



Report of a Working Group on *Beta*

First meeting — 9-10 September 1999 - Broom's Barn, Higham, Bury St. Edmunds, United Kingdom

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compilers**



European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR)



IPGRI is an institute
of the Consultative
Group on International
Agricultural Research
(CGIAR)

The International Plant Genetic Resources Institute (IPGRI) is an autonomous international scientific organization, supported by the Consultative Group on International Agricultural Research (CGIAR). IPGRI's mandate is to advance the conservation and use of genetic diversity for the well-being of present and future generations. IPGRI's headquarters is based in Rome, Italy, with offices in another 19 countries worldwide. It 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 2000, had been signed and ratified 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 ensuring the long-term conservation and facilitating the increased utilization of plant genetic resources in Europe. The Programme, which is entirely financed by the participating countries and is coordinated by IPGRI, is overseen by a Steering Committee (previously Technical Consultative Committee, TCC) composed of National Coordinators nominated by the participating countries and a number of relevant international bodies. The Programme operates through ten broadly focused 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, technical 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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Preface

The third meeting of the Technical Consultative Committee of the ECP/GR had recommended that the ECP/GR in its Phase III enhance collaborative activities for *Beta*. Consequently, in 1987 a *Beta* workshop was convened at the Centre for Plant Genetic Resources (Wageningen, The Netherlands) in order to develop a collaborative programme on *Beta* genetic resources. In 1989 IPGRI launched the concept of self-sustaining crop networks. The World *Beta* Network (WBN), which was founded the same year, served as a model crop within the framework of the new concept. The goal of all crop-specific networks is to improve international collaboration between curators of collections and researchers and users of germplasm, and, through task-sharing, to enable maximum use of the often limited funds for conservation and utilization. The WBN is a voluntary association with no membership fee or any formal obligations for the members. Scientific input and financial support come from various partners of the public and commercial sectors. It is the common interest of researchers and plant breeders working with this crop that provides the impetus for the activities of the WBN, which benefit the entire user community of *Beta* collections. Since its establishment the WBN has met in Braunschweig (Germany, 1991), Fargo (USA, 1993) and Izmir (Turkey, 1996). However, while research on the genus *Beta* and the utilization of exotic germplasm is progressing, the joint management of European *Beta* collections tended more and more to lag behind. There was therefore a growing need for stronger involvement of curators from European *Beta* collections in the international activities through an ECP/GR *Beta* Working Group. This working group was established by the ECP/GR Steering Committee meeting held at Braunschweig, Germany in 1998. This report describes how the WBN, together with the ECP/GR group, intends to improve conservation and use of *Beta* genetic resources collections in the USA, Europe, Asia and Africa.

World *Beta* Network Coordinating Committee (1996-1999)

M. Asher (UK)
L. Frese (Germany)
L. Panella (USA)
Sun Yi Chu (P.R. of China)

Local Organizing Committee

M. Asher
M. Allison

Contributing organizations and companies

British Sugar plc (UK)
Dieckmann-Heimburg (Germany)
English Sugar Beet Seed Company (UK)
Kleinwanzlebener Saatzucht AG (Germany)
The British Sugar Beet Seed Producers Association (UK)

Part I of this report summarizes the discussions and recommendations of the first ECP/GR meeting of the Working Group on *Beta*, jointly held with WBN members on 9-10 September 1999. Part II includes country reports on the status of *Beta* genetic resources and a few technical and scientific papers presented at the meeting. Part III is a collection of summaries of the scientific presentations and the posters presented on 8 September 1999, during a WBN scientific session that preceded the ECP/GR meeting. The full papers will be published in the *Journal of Sugar Beet Research*.

Part I. Discussion and Recommendations

Introduction

Dr John Pidgeon, Director of the Institute of Arable Crops Research at Broom's Barn, welcomed the participants to the research station.

As part of the UK's Institute of Arable Crops Research, Broom's Barn was founded in 1962 to study all aspects of agronomy, physiology and crop protection in sugar beet. One of the current projects is the evaluation of *Beta* germplasm (under GENRES CT 95-42) for disease resistance, and genetic and molecular marker studies of resistant sources.

