help of automated procedures. Fig. 3 gives a flow diagram of procedures for duplicate check and logging implemented in the MCPD update procedures of the IDBB.

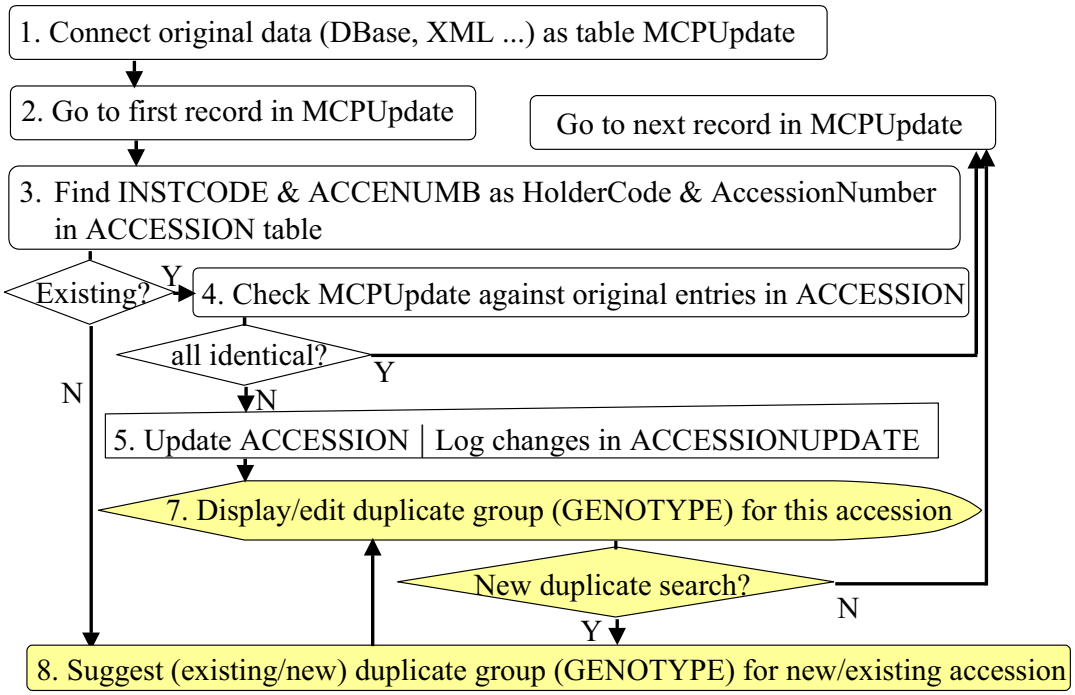

Fig. 3. Flow diagram for the MCPD update procedures.

- **Providing automatic procedures assisting identification of duplicate accessions**

A common definition of duplication in genetic resources collections refers to a common origin, which may be known from data documenting the exchange between genebanks (accession information) or may be assumed by similarities in passport data referring to the origin of an accession (collecting or breeding information/genotype information). Table 2 gives an overview of these types of information and resulting strategies for searching duplicates.

Algorithms implemented in the IDBB for searching duplicates compare the numeric parts of accession identifiers (accession numbers, donor numbers, collecting numbers, accession names) and make an in-string search for finding accessions with similar accession names.

Table 2. Sources of information and strategies for duplicate search

Accession information					Genotype information				
Holder	**Accession-Number**	**Acqu.-Date**	**Donor**	**Donor – Number**	**Breeder**	**Stock-Number**	**Collector**	**Coll.-Number**	**Coll.-Date**
1. Following up information about holders, accession numbers, donors, donor numbers and acquisition dates					2. Tracing identical or similar identifiers like accession names, breeding stock numbers, collecting numbers 3. Tracing identical or similar collecting sites				

- **Providing a framework for categorization of duplicates and sharing of responsibilities for duplicate groups**

Biological duplication categories have been described by Hintum and Knüpffer (1995). These are listed in Table 3 with 3-letter codes, which will be found in the descriptor "duplicate type" within the ACCESSION table. It will not always be possible to assign a sample to one of the biologically meaningful categories shown in Table 3a, as the origin of a sample and its maintenance history, both of which have a great influence on the genetic composition of a duplicate accession, can be obscure. But if details of the sample's history are known, it can facilitate decisions on the maintenance responsibility (Table 3b). Decisions on sharing of responsibilities will be agreed upon in forthcoming discussions within the working group and will be documented in the descriptors "responsibility" and "restriction" within the ACCESSION table. Primary responsibility is assumed by a partner genebank for primary genetic resources (PGR), which may be most original samples (MOS) in the biological sense or for political reasons (sovereign rights over national genetic resources). But primary responsibility is defined not necessarily from biological or geographic criteria. It rather describes the duty of fulfilling certain standards of maintenance of and access to the germplasm, which includes holding a base sample and an available active sample of the accession as well as storing samples as safety-duplicates at partner genebanks. Thus the responsibility agreed on for an accession determines its status in the store and the maintenance efforts that have to be provided by the holding genebank (Table 4). Relevant for trusteeship in sharing of responsibilities are responsibilities for primary genetic resources (PGR) and safety-duplicate samples (SDS), which were agreed on during the first meeting of the Working Group on *Beta* (Discussion and recommendations, pp. 1-14 *in* Maggioni *et al.* 2000).

Table 3. Duplication and responsibility as a basis for a differential storage management concept

a) Duplication (Hintum and Knüpffer 1995; Knüpffer *et al.* 1997)	
MOS	Most original sample
IDD	Identical duplication: genetically identical (e.g. clones)
COD	Common duplicates: derived from the same original population
PAD	Partial duplicates: selected from the same original population
CPD	Compound duplication: one accession is a selection from the other
PRD	Probable duplicate: duplication indicated by identical or similar passport data

b) Responsibility (modified after Bücken and Frese 1999)					
Responsibility		**Restriction**		**Storage Status**	
PGR	Primary genetic resource	PUB	Public	ACO	Active collection
REF	Reference sample	RES	Restricted	BAS	Base collection
SDS	Safety-duplicate sample of other institutions	EMB	Embargoed	BAS	Base collection
PEN	Pending responsibility	TOC	Temporarily out of collection	NEW	Newly acquired accession
REJ	Responsibility rejected	EXE	Lost or discarded	DAT	Sample lost or withdrawn, only information available
DMS	Demonstration sample	PUB	Public	ACO	Active collection
PRO	Project / working sample	RES	Restricted		

Table 4. Seed stock management in regard to the responsibility status of a genebank

a) Necessary seed stock in regard to responsibility for a given accession					
Status of an accession in the genebank			**Necessary samples in genebank seed stock**		
Documented in table ACCESSION			**field SEEDSTOCK.Activity**		**table SAVESTORE**
Responsibility	**Restriction**	**Storage status**	**Active sample (*ACO*)**	**Base sample (*BAS*)**	**Safety-duplicate sample (*SDS*)**
PGR	*PUB*	*ACO*	Yes	Yes	Yes (located at partner facilities)
SDS	*EMB*	*BAS*	No	No	Yes (stored for partners in own facilities)
REF	*EMB*	*BAS*	No	Yes	No
REF/PRO	*PUB/RES*	*ACO*	Yes	No/(Yes)	No
DMS	*PUB*	*ACO*	Yes	No	No
b) Management duties for the different parts of the seed stock					
			Active sample (*ACO*)	**Base sample (*BAS*)**	**Safety-duplicate sample (*SDS*)**
Storage conditions			STS[1]/LTS[2]	LTS	LTS
Available for seed exchange			Yes	No	No
Germination monitoring			Yes	Yes Each 10 years	No
Regeneration of seeds			Yes	Yes	Exchange on regeneration of the base sample

[1] STS: short-term storage conditions
[2] LTS: long-term storage conditions

Genebanks are free to store further samples if they wish, for example if a specific sample is frequently used and quick users' access has to be guaranteed. Reference samples (REF), project or working (PRO) and demonstration samples (DMS) can be held even if from the global point of view they are superfluous as they belong to a duplicate group for which a partner genebank has accepted primary responsibility. Reference samples (REF) may remain as duplicates in the base collection because they have been referenced in scientific publications or are considered valuable for other reasons, project samples (PRO) may be held as an active working collection for project purposes, demonstration samples (DMS) for public awareness raising projects. Decisions on responsibility for certain duplicate accessions may be pending (PEN). If a genebank rejects (REJ) the responsibility after consulting its partners, the accession can be returned to the original donor, reside inactive in the collection or be discarded.

Several restrictions may be applied to accessions of different responsibility type. Normally accessions belonging to a genebank's primary responsibility have to be kept available and public (PUB). They belong to the active collection (ACO). Access to others may be restricted (RES) or even embargoed (EMB), especially if there is no primary responsibility of the holding genebank.