L. Maggioni, ECP/GR Coordinator, welcomed all the participants on behalf of IPGRI and thanked Mike Asher, Melanie Allison and their colleagues from Broom's Barn for the tremendous work invested in the excellent organization of a complex meeting such as this. He then mentioned the presence of observers from Belarus and from the Caucasian countries – Armenia, Azerbaijan and Georgia – who were all attending an ECP/GR meeting for the first time. He wished that this could be the start of a continuing collaboration of these countries with ECP/GR. The presence of Dr W. Beyer, representing ASSINSEL, was also acknowledged with pleasure. L. Maggioni informed the Group that N. Stavropoulos, Greece and M. Malangier, Belgium, were also invited, but were unable to attend. He also mentioned the receipt of a letter from FAO expressing interest in this meeting although it was not possible to send a representative. Finally, the ECP/GR Coordinator thanked the members of the World *Beta* Network for their presence, offering the unique opportunity to discuss and integrate the Group activities within a wider international context.

The Group was then reminded that the first workshop setting the basis for collaborative work on *Beta* genetic resources in Europe had been organized by ECP/GR in 1987 in Wageningen, The Netherlands. On that occasion the first agreements were established, initiating the development of the International Database for *Beta*, improving the exchange of data on seed availability, characterization and evaluation, and encouraging systematic safety-duplication of the collections. After 10 years of continued cooperation within the context of the World *Beta* Network, a proposal to establish an ECP/GR Working Group on *Beta* was successfully submitted to the ECP/GR Steering Committee by Lothar Frese, Acting Secretary of the WBN, also on behalf of the WBN Coordinating Committee (see full proposal, Appendix I). The intention of the proponents was that this Working Group should facilitate the interaction of the European collection curators with the WBN members. At its seventh meeting (Braunschweig, Germany, July 1998) the ECP/GR Steering Committee approved the establishment of the Group.

In agreement with the Group, L. Maggioni asked L. Frese to chair the meeting and he kindly accepted.

L. Frese then asked the members and observers to briefly introduce themselves and the provisional agenda was subsequently adopted by the Group (see Appendix II). He explained that the establishment of the ECP/GR *Beta* Working Group should be seen as a European contribution to the WBN, improving the function of this international network. The ECP/GR *Beta* Working Group is an integral part of the WBN. Any recommendation addressed to the WBN includes obviously the ECP/GR Group and *vice versa*.

Information on ECP/GR

Considering that the audience was in large part unfamiliar with the European Cooperative Programme, L. Maggioni gave a presentation explaining the history, scope, objectives and achievements of the programme, as well as its mode of operation in the current Phase VI. While presenting the operational structure of the Programme (see Fig.

1), he clarified that the various ECP/GR Working Groups will continue as in the past to be the operational units for the implementation of workplan activities, to be carried out as inputs in kind by institutions of the member countries. It was explained that the role of the Networks will be enhanced with the establishment of Network Coordinating Groups, composed of Working Group Chairs and Vice-Chairs or Database managers. These groups will work closely with the Secretariat to which they will submit proposals for activities and review progress, achievements and future workplans of the Working Groups.¹ It is hoped that an enhanced internal coordination within the Networks will facilitate better planning and follow-up of the agreed workplans. At the same time, a reduced number of Working Groups meetings is envisaged, which should enable the Programme to invest funds in small technical meetings addressing relevant issues identified within the Networks. An increased scope and flexibility of operation is the expected result of these operational changes. Regarding the Industrial Crops and Potato Network, it was clarified that two new Working Groups, on *Beta* and Potato, are planned to be activated and coordinated by the Industrial Crops Network Coordinating Group, which meets for the first time at Bury St. Edmunds, UK, on 11 September 1999, right after the WBN and ECP/GR *Beta* meeting. A meeting of the whole Network, comprising the members of the two Working Groups on *Beta* and Potato, is foreseen by the ECP/GR workplan and should be held at some date to be determined between 2001 and 2003. Although no Working Groups meetings are planned during Phase VI, the ECP/GR coordinator explained that funds allocated to small technical meetings were used on this occasion, in agreement with the Steering Committee, to allow the convening of the first *Beta* Working Group meeting jointly with the WBN meeting. The opportunity to organize in 2002 the Industrial Crops Network meeting, again jointly with the next WBN meeting, was proposed for the consideration of the Group.²

In the discussion following, H.M. Srivastava asked whether it were possible for India to become a member of ECP/GR and L. Maggioni replied that, although technical cooperation and collaboration with other regions had always been encouraged within the Programme, the possibility to include members from outside of Europe had never been seriously taken into consideration. He concluded by saying that a similar request would need to be formally presented to the Steering Committee for proper consideration. M.N. Arjmand (communication sent by fax on 8 September 1999) requested that IPGRI consider a programme for the Asian region similar to the ECP/GR Programme to strengthen links between countries in the region. He informed the Group that the Sugar Beet Seed Institute (SBSI) in Iran is ready to cooperate with international and national programmes in the field of germplasm exchange, collecting of *Beta* species, safety-duplication, evaluation and characterization. M.N. Arjmand conveyed his best regards to the participants and expressed his wish to join the Group at the next opportunity. By correspondence dated 19 August 1999, Sun Yi Chu from the Institute of Sugar Beet (Chinese Academy of Agricultural Science, P.R. of China) expressed his regret for not being able to attend the meeting this time. He conveyed his best regards to the participants and wished them a successful meeting. Sun Yi Chu indicated that he would like to maintain contact with the WBN and that he would be available for inquiries.

¹ Report of the Seventh Steering Committee Meeting, Braunschweig, Germany, 29 June and 4-5 July 1998. IPGRI, Rome, Italy.

² On 11 September 1999, The Industrial Crop Network Coordinating Group proposed that the two Working Groups on *Beta* and on Potato meet independently from each other. A second meeting of the Working Group on *Beta* was proposed for 2002, to be jointly held with the WBN meeting.