There is no access to the safety-duplicate collection which thus is also embargoed (EMB) and belongs to the base collection (BAS) of a genebank. Accessions may be temporarily out of an active collection (TOC) for technical reasons or if important information such as taxonomy is unclear.

B. Characterization and evaluation modules - A data model for evaluation and characterization of plant genetic resources

1. Introduction

Characterization and evaluation data form an important part of genetic resources documentation. Much more than passport data, they are characterized by great heterogeneity, which is a result of the various potentially useful traits, of different methodological approaches and the scientific and methodological progress in characterizing and evaluating crops.

Resulting from projects initiated in the framework of the Council Regulation 1467/94 of the Commission of the European Countries ("GENRES"), a wealth of characterization and evaluation data has been accumulated, which must be documented and made available on the Internet. More than 20 000 observations have been entered into the IDBB as a result of the project GENRES CT95-42, which is about half of all characterization and evaluation data currently available from the database (44 750). They deal with 689 evaluated accessions of a larger core collection and 577 accessions which were characterized mainly during seed multiplication. In total, 44 descriptors were applied within this project: they were evaluated using 50 methods in 54 experiments.

This contribution gives an overview of database structures handling characterization and evaluation data, as currently implemented in the IDBB, with special reference to practical considerations relevant for contributors of data. Fig. 4 gives an overview of basic modules interacting for documentation of characterization and evaluation data and for providing important interfaces to passport and breeding data.

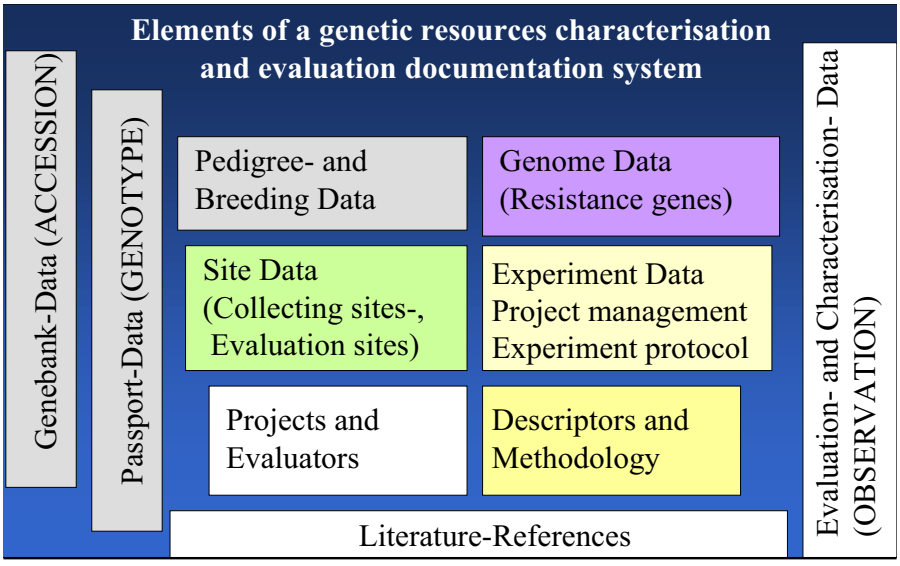

Fig. 4. Modules for characterization and evaluation data and related passport, breeding and genome modules.

2. The observation table

- **The single observation concept**

The observation table (ACCESSIONOBSERVATION) represents the core of the characterization and evaluation module within the IDBB. As early as 1992 a design principle was introduced to the IDBB (Hintum and Hazekamp 1992), which is also used in the GRIN databases (http://www.ars-grin.gov/npgs/aboutgrin.html, USDA Germplasm Resources Information Network) and denoted there as the "single observation concept". This means that different descriptors are not presented in a spreadsheet-like manner as attributes (columns of a table, see Table 5a), but as foreign keys within tuples (rows) relating to descriptive tables (Table 5b). Each row (tuple) represents exactly one observation regardless of descriptor, method and experiment. These are explained by reference to descriptive tables (Fig. 5). All tuples (observations) have a common set of attributes giving observation details such as date of observation, development stage of the crop observed, various dimensions of observation results (measurements, percentages and scores), descriptive statistics (mean, median, maximum, minimum), distribution parameters, etc. (Table 8).

Table 5. Two contrasting design concepts for characterization and evaluation data

a) The compound observation concept

Holder-Code	Accession	Experiment	Treatment	Descriptors																								
				4.1.1.	4.1.2.	4.1.3.	...	4.2.1.	4.2.2.	4.2.3.	...	...	6.1.1.	6.1.2.	....	6.2.1.	6.2.2.	..	7.1.1	7.1.2.	7.1.3	...	8.1.1.	8.1.2	8.1.3	...
BEL004	125V	1	$N_0P_0K_0$																							
BEL004	125V	1	$N_1P_1K_1$																							
BEL004	175V	1	$N_1P_1K_1$																							
...	...																									
CHE001	80.5001	2	$RsAG_2$																							
...	....																									

b) The single observation concept

Holder-Code	Accession	Experiment	Treatment	Descriptor	Method	OriginalMeasurement	ScoringDate	ScoringStage	Replications	PlantsTested	AbsoluteValue	Percentage	NumericScore	Homogeneity	StandardDeviation	StandardError	VariationCoefficient	Skewedness	Kurtosis	Minimum	Median	Maximum	OriginalScore	UniversalScore
BEL004	125V	1	$N_0P_0K_0$	433	4331																			
BEL004	125V	1	$N_1P_1K_1$	433	4331																			
BEL004	175V	1	$N_1P_1K_1$	434	4341																			
...	...																							
CHE001	80.5001	2	$RsAG_2$	834	8341																			
CHE001	80.5001	2	$RsAG_2$	834	8342																			
..	..			...																				

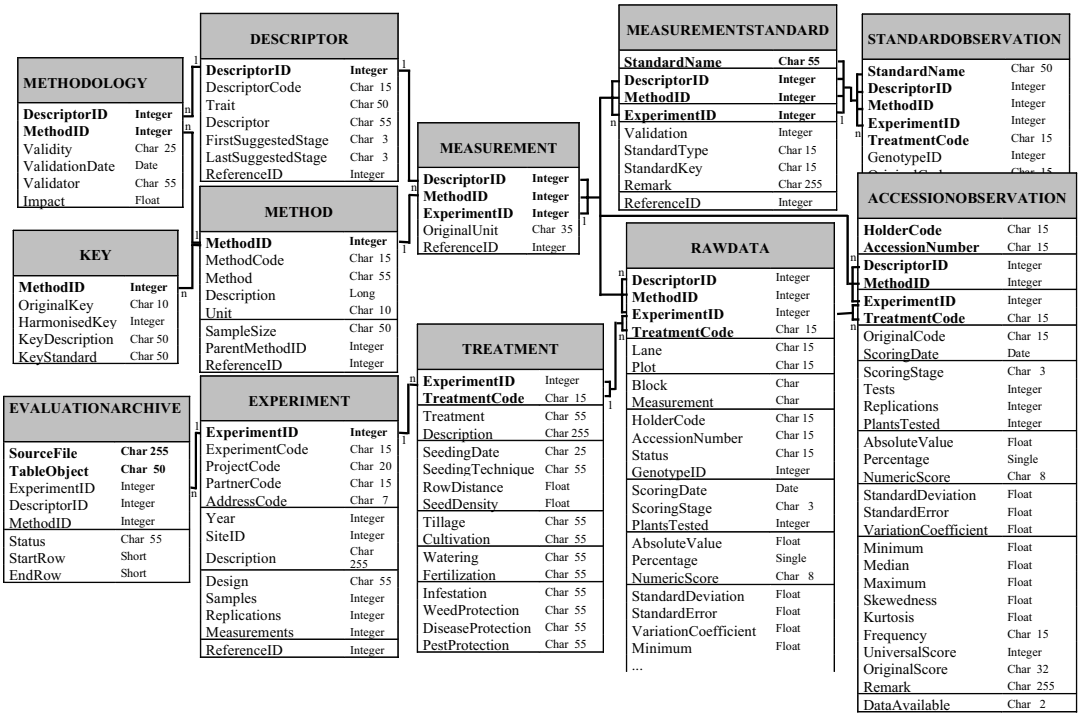

Fig. 5. Data model for the documentation of characterization and evaluation data.

It is obvious from Table 5 and Fig. 5 that the main advantages of this design are the possibility of explaining observation methodology in much more detail (given by all the attributes within a complete set of tables: DESCRIPTOR, METHOD, KEY, see Fig. 5) and to have room for additional explanations for each observation (date of scoring, development stage, statistics) through the attributes within the observation table (Table 9). Table 6 lists some of the advantages and shortcomings encountered with the single observation concept.