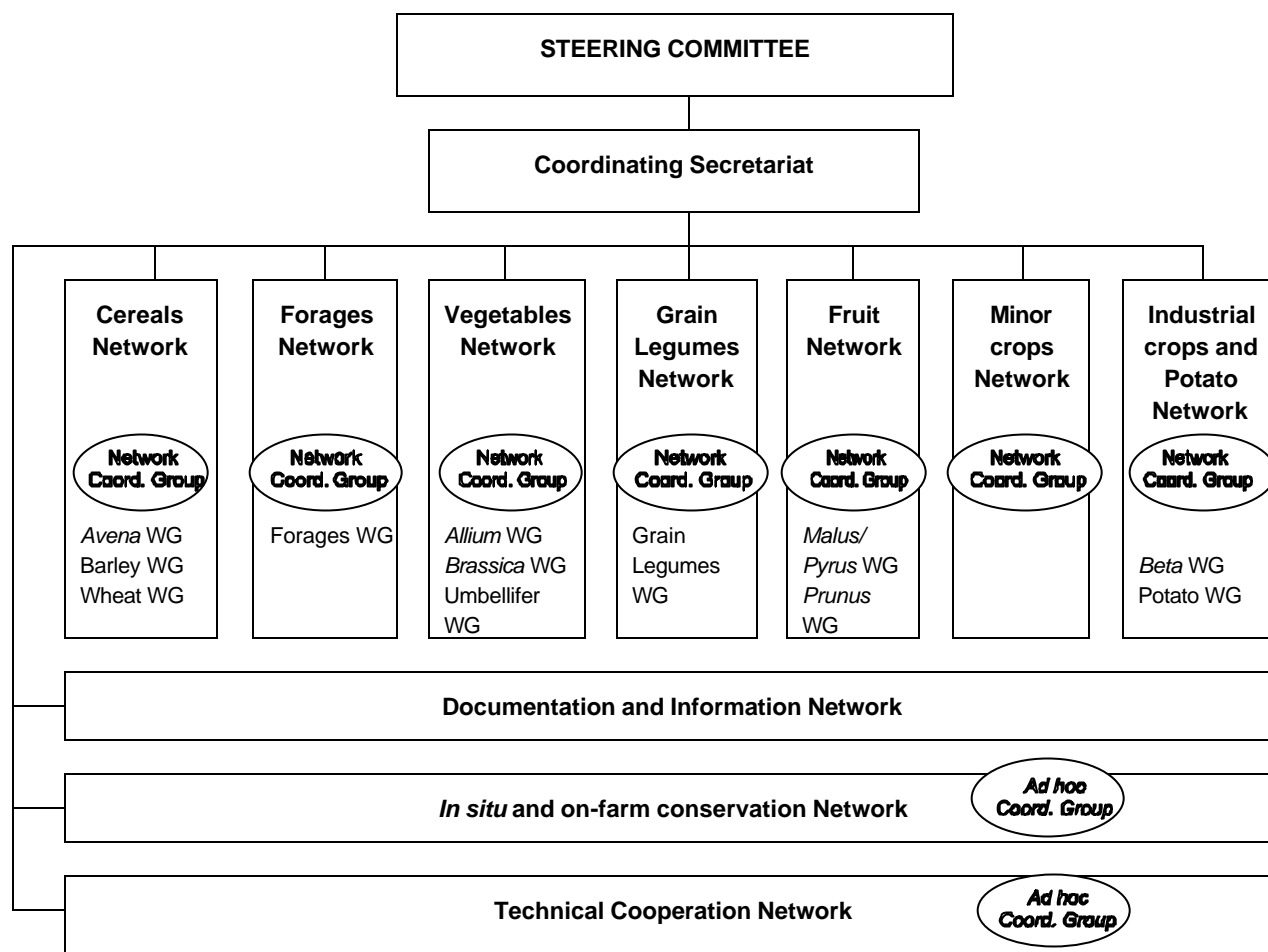


Fig. 1. Operational structure of ECP/GR, Phase VI.

Report of the WBN Secretary

The WBN Secretary reviewed the history of the WBN. He noted that in 1986 the Dutch-German cooperative programme on genetic resources provided additional manpower for the establishment of the European Database for *Beta* which became operational in 1987. The same year an *ad hoc* ECP/GR *Beta* Working Group including a scientist from the USA convened at Wageningen, The Netherlands. An International *Beta* Genetic Workshop was organized by the Centre for Genetic Resources (CGN) and IPGRI at Wageningen in 1989. On the initiative of IPGRI the World *Beta* Network (WBN) was founded at the end of this meeting as the first in a series of international networks that should become self-sustaining. Since then the WBN has met at Braunschweig (Germany, 1991), Fargo (USA, 1993), Izmir (Turkey, 1996) and Higham (United Kingdom, 1999).

The WBN is a voluntary association of experts. A steering committee called the *Beta* Coordinating Committee (BCC) promotes network activities and maintains contacts between the network and organizations such as IPGRI, the ECP/GR Programme and the International Institute of Sugar Beet Research (IIRB). The Network has a central crop database – the International Database for *Beta* (IDBB) – storing passport information donated by 28 national holdings. It serves as the central link within a network of decentralized collections. In 1989 network members agreed upon a number of collaborative activities.

L. Frese reviewed the technical workplan and the achievements of the past 10 years.

Passport data have been exchanged through the IDBB and the inventory of passport data of all collections has been completed, except for datasets available in China. Data published in a book on vegetable crops have been translated, processed and sent to the IDBB by Ma Yahuai (Institute of Sugar Beet, Chinese Academy of Agricultural Science). The whole dataset contained in the genebank information system of the Chinese genebank, however, is much larger. The IDBB manager will take up the initiative for exchange of further data between the Chinese collections and the IDBB. For the 28 holdings already documented by the IDBB, a permanent update of the IDBB is required as national holdings will change in size and composition.