- **Attributes and data types in the observation table**

Characterization and evaluation data are found in numeric and text format. Table 7 lists advantages and shortcomings of these data types. Numeric data are more suitable for ranking and sorting, comparison and statistical analysis. Measurement procedures are preferable: documentation of measurement data, if available in its original state, has priority. Qualitative traits like colour or habit in most cases can be ordered on a numeric scale (e.g. brightness, soil covering, agronomic value). The design of rating keys should follow such scales in order to make an algebraic comparison, sorting and averaging of scores meaningful.

The observation table should contain attributes enabling documentation of experimental results as closely to the original as possible . Column "OriginalScore" keeps original data, which have to be transformed to make them compatible with the implemented analytical and comparison operations in the database. Different data types and dimensions (measurements, percentages, frequencies) are kept in separate columns (Table 8). In addition to identifiers for accessions (holder, accession number or cultivar name), descriptors, methods, experiments, treatments and plots, scoring date, number of replications and tested plants and their development stage are documented for each observation.

To facilitate a rapid overview, the database transforms original data into universal scores (1-9; see below, section 6). This can be more or less easily done with automatic procedures, while original measurements not documented cannot be reconstructed from harmonized scores.

Table 6. Advantages and shortcomings of the compound vs. single observation concepts

The compound observation concept	The single observation concept
Advantages: Data retrieval relatively simple	**Shortcomings:** Data retrieval more complicated (cross table queries)
Shortcomings: - Detailed explanation of descriptors and methodology lies beyond standard procedures supported by relational database management systems. - Use of different descriptors and methodology in different experiments often results in unclear NULL values. - The table tends to increase to an extreme width or to necessitate extreme standardization in observation methodology. - Attempts to document descriptive statistics exacerbate all the problems associated with this design.	**Advantages:** - Explanation of descriptors, methods and experiment is achievable by foreign keys to descriptive tables and easily extendable in a relational design. - The table has a fixed and normal number of attributes. - All entries represent well defined observations. Observation methodology is well described for each observation. - Descriptive statistics form part of the attributes within the observation table. They cause no problem with this design.

Table 7. Advantages and shortcomings of data formats for characterization and evaluation

Numeric data	Text Data
Advantages: - Easy to sort and to query. - Allow for algebraic comparison, aggregation and statistical analysis. - > Facilitate automated data retrieval	**Shortcomings:** - Sorting, ranking and querying mostly cumbersome. - Algebraic comparison, aggregation and statistical analysis not applicable. - -> unsuitable for automated data retrieval
Shortcomings: - Need for more elaborate and more standardized, quantifying methodology. - Need for greater abstraction of data. - Heterogeneous populations and peculiarities are more difficult to describe.	**Advantages:** - High flexibility in accepting any information. - Little or no need for methodological standardization and data abstraction. - Heterogeneous populations and peculiarities describable in a more (Hintum 1989) or less formalized way.

Table 8. Basic structure of the observation table(s)

Identifiers		**Numeric data**		**Text data**	
GENOTYPE/ACCESSION			***OBSERVATIONS***		
HolderCode	Char 15	ScoringDate	Date	OriginalScore	Char 8
AccessionNumber	Char 15	ScoringStage	Integer	Homogeneity	Char 15
GenotypeID	Integer	Tests	Integer	Remark	Char 70
StandardName	Char 50	Replications	Integer	DataAvailable	Char 2
		PlantsTested	Integer		
		AbsoluteValue	Float		
		Percentage	Float		
		NumericScore	Float		
METHODOLOGY		***STATISTICS***			
Descriptor	Integer	StandardDeviation	Float		
Method	Integer	StandardError	Float		
		VariationCoefficient	Float		
EXPERIMENTAL		Minimum	Float		
Experiment	Integer	Median	Float		
Treatment	Char 15	Maximum	Float		
		Skewedness	Float		
		Kurtosis	Float		
		Frequency	Float		
ORIGINAL PLOT		***STANDARDIZED DATA***			
OriginalPlot	Char 15	UniversalScore	Float		

3. Raw data

Characterization and evaluation data from project GENRES CT95-42 have reached the database as aggregated data (means of field replications). Several project partners also sent additional descriptive statistics, such as minimum, maximum, standard deviation, standard errors or additional frequencies (e.g. of infected plants) to the database manager.

Table ACCESSIONOBSERVATION and the importing procedures were originally designed to deal with such data. For enabling re-evaluation or additional statistical analysis, it would be preferable that the database stores single plot or single plant results ("raw data"). For this purpose an additional table RAWDATA has been included in the characterization and evaluation module of the IDBB (see Fig. 5).

The database application generates aggregated data (mean, standard error, range) from the raw data automatically and writes them into the tables ACCESSIONOBSERVATION and STANDARDOBSERVATION. The latter table keeps experimental results for genotypes explicitly used as standard cultivars apart from the accession results. This makes algebraic operations involving comparisons with standard cultivars easier to perform.

4. Scoring heterogeneous populations

Special problems are related to heterogeneous populations as often found in accessions of landraces or wild populations. Heterogeneity can be indicated by distribution parameters (range, mean, median, skewedness, kurtosis) if the principle of one row (tuple) per observation is adhered to. Another, more complicated approach would be using the percentage field for relating scores or measurement results to frequencies within one plot.

Hintum (1989) described a coding system facilitating description of heterogeneity in field work. It implies use of characters and special signs and thus is not very appropriate for automatic analysis but is very useful as an easy-to-use standard text format for describing heterogeneity in field work. Procedures for automatically extracting numeric data can be easily made available. With slight modifications, this coding system is generally suggested for communicating heterogeneity observed in characterization and evaluation plots to the IDBB. It follows the procedure listed below:

1. Put the scores of the separate fractions in decreasing order of frequency. The most frequent score(s) should be 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 three fractions.

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%.

Algorithms have been implemented in the database application, extracting a mean value and the range from inputs, keeping these conventions and storing them in additional numeric fields, which facilitates look-up and sorting procedures within these data.

5. Suggestions for the transfer of future evaluation and characterization data to the IDBB

Importing mechanisms for evaluation and characterization data to the IDBB are now implemented for importing data from various Excel data sheets. The database automatically generates descriptive statistics as means, standard errors, coefficients of variation, minimum, maximum etc. It would be preferable if all raw data, not only aggregated data (means) were delivered to the database (see above, section 3). Also, data would be better explained if respective development stages of the crop, or at least the date of the observation, could be provided. Repeated measurements or scores can be imported from multiple columns as well

as from multiple rows. Naming of columns is not of importance (only 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. As seen in Fig. 5 they can be stored in tables EXPERIMENT, SITE (not shown in Fig. 5), TREATMENT, DESCRIPTOR, METHOD and KEY.

From experience with the implementation and testing of importing procedures for Excel sheets, some suggestions can be made for further data transfer to the database. Keeping to certain standards within the Excel files, whose data need to be imported into the database makes this task easier to automate:

- 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. 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) in one column should be avoided.
- Coded scores should keep to the standards of the descriptor lists (scores 1-9 or 0,1 in most cases). 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 (section 4). The database is able to store these data in their original form as well as extract a mean, minimum and maximum value.

Table 9 shows an example of a worksheet optimized for easy gathering of detailed data in the field and automated import into the database

Table 9. 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				
	...	....																

6. Original and harmonized data

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

1. Store all data in its original form as far as possible.
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 available.
3. Offer the user an easy-to-read universal score (1-9) for initial guidance, but also allow him to access the original data.

To achieve these tasks, several procedures for harmonizing original data, which are first stored in the field OriginalScore and which can generate a universal score, are implemented in the database application (Fig. 6).

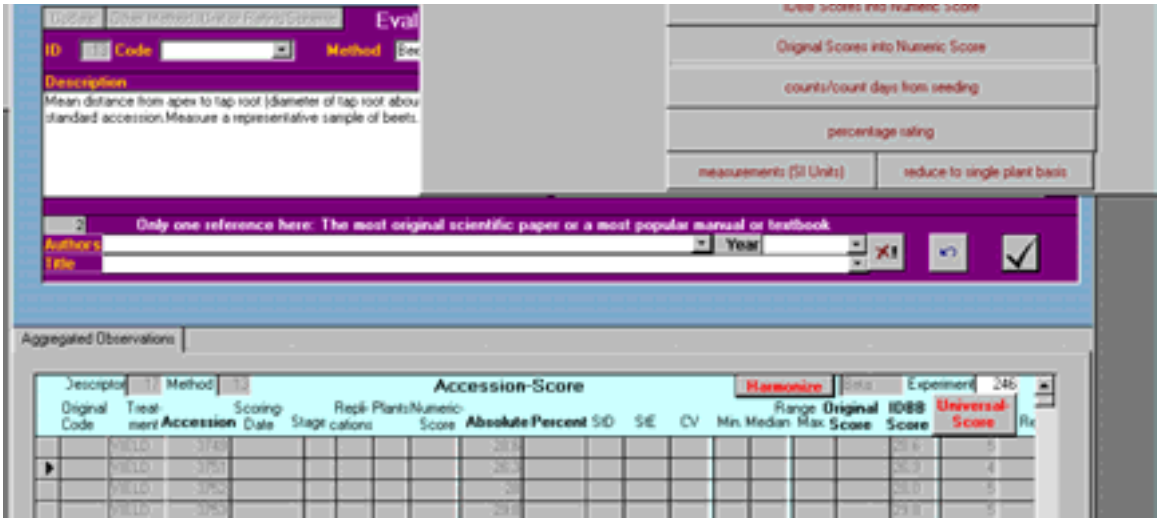

Fig. 6. Database application showing observation data, harmonizing observations and generating universal scores.