Two concepts for documentation of characterization and evaluation data were discussed in 1993. Particularly plant breeders expressed the wish for a central documentation of evaluation data. Lack of manpower capacity was considered as a major constraint for the development of the IDBB. The WBN recommended finding a collaborator to develop a concept for documentation of exact evaluation data, to create the required logical structures in the IDBB and compile evaluation data. Attempts to acquire additional funds required for the IDBB improvement failed. L. Frese noted that the whole genebank information system of the BAZ Gene Bank would need a revision until late 1999 in view of a possible Year-2000-problem and that the IDBB, as one of the smaller databases managed by the BAZ Gene Bank, is currently used to investigate the best possible solution of the problem. As a result of this exercise, a new IDBB is being developed that will allow recording of characterization and evaluation data (see contribution of C. Germeier, p. 55).

The Group had recommended to transmit data on essential agreed characters to be observed during regeneration. A minimum descriptor list of characterization data was developed and published in the IPGRI Descriptors for *Beta*.

It had been recommended to send plans of national programmes for regeneration of accessions at 2-year intervals and the exchange and documentation (mainly of data from the holding at the University of Birmingham) of seed stock data was initiated. However, the coordination of a joint seed-increase programme required too much additional manpower and it proved very difficult to organize joint seed-increase activities according to a priority list of material requiring urgent regeneration.

Lack of sufficient amounts of seed was seen as a constraint to evaluation. During the meeting at Fargo (USA), the Group recommended persuading genebanks to fill the gap between seed increase and evaluation capacity by sending surplus seed lots from their yearly routine seed-regeneration programmes to Braunschweig, from where it can be forwarded to the various researchers. Surplus seed from the yearly seed production has been provided by the Czech, Russian, Iranian and German counterparts and mainly used to feed evaluation projects in the USA, Europe and Asia. Considerable progress has been achieved in the field of evaluation of collections, mainly through the systematic evaluation programme of the USDA-ARS in the United States and since 1996 through the EU-funded project GENRES CT95-42 and related ECP/GR-funded evaluation projects in Russia and Poland. For the first time, in Poland horticultural characters have been evaluated as discussed and recommended during the WBN meeting at Izmir (1996). The garden beet crop is a very important storage vegetable in East European countries.

The use of standard checks in germplasm evaluation was proposed in 1989 to improve the quality of data documented in genebank information systems. Today, standard checks are widely used in *Beta* germplasm evaluation programmes. L. Frese noted that very good progress has been achieved in the field of evaluation and utilization programmes (for example pre-breeding projects of the French network).

The WBN had recommended analyzing the information of the IDBB for selective germplasm collecting. Geographic gaps in collections were identified and targeted collecting missions implemented by various partners in Iran, Italy, Turkey, the Caucasian

countries, Egypt, China and others. Considerable progress has been made, although some geographic gaps still exist.

The WBN proposed to promote specific research on problems affecting the development of the Network. During recent years much research work on taxonomic and biosystematic aspects have been implemented and our understanding of the patterns of diversity has considerably grown since 1989. However, results published by various research groups could be more meaningful for the management of germplasm collections if there were a coordinated research approach.

In 1993 WBN members felt that meetings in 3-year turns would be sufficient if communication within the Group is maintained by a WBN Newsletter. It was proposed that the WBN Coordinating Committee and one reporter from each region should serve as editors and that the newsletter should be published twice a year, printed in India or published on the BAZ Gene Bank homepage. No progress has been achieved in that matter owing to insufficient work capacity.

The publication of technical WBN reports had been suggested and a pamphlet on seed increase procedures as applied by members envisaged. L. Frese suggested using a *Beta* seed increase protocol prepared by the BAZ Gene Bank as a starting point for the first WBN technical report.

The genus *Beta*, in particular landraces of leaf and garden beets, occurs in countries which have never been involved in WBN activities. In the past, WBN members had expressed the wish to participate of countries like Pakistan, Afghanistan, Iraq, Syria, Lebanon, Algeria, Albania and Spain. Lack of persons interested in the genus *Beta*, other national funding priorities and political reasons were identified as the main constraints with respect to the involvement of these countries.