For easy interrogation of the database and to provide a quick overview of data, universal scores (1-9), which make the data easily comparable regardless of descriptors, methodological or experimental details, should be provided for all data. They imply a major simplification of the original data and a great loss of information. Thus they should not be the primary way to store data in the characterization and evaluation module, but an additional feature assisting the user to gain a quick overview of the data.

Algorithms for generating universal scores may be based on distribution parameters for an experiment, on regression models taking into account environmental and agronomic experimental information or on standard cultivars. Some approaches for generating universal scores and some advantages and shortcomings are listed in Table 10. These algorithms and resulting entries in the field "UniversalScore" are capable of regular improvement and adaptation to descriptors and methodology.

Table 10. Algorithms for generating universal scores from characterization and evaluation data

1. Based on experiment statistics									
	Example with skewed distributed observations								
- Simplest algorithms	Minimum				Mean		Maximum		
- Biased for experimental sample	1	2	3	4	5	6	7	8	9
2. Regression approaches based on environmental and experimental information									
- Necessitates highly complex multivariate approaches and a broad data base.									
- Practicability for highly interacting traits questionable.									
- Different approaches for different reaction types (intensive, extensive types) necessary.									
3. Based on standard cultivars									
- Standard cultivars have to be defined for all descriptors used in evaluation and characterization.									
- Standard cultivars have to be used over long periods of time.									
- Reaction types (intensive, extensive) have to be taken into account for each standard cultivar.									

Standard cultivars should be defined within descriptor lists and method descriptions and should be used in all evaluation and characterization work.

7. Some considerations for the design of descriptors and keys

Algebraic and statistical analysis greatly improve the usefulness of characterization and evaluation data. This should be kept in mind when designing methodology, especially scoring systems. The suggestions listed below for the design of rating keys lead to a more consistent quantification of scoring results:

- Transforming qualitative observations (colours, habit descriptions, site descriptors, etc.) into numbers makes sense, if this is intended as a step to quantification and the figures are open to meaningful algebraic and sorting procedures. In other cases, use of short words instead of keys avoids confusion and the possibility of unjustified quantification.
- Quantification of qualitative traits is feasible if it leads to a meaningful ranking, e.g. using scales from bright to dark, low to high, sparse to complete soil cover or indicating economic value. The design of rating keys should strictly follow such rankings.
- Rating keys should be restricted to figures (preferably 0-9) and not contain characters or special signs (0,1 instead of -,+ etc.)
- The availability of example cultivars greatly facilitates the use of rating keys. Example varieties are defined for rating keys of several descriptors by UPOV descriptor lists and the German BSA (Federal Office of Plant Varieties).

8. Characterization and evaluation data in the IDBB

Table 11 lists evaluation and characterization data currently available for various descriptor groups in the IDBB. Most data are available for growth habit, seasonality, fungal and virus diseases, leaf, beet, stem and seed characters.

Table 11. Groups of characterization and evaluation data available in the IDBB

Descriptor group (trait)	Descriptors	Methods	Observations
Habit	15	16	**7852**
Seasonality	9	13	**7830**
Fungal diseases	6	13	**4703**
Leaf	11	13	**4688**
Beet	14	20	**4176**
Stem	4	5	**3521**
Virus diseases	6	14	**2853**
Seed	3	3	**2738**
Inflorescence	9	15	**2487**
Breeding system	7	8	**1408**
Yield	13	18	**1188**
Abiotic stress resistance	2	2	**1138**
Quality	15	19	**54**
Pests	1	1	**35**
Total	**117**	**141**	**44671**

9. A new PHP application for on-line retrieval of data from the IDBB

In cooperation with Dr G. Weber and Ms B. Hipko, the CIMDATA Academy for digital media, Berlin and ZADI/IBV a new on-line application for the IDBB based on PHP technology has been designed and will be available from the beginning of 2003 at www.genres.de/eccdb/*Beta*.

An implemented SQL generator will enable the user to generate complex queries involving passport, characterization and evaluation data in an easy, intuitive way and special download procedures will provide Excel files of the results:

- Passport and accession data,
- Addresses of institutions holding the accessions,
- Characterization and evaluation data as cross tables with universal scores or as detailed list including descriptive statistics,

- Experiment site, experiment design and experimental treatments,
- Methodology used in determination of the descriptors.

Fig. 7 shows the query interface and Fig. 8 the reports displayed by a Web browser.

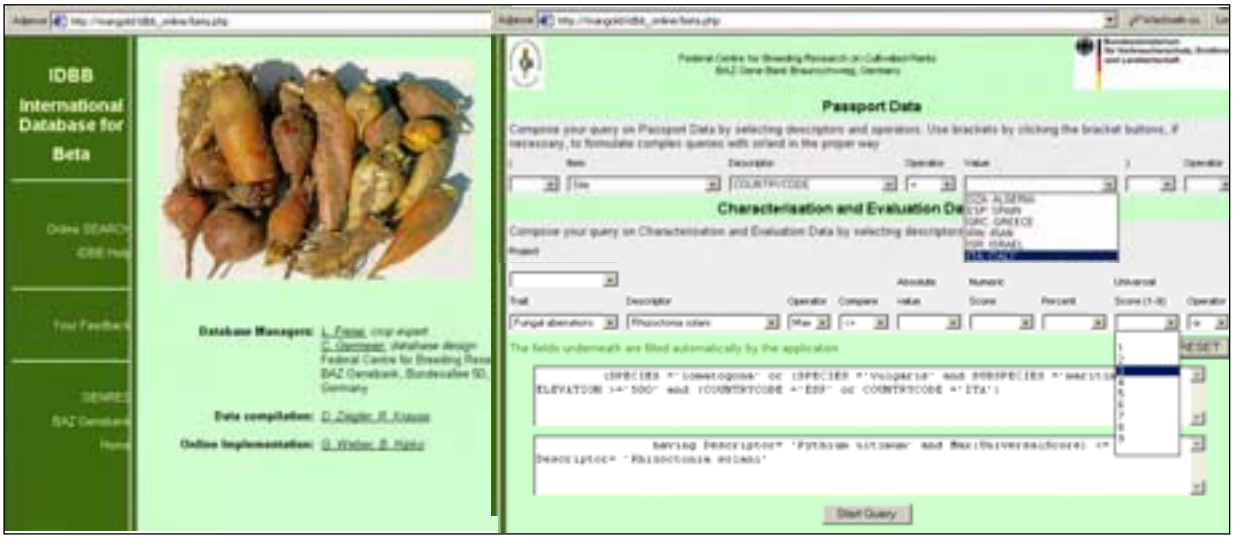

Fig. 7. Query interface for the on-line IDBB.

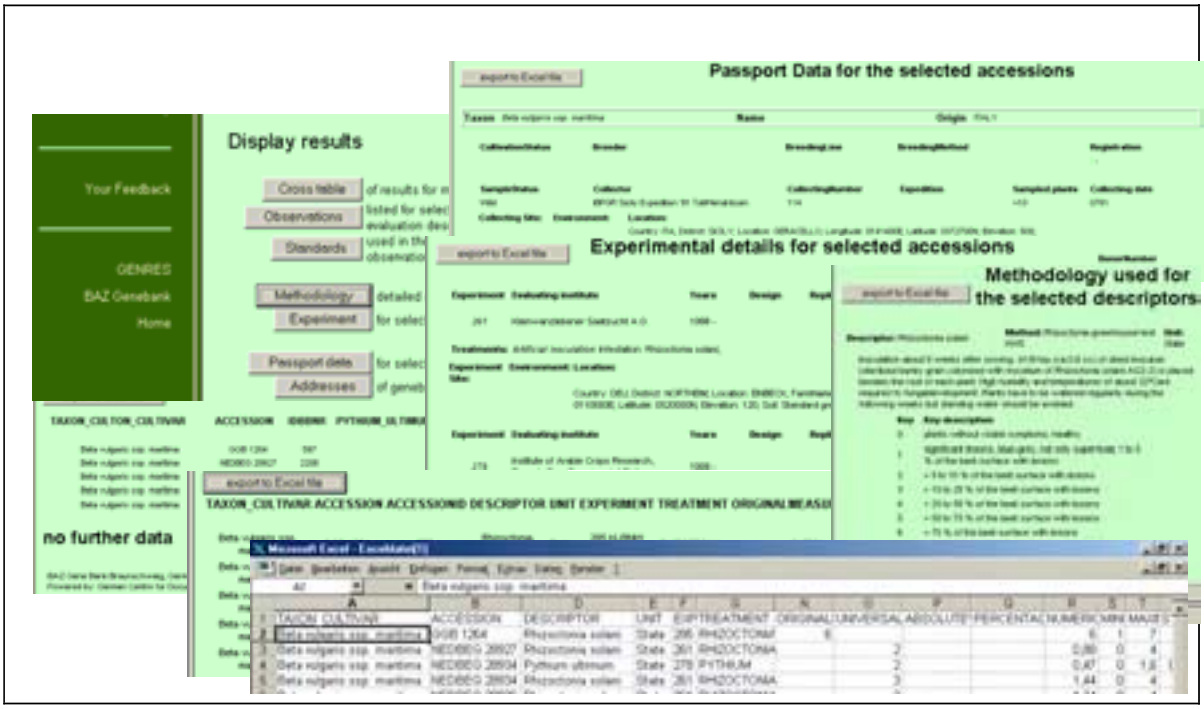

Fig. 8. HTML and Excel reports available from the on-line IDBB.

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Scientific Presentations

The sea beet of the Po delta

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Introduction

The sea beet, classified *Beta vulgaris* L. subsp. *maritima* L. Arcang. by Lange *et al*. (1999), is quite common along the Adriatic coast of the Po delta (Barstch 1999). The species, considered to be the progenitor of cultivated beets (McGrath *et al.* 1999), is characterized by a remarkable genetic and phenotypic variability. Its adaptive ability allows it to grow even on salty soils and in conditions of limited availability of water. This genetic variability may be an adaptive response to environmental stresses (Hanson and Wyse 1982). Besides being a source of genetic resistance to sugar beet diseases such as cercospora and rhizomania, the sea beet is also arousing great interest as possible source of resistance to abiotic stress (Luterbacher and Smith 1998).

Resistance to cercospora leaf spot and to rhizomania

Hybridization between sugar beet and sea beet is easy due to their genetic affinity (Hjerdin *et al*. 1994). Experiments in transferring useful traits to the cultivated varieties began toward the end of the 19th century in different countries, but only the work carried out by Munerati brought significant results (Munerati *et al.* 1913).

In the summer of 1909, this author collected seed on the right bank of the Po di Levante river (Fig. 1), close to its mouth at the Adriatic sea (Munerati 1946).

Mass selections from the plants sown in cultivated soil were followed by several cycles of inbreeding with the objective of fixing the biennial trait. Using predominantly biennial lines, he began to cross it with sugar beet, continuing by a number of backcrossings to eliminate the negative traits of the wild parentage (fangy and fibrous root, tendency to bolting, etc.). Munerati does not mention the specific programme to improve the resistance to cercospora leaf spot (CLS), to which even the sea beet of the Po delta is normally susceptible. Around 1925, he selected genotypes able to reduce or delay the development of the fungus on the leaves. Some lines were forwarded to the breeders working for the US Department of Agriculture (Coons *et al*. 1955).

Further selections improved bolting resistance and after ten years it was possible to release the line R 581, which was considered to show the first substantial progress against the disease (Coons *et al*. 1975). The line was distributed to public and private breeding stations, and was used directly for a number of commercial varieties classified as CLS-resistant.

Presently, the increased effort of the breeding companies has produced several improvements in sugar yield and bolting resistance, which only a few years ago were the main disadvantages of the resistant varieties. With the recent breeding progress, the sugar yield of these varieties is today similar to that of the varieties susceptible to CLS (Skaracis and Biancardi 2000). Even with the protection given by genetic resistance and fungicide, the control of the disease is not complete (Stevanato *et al.* 2002), and a lot of breeding activity is still necessary, especially to reduce the use of fungicides on the crop.

The origin of rhizomania resistance, recently reviewed by Biancardi *et al. (*2002), is probably to be sought in Italian CLS-resistant materials derived from the above-mentioned

crosses with sea beet. The authors confirm the hypothesis of the common origin of the supposed qualitative (monogenic) rhizomania resistances well known as "Rizor type" and "Holly type". The Italian sea beet genotypes, from which CLS resistance was obtained, probably also provided the quantitative (multigenic) resistance to rhizomania shown by the multigerm variety 'Alba P'. Other authors confirmed the presence of rhizomania-resistant genes in sea beet biotypes collected in many parts of the world (Whitney 1989).

Fig. 1. Sea beet habitat (Porto Levante).

Fig. 2. Sea beet populations of the Po delta.

Distribution and description of sea beet populations

In recent years, the distribution of sea beet populations along the Po delta coastline has been examined with the objective of studying the genetic variability of the different populations and to evaluate the possible presence of hybrids with cultivated beets (Bartsch *et al.* 2002). Five principal sites were located (Fig. 2).

The coastline from the Venice lagoon to the southern part of the Po delta appeared the most densely populated. This is probably due to the relatively high presence of undisturbed natural habitats (Stevanato *et al.* 2001). Representative samples of seed were collected from each population and stored in controlled conditions. The seed is available for breeding purposes and for research centres involved in protection of genetic resources.

Sea beets were identified in some restricted areas in the northern part of the Po delta. Only in few places between the mouths of the Po di Levante and Po di Maestra can the populations be considered sufficiently protected from foreign pollination because of the distance from the sugar beet fields. Great variability in the form of the seed stalk, number of flowers per flower cluster, shape of leaves and roots, etc., was immediately observed. The plant prefers the banks very close to the seawater, which is certainly important for the dispersion of the species. Some plants grow without any apparent ill effects, with the fibrous roots partially submerged. Probably due to the lack of competitive ability, the sea beet seems to suffer from the presence of weeds (Graminaceae), which grow partially uncontrolled along the banks. The seed collected at different times reached the maximum germination of 20% in the harvest made on 20th July (Biancardi and De Biaggi 1979).

Germplasm evaluation and conservation

During the months of July and August 2000, the previously located populations of wild beets were sampled. The aim of the investigation was to study the genetic traits of the different

populations and identify possible crosses with cultivated beets. Two or three young leaves were sampled from each plant. The DNA was extracted from each leaf using the methods of Doyle and Doyle (1987) and analyzed using the AFLP technique (Bartsch *et al.* 2002).

In order to determine the extent of genetic variation of the morphophysiological characters involved in the mechanisms of response to water and nutritional stress, the parameters "root length" and "sulfate uptake rate" were measured after water/nutritional stress in 30-day-old sea beet seedlings grown in hydroponics. The objective of this research was to study the mechanisms of adaptation to water/nutritional stress with the aim of identifying the morphological and physiological markers useful for the selection of genotypes tolerant to abiotic stresses (Saccomani *et al.* 2002).

The wild populations must be catalogued and conserved in order to avoid genetic erosion and the risks of gene flow from cultivated to wild beet. Gene flow is possible in the current situation, but it would be more worrying if transgenic varieties were to be grown. As is known, transgenic varieties of sugar beet resistant to herbicides, nematodes and rhizomania are currently under advanced field experimentation (Wenzel 1998). Several researchers pointed out the risk of gene flow caused by the transfer of transgenes from the commercial seed breeding centres in Emilia-Romagna and Veneto to the Adriatic coastal areas. The diffusion of transgenes carried by pollen within the wild populations would probably confer a selective advantage on the hybrids, and therefore it could modify the genetic structure of the populations themselves (Bartsch *et al.* 1999).

The ISCI-Sezione di Rovigo has begun collaboration with the Po Delta Regional Park in order to preserve the natural populations of sea beet. Owing to the decreasing number of plants in the main area concerned (Barstch *et al.* 2002), the cultivation of plots located in more isolated sites was initiated. The aims of such activity can be summarized as follows: i) identification of the different populations of sea beet and recording of their geographical coordinates; ii) evaluation of the dimensions and phenotypic variability of each population and monitoring of the numeric variation over time; iii) collection and conservation of the seed of populations under genetic erosion. The inspections will permit a complete mapping of the localities and characterization of the factors that determine genetic erosion. The long-term storage of the seed will allow the conservation of the various populations and, if necessary, the restoration of their numbers.

Conclusions

The sea beet of the Po delta is of great interest as a source of genetic resistance useful for the cultivated varieties. Because of the land reclamation works and the expansion of the tourist facilities, the number of plants of sea beet is declining in various localities. The main populations were mapped and AFLP analysis of the genetic structure has been performed. In order to preserve this resource, it is necessary to analyze the biodiversity in order to determine the genetic structure of each population. This should allow the detection of any possible future modifications caused by gene flow. It is also necessary to reconsider the policy of *in situ* conservation of sea beet germplasm in this area.