L. Frese noted that finding financial means for WBN meetings has always been the prominent occupation of the *Beta* Coordinating Committee. He also noted that without the continued financial support received from IPGRI and various breeding companies the self-sustaining World *Beta* Network would never have been able to operate successfully over a period of 10 years. The establishment of the ECP/GR *Beta* Working Group will therefore facilitate the organization of future meetings considerably. This development should be considered as an important step forward.

IPGRI/FAO Multicrop passport descriptors

L. Maggioni informed the Group of the recommendation made at the Documentation Workshop in Budapest (October 1996) by the European Central Crop Database managers, regarding the adoption of the IPGRI/FAO Multicrop passport list for data exchange. He pointed out that all the ECP/GR Working Groups had adopted this format for data request and data exchange. The examples were given of the Forages, *Allium*, Barley and *Avena* passport lists, where a few additional passport descriptors were included in the respective lists. It was also mentioned that all the Descriptor Lists published by IPGRI are now using the Multicrop passport list and that also the System-Wide Information System on Genetic Resources (SINGER), which is combining all the data of the CGIAR genebanks accessions, has adopted this list as a standard. After almost 3 years of use, the Multicrop list, which is likely to be continuously evolving, is under revision; feedback from the users is welcome at IPGRI. The revision process is expected to be concluded and a new version released by Spring 2000.

International Database for Beta (IDBB) – state of the art

C. Germeier presented the current status and intended further developments regarding the database. The main task for the next months is to reach Year-2000 compliance by migrating the database backend from Oracle 6.0 to Oracle 8.05 server. User interfaces (Frontend applications) will be developed in Access 97 and Oracle Developer 2000. For downloadable off-line versions also the database backend will be available in Access 97. Internet access at present is provided by the German Agricultural Information Network (DAINET) on a BASIS server (<<http://www.dainet.de/genres/beta>>). Further development is to be sought in collaboration with ZADI, which is the provider of DAINET.

Main efforts are undertaken to modernize the database architecture by implementing a "human design" avoiding codes, abbreviations and underlining in naming tables, columns and keys, expanding the relational structure including additional tables for literature references, characterization and evaluation data, as well as consistent implementation of IPGRI Multicrop passport and FAO WIEWS descriptors.

A main structural change in passport data consists of dividing passport information into two new tables. The ACCESSION table holds information on single genebank accessions including accession numbers, identifiers for the holding genebank, reception dates and the donating institutions, but also original passport information provided by the holding genebanks. The ORIGIN table keeps information on genetic entities (duplication groups identified by L. Frese in the IDBB), which are presented as duplicated accessions in several genebanks. It holds collecting and taxonomic information in one data set for each duplication group, presented in a standardized style and updated by the latest knowledge provided to the database manager, especially regarding taxonomy. It has the MONIDBBNR, introduced by Th. van Hintum and L. Frese for identification of duplicate groups, as its primary key. Minor modifications relate to transformation of the field sample category into two new fields for duplication type and activity status and the field origin type into the new field collecting source according to the Multicrop Passport Descriptors.

The new concept for passport data will consist of five major tables (ACCESSION, ORIGIN, TAXON, COLLECTINGSITE, ADDRESS) and six decoding tables.

Evaluation and characterization data will be implemented into the database as suggested by the WBN meeting in 1993. A basic relational structure was adopted in 1992 from the CGN documentation system, including information on evaluation projects, descriptors, agronomic measures in field experiments and evaluation methodology, standard cultivars, experimental design, experiment sites and scores including statistical parameters. The new structure will be enlarged to 16 tables, thereby more efficiently coping with this information.

Discussion

In the discussion following, M. McGrath inquired about the possibility of including molecular data in the IDBB. He also mentioned that the USDA Genetic Resources Information System (GRIN) has no capacity for molecular markers data; however, the USDA National Agricultural Library has several crop-specific genome databases hyperlinked to their respective GRIN collections (*Beta* is not part of this yet).

C. Germeier replied that there has been thinking about this option, which is technically feasible. He informed the Group that a database including molecular data is under consideration by the Group for molecular genetics in cereals, IPK Gatersleben, and this may become a model to be used elsewhere.