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Deployment of Beta *genetic resources*

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Wild species of cultivated crops often contain genetic variability that is likely to be useful in breeding programmes. If the specific genes are known or can be easily identified, the task of introgressing such genes into crops is straightforward. For the majority of accessions in germplasm collections this is not possible, since we are not aware of the specific genes that control and influence agronomic and horticultural characters. Thus, plant breeders are generally reluctant to introgress wild germplasm into elite genotypes because of the loss of agronomic performance associated with such crosses, unless the specific solution requires the effort needed to backcross for acceptable performance that often adds years to varietal release. Although exact numbers are not known, the amount of allelic diversity present in wild beets may exceed that in sugar beet by 10-fold or more. An assumption is that most of this diversity is not useful, but if only 1% of the allelic variation in the wild species would enhance the agronomic performance of cultivated beets, now or in the future, then efforts to introgress this diversity should be attempted.

Introgression of *Beta* germplasm in varietal development is an enormous task given the number of accessions collected, the number of genes in beet, and the number of environments where beet is grown. Over 2500 Plant Introduction accessions in the U.S. National Plant Germplasm System, over 10 000 Plant Introductions in the BAZ Gene Bank, and germplasm collections throughout the beet growing world, both *ex situ* and *in situ*, are held in trust for the preservation of genetic diversity. Part of the justification for collecting and maintaining *Beta* germplasm is that genes present in wild species, local landraces, alternate crop types, public germplasm releases, and obsolete varieties may contribute to future enhanced germplasm to meet unforeseen genetic crises. Since these are impossible to predict, a balance between the breadth of germplasm collections and the cost of their maintenance requires wise choices of germplasm to include or exclude from collections.

All germplasm should be saved by default, but this is impractical. Stratification of collections based on taxonomy, geographic location, representative subsets (e.g. core collections), crop end use, molecular markers and phenotypic characterization (e.g. crop descriptors) are useful in stratifying collections, assessing the depth of collections, and choosing promising accessions for specific genetic deployment. This information will remain the best predictor for germplasm utilization. In the near future, germplasm curators, breeders, and others will have access to additional information that may positively impact germplasm conservation and the practice of its utilization. This paper seeks to identify some of those trends, how they might be important, and how activities related to germplasm conservation may help facilitate incorporation of novel *Beta* germplasm into improved crop types.

Genomic technologies represent the current opportunity to investigate biological form and function. These technologies have evolved from methods developed to investigate the action and inheritance of single genes and genetic elements, but current applications have allowed massive scaling in to look at hundreds and thousands of genetic elements simultaneously or over a short time period, leading to massive amounts of data collected about individual biological processes. Costs of an individual data point have declined dramatically, and this trend is likely to continue to the point where many programmes will be able to apply these technologies locally.

The application of these tools to germplasm conservation and germplasm enhancement is receiving high priority. However, the tools have not been sufficiently developed in sugar beet and related species that these applications have become obvious or routine. Reasons for this lack of tools include the rapid, continuing development of the industrial aspects of genomics, which presents a moving target of opportunity for those wishing to make costly capital investments in instrumentation. Also, insufficient time has elapsed for the sugar beet community to have embraced the scale and magnitude of these technology changes and their potential to reveal fundamental and practical information. Further, few examples have been published in sugar beet that might illustrate where and how this technology might best be applied.

Perhaps the most compelling reason for adopting these technologies is the ability to survey global gene expression during development or contrasting environments. This ability has never been available routinely to plant breeders, and this change could be profound. Genes cannot and do not work in isolation because the sum total of all genes operating in a plant represent the phenotype, visible at the macrobiotic level but invisible at the molecular level. Parallel gene expression analyses of all, most, or an interesting subset of genes under sets of contrasting conditions can provide a molecular phenotype. Learning to interpret such phenotypes is a challenge, but once known they can be used as any other selection or germplasm characterization criteria. Learning to read the molecular phenotype will be facilitated by extension among all plants, as vascular plants are a monophyletic lineage, and in general and on average, molecular processes will be common in beets and other species. One of the tasks ahead is identify molecular processes in beets that are similar and those that have diversified between plant lineages and within *Beta* populations.

Few crops are in a position to apply molecular phenotypes at present. Investment in gene sequences is required, and this work has just begun for sugar beet. The task will be to obtain sufficient nucleotide sequence information on as many expressed genes as possible, assuming the majority of work in building a plant is accomplished with proteins. With as many as 25 000 identified and putative genes in diploid species such as *Arabidopsis* and rice, two plants whose entire genomes have been essentially sequenced, a similar number of genes in the sugar beet might be expected. Ideally, all expressed genes will be sequenced but this may also be impractical as some genes may be expressed at extremely low levels or for an extremely short time period or under very specialized conditions. To be able to confidently declare completion of a sequencing effort is virtually impossible with this strategy. The complete genome sequence of sugar beet would be required to begin to address this issue. For *Beta* species, the entire genome sequence is unlikely to be obtained soon, but progress in developing other genomic tools for beet may accelerate this process.

Characterization of the allelic nucleotide sequence diversity at agronomic loci in germplasm collections would be one application in germplasm characterization. Expected decreasing costs in the analyses of Single Nucleotide Polymorphisms (SNPs), for example, would make this practical, at least for alleles with reasonably high frequency in germplasm accessions. SNP analyses may better predict phylogenetic relationships between accessions since their genomic locations within the *Beta* genome(s) would be known (by their virtue of residing in a gene of agronomic importance as identified by functional and inheritance data), and the distribution of different SNP-detected loci could assure reasonable coverage of linkage groups in these phylogenetic studies. Allelic synteny relations, if any, between accessions could also be assessed. This information could be valuable for predicting, for instance, whether sufficient allelic variation exists in any given accession in the case where a Quantitative Trait Locus (QTL) has been identified but the underlying gene(s) have not yet been identified.

Deploying *Beta* germplasm resources may be facilitated by technological innovations but it cannot supplant agronomic evaluation. This will continue as the most challenging aspect of effective and efficient utilization of germplasm resources. An approach for efficiently deploying germplasm is to specifically introgress wild-type alleles for agronomic traits into cultivated germplasm. These alleles would have been identified at the molecular level by expression profiling as above, or otherwise known through genetic mapping of SNPs, for instance. Once polymorphisms have been identified, generating inbred lines from crosses between the accession(s) carrying the desired allele with a male-sterile, self-fertile tester will be relatively straightforward, and the phenotypic effect of the transferred allele, if any, could be examined. Such an approach would be complemented by gene expression profiling at the molecular phenotypic level, as many genes introgressed in this manner could have subtle effects on expression of other genes at unlinked (or linked) loci but may not have gross phenotypic effects. In particular, genes whose products perceive, transmit, or effect response to stress may show this kind of behaviour.

A reasonable alternative in the meantime may exist if, in every seed multiplication, a self-fertile and male-sterile plant was included to capture the genetic diversity present in the increase. Seed from such hybrid plants could be grown under field conditions, vernalized if necessary, and self-pollinated by bagging single plants. The actual number of hybrids to be selfed would depend on the cooperators, but a target number of 10 F_2 populations for each accession might be a reasonable compromise. Each of these F_2 populations would then enter into an agronomic evaluation, and promising genotypes would be selected for further inbreeding or outcrossing as desired. Characters normally masked in the wild species, for instance, may surface in later generations and some of these characters could be advantageous for beet breeding. A limitation to this approach is that a sample of genetic diversity from the donor accession will be present in the hybrids chosen for selfing: in the case of 10 hybrids, only 10 donor gametes will have been sampled and rare alleles will be unlikely to be transferred in most instances.

The game of germplasm utilization is one of numbers; of accessions, of genes, and of environments. The challenge is to assure that only the most promising materials are used, and developments in functional and structural phenotyping of populations can assist in making wise germplasm deployment choices.

Exploiting disease resistance in Beta *germplasm*

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The evaluation of ca. 600 *Beta* accessions from the BAZ Gene Bank for resistance to eight diseases of major economic importance in the European sugar beet crop was carried out under GENRES CT 95-42. Results obtained from the eleven collaborating institutes showed that highly resistant (category 1: no detectable infection) accessions occurred at a frequency of between 0.2 and 5.0%, depending on the disease. If category 2 (trace of infection) accessions were included, the proportion of resistant accessions increased to between 2.0 and 21.0%.

Published information on the identity and location of disease resistance genes in *Beta vulgaris* is extremely sparse, compared to most other major crop species. Only six major genes, governing resistance to curly top virus, cyst nematode and rhizomania (BNYVV), and located on three chromosomes, have been mapped to date. To improve our understanding of the distribution and interrelationships of major disease resistance genes in the sugar beet genome, mapping populations have been developed from resistant *B. vulgaris* sources identified in the GENRES programme.

For the diseases caused by beet mild yellowing virus (BMYV), beet yellows virus (BYV), *Erysiphe betae* and *Aphanomyces cochlioides*, individual plants from each resistant accession were selected following evaluation. Resistant plants (mainly *B. vulgaris* subsp. *maritima)* were crossed with a common genetic male-sterile sugar beet line to develop F_1 hybrid populations for analysis.

Twenty five individuals from each F_1 generation were screened for resistance using established artificial inoculation techniques under controlled environmental conditions. Segregation was observed in many of these test populations, indicating that the parent had been heterozygous for resistance, and that the F_1 generation was suitable for mapping. In cases where no segregation was observed, indicative of a homozygous resistant parent, highly resistant F_1 individuals were selected for selfing and simultaneous backcrossing to the male-sterile line to produce the segregating F_2 and BC_1 generations required for mapping.

To date, approximately 450 F_1 or F_2 mapping populations have been produced, covering sources of resistance to seven diseases. Preliminary screens are being carried out on all of these populations to identify resistance that appears to be under relatively simple genetical control. Future work will involve the genetic analysis of mapping populations, where single genes of large effect have been implicated in the resistance, utilizing AFLP and microsatellite markers to locate genes to chromosomes.

Evaluation of drought tolerance in Beta *germplasm*

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Introduction

Drought limits sugar beet yields in regions such as the UK where seasonal rainfall is insufficient or too erratic and where irrigation is usually not an option. However, to improve the drought tolerance of commercial varieties, sources of drought-tolerant germplasm must be identified. To provide this information, we have developed three controlled environment (CE) screens and one field screen to evaluate diverse *Beta* germplasm obtained from genebanks and plant breeders: 1) young, pot-grown plants were subjected to a series of stress/recovery cycles – primarily to evaluate shoot growth during and recovery from water deficit; 2) growth of seedlings during four days in vermiculite at high or low matric potential – evaluating ability of roots to grow in dry soil; 3) growth of seedlings for 20 days in sand at high or low penetration resistance – evaluating ability of roots to penetrate hard soil, which usually accompanies soil drying; 4) plants grown to maturity in the field and subjected to a terminal drought – evaluating the yield response and ability of plants to access soil moisture and maintain growth.

Results

Screen 1

594 accessions were screened as part of the GENRES CT95-42 project. The genotypes with extreme (high and low) drought scores identified in this study will be studied in greater detail. Also, this method is now being used to test genotypes that have been characterized in the field screen (screen 4) to assess the relationship between the two types of screens. The limited number of genotypes (35) tested so far indicates poor correlation between the drought Susceptibility Index (SI) observed in the field and SI observed in the CE screen. However, the CE screen may be used to identify physiological traits expressed differentially in contrasting, divergent genotypes. This information could be used to explore the genetic basis of specific traits.

Screen 2

Preliminary results from 12 genotypes indicate significant genotype x matric potential interactions, indicating that the screen was able to differentiate between genotypes exhibiting different growth responses to dry soil. In particular, the seedling root:shoot ratio increased under dry conditions, and there were large genotype differences in this partitioning of growth.

Screen 3

Preliminary results from only 7 genotypes showed that the screen was able to differentiate between genotypes in terms of total root length in packed versus loose sand. Work is still needed to adapt the method to large-scale screening of numerous genotypes.

Screen 4

A diverse set of 46 genotypes have been tested in the field over 3 years. There were significant differences in drought SI and other yield parameters. The data also showed

significant genotype x environment interactions for other traits such as amino-N accumulation. The field screen supplies a basis against which the applicability of the CE screens can be measured.

Summary

The CE screens evaluate different aspects of the drought response of each genotype. The various requirements of the screens, such as cost, number of entries, time for each test, control of stress level, etc., must be considered for optimum performance. The CE screens may be more useful for phenotype mapping of populations than for pre-breeding in a crop improvement programme. There are possibilities of improving the drought tolerance of crop plants through transgenic manipulation. However, for *Beta vulgaris*, in the short and medium term, the resources for genetic improvement exist within germplasm collections. There is now progress toward identifying those materials.

Evaluation of red beet working collections and donor material in Lithuania

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Introduction

Conservation and evaluation of genetic resources of Lithuanian horticultural plants started in 1996 (Bartkaitė 2000). The first step was characterization and description (according to IPGRI descriptors) of Lithuanian horticultural plant varieties (Petronienė 1998). The most valuable accessions of Lithuanian origin were placed in long-term storage (Būdvytytė *et al.* 1997). Evaluation of red beet working collections to identify donors of valuable characters started in 1998.

Materials and methods

Investigations on red beet genetic material were carried out at the Lithuanian Institute of Horticulture (LIH) trial field during the period 1998-2002. The sowing date was 15-18 May on each year of the study. A manual drill was used; plant spacing was 70 cm between rows, 2 seed rows. The trial consisted of 4 randomized blocks. The initial trial plot was 7 m^2, record – 5.6m^2. All the investigated varieties of red beet were on the national list of varieties.

The investigated Lithuanian varieties were intercrossed and crossed with foreign varieties using topcrossing to determine their possibilities to transmit valuable characteristics to the progeny.

The following agronomic characters of the investigated varieties and F_1 hybrids were evaluated: productivity, appearance, biochemical composition, storage durability, resistance to leaf and root diseases, sprouting of mother plants.

The donor characteristics of accessions were determined by the progeny test.

Results and discussion

The hybrid 'Pablo' was most productive (47.7 t/ha) over the experiment period (Table 1). The commercial yield (43.3-41.1 t/ha) of hybrid 'Wodan' and cylindrical varieties 'Rocket' and 'Ilgiai' was significant. Compared with the hybrid 'Pablo', the productivity of Lithuanian varieties was significantly lower. The roots of the variety 'Rocket' and all hybrids had the best appearance.

Lithuanian red beet varieties had better biochemical composition. Lithuanian round-shaped varieties had a significantly higher content of dry solubles compared with the standard variety 'Wodan'. The standard variety 'Wodan' had the lowest dry matter content (11.1%). Hybrids were more susceptible to the investigated leaf diseases – phoma leaf spot (*Phoma betae* Frank.) and cercospora leaf spot (*Cercospora beticola* Sacc.). The severity of cercospora leaf spot in the standard variety 'Wodan' in 2001 was 75% and that of phoma leaf spot 50%. The leaves of other investigated varieties were less affected.

Cylindrical red beet was not affected by dry common scab (*Streptomyces scabies* (Taxt.) Wacman et Henrici). The roots of hybrid progeny were affected (5.2-3.2%).

The roots of hybrid 'Wodan' were most damaged (26.5%) by brown root rot (*Rhizostonia aderholdii* Kolosch.) during storage. Significantly less damage was identified on the roots of the varieties 'Kamuoliai 2', 'Ainiai', 'Nevėžis' and 'Rocket'.

Table 1. Red beet productivity, dry solubles content and disease incidence (Babtai, 1998-2002)

Variety / hybrid	Commercial yield (t/ha)	Dry solubles (%)	Leaf diseases (%)			Root diseases (%)
			phoma leaf spot	cercospora leaf spot	common scab	brown root rot
Kamuoliai 2	35.0	15.2	4.8	9.6	0.8	8.7
Ainiai	37.8	14.3	4.6	5.2	0.9	18.3
Nevėžis	30.0	15.4	5.2	8.1	0.8	15.3
Vytėnų bordo	33.5	14.6	5.4	19.6	1.7	20.0
Joniai	37.5	14.5	4.1	5.4	0.6	24.7
Ilgiai	41.1	13.4	5.4	7.6	0.0	23.7
Pablo F_1	47.7	13.2	6.0	10.4	3.2	20.3
Wodan F_1	43.3	11.1	31.0	37.6	5.2	26.5
Rocket F_1	42.5	11.9	7.8	5.1	0.0	11.0
LSD_{05}	9.3	2.9				7.6

The value of the genotype was determined by its ability to transfer the investigated characters to progeny (Table 2). The varieties 'Kamuoliai' and 'Nevėžis' appeared to be donors of the following traits: dry solubles, scab resistance and good sprouting of mother plants. The hybrid 'Pablo' and the variety 'Rocket' were donors of productivity, good appearance and uniformity. The varieties 'Kamuoliai *2*' and 'Rocket' were donors of root storage durability and resistance to different rots.