Replying to a question by L. Frese, C. Germeier also mentioned the inclusion of literature data. Basic data are available from a collaboration with KWS and with Assoc. Prof. Ma Yahuai, Institute of Sugar Beet (CAAS) for inclusion in the database. These will

help to understand the origin of accessions mentioned in the literature, and the experimental conditions and methodology used in evaluation and characterization experiments.

According to B. Desprez the usefulness of the database could be improved if it contained maps showing the distribution of accessions with specific properties, such as disease resistance. C. Germeier replied that this would be possible with the introduction of a Geographic Information System software and that this would be an interesting project for which funds should be sought.

W. Beyer commented that the inclusion of more complex information in the IDBB is bound to reduce its user-friendliness. He suggested that it would be useful to maintain easy access to the most important data, such as those related to the core collection.

L. Panella recommended that the IDBB should be available in a downloadable form and C. Germeier confirmed that this will be the case.

A proposal was made by C. Germeier that the evaluation data from the GRIN system could be merged into the IDBB. These data, together with those produced by the EU-funded project partners, would form a valuable core of evaluation data. It was considered important and feasible to merge the data, rather than to simply hyperlink the two databases. This last option would limit access to users connected to the Internet, but would exclude several others, especially in the developing countries. A collaboration with GRIN Database managers was considered essential to understand the structure of the US system. L. Panella offered to facilitate the contact with the GRIN people and the provision of the GRIN database architecture.

Recommendations

The Group thanked C. Germeier for his work dedicated to the improvement of the IDBB and agreed on the following:

- *The elaboration of a database with a "human design", as presented by C. Germeier, should be continued by the IDBB manager.*
- *Characterization and evaluation data available from the genebanks and the national programmes should be sent to BAZ for inclusion in the IDBB, as proposed in the 1993 meeting.*
- *The IDBB should be provided with GIS software.*
- *The offer from L. Panella to facilitate the contact between BAZ and the GRIN database managers was welcomed and the IDBB manager was invited to look into the possibility of merging the US and European evaluation data.*
- *It is suggested that the IDBB manager should prepare a funding proposal to hire additional staff in charge of entering GRIN, GENRES and additional evaluation data into the database.*
- *The origin of all the IDBB data will have to be clearly acknowledged and immediately understandable for the database users.*

EU project GENRES CT95-42

On 7 September 1999 the fourth coordination meeting of the EU project took place at Broom's Barn. L. Frese summarized the objectives and output of the project. The EU-funded project 'Evaluation and enhancement of *Beta* collections for extensification of agricultural production' is carried out by 11 partners located in six European countries. The objectives of the project are: improvement of conservation, evaluation on disease and stress resistance, rationalization of collections, and documentation. Seed samples of the Synthetic *Beta* Core Collection (SBCC) have been multiplied by partners and sent through the project coordinator (BAZ Gene Bank) to project partners for evaluation. Five project partners charged with evaluation work have screened in total more than 2000 entries on disease and drought resistance. Accessions with promising variation for resistance to

Rhizoctonia solani, BMV, BYV, *Aphanomyces cochlioides*, *Pythium ultimum*, *Erysiphe betae*, *Cercospora beticola* and BNYVV have been detected.

L. Frese noted that three East European projects at the University of Kraków (Poland), the Czech Gene Bank, and the Vavilov Institute (Russia) were co-funded by the ECP/GR. The framework title for all three projects was 'Promotion of the use of East European *Beta vulgaris* germplasm collections'. Two of the projects were organized such that they supplemented and enforced the GENRES CT95-42 work programme (Russian and Czech activities). The Department of Genetics, Plant Breeding and Seed Science (University of Kraków) investigated the structure of genetic diversity of 40 garden beet accessions. For that purpose horticultural characters were evaluated in field trials. The same set of accessions was described by RAPDs. Based on the results of this project, improvements of the Synthetic *Beta* Core Collection have been proposed.