Table 2. Transfer of various traits of red beet parental forms to hybrid progeny (Babtai, 1998-2002)

Variety / hybrid	Characters						
	Root					Leaves	
	Productivity	Appearance	Biochemical composition	Disease resistance	Storage durability	Disease resistance	Leaf sprouting of mother plants
Kamuoliai 2	-	-	+	+	+	+	+
Ainiai	-	-	-	+	-	+	+
Nevėžis	-	-	+	+	-	-	+
Vytėnų bordo	-	-	+	-	-	-	+
Joniai	-	+	-	+	-	+	+
Ilgiai	+	-	-	+	-	-	+
Pablo F_1	+	+	-	-	-	-	-
Wodan F_1	-	-	-	-	-	-	-
Rocket F_1	+	+	-	+	+	+	-

Conclusions

- Investigations of genetic resources of red and fodder beet suggest that most of the accessions are donors of various agronomically valuable characters.
- Varieties 'Kamuoliai' and 'Nevėžis' were found to be donors of the following traits: dry solubles, scab resistance and good sprouting of mother plants. Varieties 'Kamuoliai *2*' and 'Rocket' were donors of root storage durability and resistance to different rots. The hybrid 'Pablo' and the variety 'Rocket' were donors of productivity, good appearance and uniformity.

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APPENDICES

Appendix I. Abbreviations and acronyms

AARI	Aegean Agricultural Research Institute, Turkey
ABI	Institute for Agrobotany, Tápiószele, Hungary
AFLP	Amplified Fragment Length Polymorphism
AIS	Agricultural Institute of Slovenia
ARI	Agriculture Research Institute, Shumen, Bulgaria
BAZ	Federal Centre for Breeding Research on Cultivated Plants, Braunschweig, Germany
BGRC	Braunschweig Genetic Resources Collection, Germany
BMYV	Beet Mild Yellowing Luteovirus
BNYVV	Beet Necrotic Yellow Vein Virus
BREBSS	Belarus Regional Experimental Breeding Station for Sugar beet
BRIAFF	Belarus Research Institute of Arable Farming and Fodders, Zhodino, Belarus
BRIVC	Belarus Research Institute of Vegetable Crops, Samohvalovichi, Belarus
BYV	Beet Yellows Closterovirus
CAAS	Chinese Academy of Agricultural Science, P.R. of China
CAPS	cleaved amplified polymorphic sequence
CBD	Convention on Biological Diversity
CCDB	central crop database
CGN	Centre for Genetic Resources, The Netherlands
CLS	cercospora leaf spot
CMS	Cytoplasmic Male Sterility
ECP/GR	European Cooperative Programme for Crop Genetic Resources Networks
EPGRIS	Establishment of a plant genetic resources infra-structure
EU	European Union
EUFORGEN	European Forest Genetic Resources Programme
EURISCO	European Internet Search Catalogue
FAO	Food and Agriculture Organization of the United Nations, Italy
GIS	Geographic Information System
GMO	genetically modified organism
GRIN	Genetic Resources Information Network, USA
HBP	Hodowla Buraka Pastewnego (Fodder Beet Breeding), Poland
IBPGR	International Board for Plant Genetic Resources, Rome
IDBB	International Database for *Beta*
IGC	Institute of Genetics and Cytology, Minsk, Belarus
IHAR	Plant Breeding and Acclimatization Institute, Poland
IPGR	Institute for Plant Genetic Resources, Sadovo, Bulgaria
IPK	Institut für Pflanzengenetik und Kulturpflanzenforschung, Germany
IPK	Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany
ISB	Institute for Sugar Beet, Kiev, Ukraine
ISB-CAAS	Sugar Beet Research Institute of the Chinese Academy of Agricultural Science
ISCI	Istituto Sperimentale per le Colture Industriale, Italy
ISTA	International Seed Testing Association
KWS	Kleinwanzlebener Saatzucht AG, Germany
LIA	Lithuanian Institute of Agriculture
LIH	Lithuanian Institute of Horticulture

NGB	Nordic Gene Bank, Alnarp, Sweden
NPGS	National Plant Germplasm System, USA
NSSL	National Seed Storage Laboratory, USA
PNOS	Przedsiebiorstwo Nasiennictwa Ogrodniczego i Szkolkarstwa (Enterprise for Horticulture Seed Technology and Nursery), Poland
RFLP	Restricted Fragment Length Polymorphism
RICP	Research Institute of Crop Production, Prague, Czech Republic
RWTH	Rheinisch-Westfälische Technische Hochschule Aachen, Aachen, Germany
SBSI	Sugar Beet Seed Institute, Karadj, Iran
UAAS	Ukrainian Academy of Agrarian Science, Ukraine
UPOV	Union pour la Protection des Obtentions Végétales, Switzerland
USDA-ARS	United States Department of Agriculture-Agricultural Research Service, USA
VIR	N.I. Vavilov Research Institute of Plant Industry, Russian Federation
WBN	World *Beta* Network
WRPIS	Western Regional Plant Introduction Station (of USDA-ARS)
ZADI/IBV	Zentralstelle für Agrardokumentation und –information / Informationszentrum Biologische Vielfalt (German Centre for Documentation and Information in Agriculture / Information Centre for Biological Diversity), Bonn, Germany

Appendix II. Agenda

Second Joint Meeting of the ECP/GR Working Group on Beta *and the World* Beta *Network*
23-26 October 2002, Bologna, Italy

Tuesday 22 October
Arrival of participants

Wednesday 23 October - Meeting of the ECP/GR Working Group on *Beta*

09:00 – 09:15	**Introduction** • Opening of the meeting, welcome (*P. Ranalli and L. Frese*)
09:15 – 09:35	**ECP/GR** • General briefing on ECP/GR (*L. Maggioni*, 10 min) • Report of the Working Group Chair (*L. Frese*, 10 min)
09:35 – 10:30	**Update on national collections** (brief updates on the status of national collections) Countries: Azerbaijan, Belarus, China, France, Germany, Hungary, Iran, Italy, Lithuania, Nordic Countries, Poland, Romania, Russia, Slovakia, Slovenia, Turkey, USA, Ukraine
10:30 – 11.00	*Coffee break*
11:00 – 11:30	**Update on national collections** (continued)
11:30 – 12:30	**Identification of duplicates, rationalization of collections and implementation of a database concept of sharing of responsibilities** *(C. Germeier)*
12:30 – 13:30	*Lunch*
13:30 – 15:30	**Working group sessions** (introduction to the tasks of two working groups) • **Regeneration guidelines** • **Development of a quality concept**
15:30 – 16:00	*Coffee break*
16:00 – 17:00	**Our priorities for Phase VII of ECP/GR** Joint research projects: needs, ideas, funding options
17:00 – 17:30	**Discussion on task-sharing within the Steering Committee** (BBC, ECP/GR Working Group Chair and Vice-Chair)
20:00	*Dinner*

Thursday 24 October – Meeting of the World *Beta* Network

09:00 – 09:15	**Introduction**
09:15 – 10:30	**Section I - Scientific basis for *in situ* management of *Beta*** • Taxonomy and distribution of the genus *Beta*. Achievements, criticism, research needs *(discussion introduced by L. Frese)* • Beets in Turkey *(A. Tan)* • The sea beet of the Po Delta as source of resistance for sugar beet (*P. Stevanato, E. Biancardi and M. De Biaggi*)

10:30 – 11:00	*Coffee break*
11:30 – 12:30	**Working group session on *in situ* management** Introduction of GRACE "Genetic Resources and Changing Ecosystems" Discussion on joint activities and projects
12:30 – 14:00	*Lunch*
14:00 – 15:30	**Section II - Genetic resources for beet breeding** • Deployment of *Beta* genetic resources (*M. McGrath*) • Disease resistance in wild *Beta* species (*M. Asher*) • Genetic improvement in utilization of crop species (sugar beet, fodder beet, table beet) and wild species in sugar beet breeding and production of improved varieties (*M. Mesbah*) • Evaluation of sugar beet germplasm for improvement of drought tolerance (*E. Ober*)
15:30 – 16:00	*Coffee break*
16:00 – 18:00	**Working group session on characterization and evaluation** • The International Database for *Beta*: characterization and evaluation data (report by the IDBB managers) • Update of the descriptor list for *Beta* • *Beta* core collection • Discussion on joint evaluation activities and projects
20:30	*Dinner*

Friday 25 October

09:00–13.00	*Tours of the research facilities at the Istituto Sperimentale per le Colture Industriali and local excursion / Drafting of the report by the compilers*
13:00 – 14:30	*Lunch*
14:30 – 16:00	**Plenary meeting and approval of the report**
16:00 – 16:30	*Coffee break*
16:30 – 17:00	**Election of new Chair and Vice-Chair for the Working Group** **Closing remarks**
20:00	*Social dinner*

Saturday 26 October
Post-meeting tour

Sunday 27 October
Departure of participants

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[13] This list was updated at time of publication. It is ordered by alphabetical order of country, regardless of the member status (ECP/GR member, WBN member or observer). The current composition of the ECP/GR Working Group on *Beta* can be found on the ECP/GR Web site, constantly updated (see http://www.ipgri.cgiar.org/networks/ecpgr/Contacts/ecpgr_wgbe.asp).

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