The rationalization of *Beta* collections and their use is another important objective of the GENRES CT95-42 project. Collections can be rationalized through identification of duplicates whereas the development and application of the Synthetic *Beta* Core Collection will allow a more rational use of the germplasm in evaluation projects.

L. Frese described the procedure applied to identify probable duplicates in the IDBB. About 15% of the total holdings belong to the sample category 'probable duplicates' which have been traced by collecting numbers, or by similar-sounding accession names. Within the framework of the GENRES CT95-42 project, groups of probable duplicates will be tested together with the 'most original sample' in the field (task of the BAZ Gene Bank). A seed lot of each accessions will also be described by molecular markers (task of the University of Birmingham) and results will be compared. Referring to the example of the duplicate group 'Egyptian' C. Germeier asked the Group whether they thought it useful to include pedigree information in the IDBB. In the following discussion, the opinion was expressed that the historical pedigree information would be very useful, if accurate, to identify potential sources of resistances. However, the usefulness of pedigree data was also challenged, considering that different selection methods used in the *Beta* breeding programmes would lead to completely different results, even if applied to the same genetic material. Therefore, genealogy data would not tell very much about similarities existing in the progeny.

The uncertainty about the availability or even the existence of pedigree data for *Beta* accessions was also considered an important factor and overall the Group estimated it very difficult and time-consuming to collect this information.

Recommendations

- *Considering the limited usefulness of pedigree data and the uncertainties linked to their existence, availability and reliability, the Group agreed that the inclusion of this information in the IDBB should not be a priority, although it could offer interesting insights.*
- *The IDBB manager is invited to continue with the identification of duplicates and rationalization of the collection.*

Synthetic *Beta* Core Collection (SBCC)

L. Frese described how the SBCC has been developed. Unlike the barley or *Brassica* core collections the SBCC was selected with top-down approach without any participation of partner genebanks holding a specific core collection entry. L. Frese considers this a shortcoming and a possible obstacle with respect to the general acceptance of the SBCC, which should be the ultimate goal of the WBN.

National core collections have been established by L. Panella (USA) and V. Burenin (Russia). N. Stavropoulos (Greece) had mentioned that they are planning to establish a national core collection. To make maximum use of all these efforts there is an urgent need

to combine national and international approaches. L. Frese mentioned that the SBCC currently consists of 674 accessions of which 618 have been sent to partners for evaluation. He noted that the SBCC is not an invariable set of accessions. When the EU-funded project is accomplished, data on the SBCC can be analyzed to improve the core collection jointly. The WBN agreed that the establishment of a Synthetic *Beta* Core Collection is a valuable tool which improves access to useful traits. L. Panella said that a core collection is a useful starting point for screening. It certainly does not replace the rest of the collection. It was also mentioned that if useful material has been detected on a specific branch of the collection, it can be an entry point to screen similar material in the collection.

Recommendations

It was recommended to involve more national genebanks in the process. The German Ministry of Agriculture would fund travel of L. Frese to the USA with the objective to further elaborate the core collection concept for Beta. This should be seen as a first step toward a joint approach.

It was recommended to establish a task force to look into the preliminary Synthetic Beta Core Collection and to further develop it. B. Ford-Lloyd, L. Frese, L. Panella and A. Tan agreed to participate in the task force. The task force will submit a proposal to the ECP/GR to fund a meeting. A meeting of the task force back-to-back to the IIRB Study Group meeting Breeding and Genetics (Capelle-en-Pévèle, France, September 2000) is planned. At a later stage the participation of scientists from other national collections should be encouraged.

National collections status reports

Delegates from Armenia, Azerbaijan, Belarus, Czech Republic, France, Georgia, Germany/Netherlands, India, Italy, Lithuania, Poland, Russian Federation, Slovakia, Turkey, United Kingdom and USA gave short presentations on the status of national *Beta* collections. Full reports are published in the second part of this volume.

Reports from Greece, Latvia and Switzerland were received on time for inclusion in the present document (see Part II).

Sharing of responsibilities for conservation

L. Maggioni introduced the issue of sharing responsibility for conservation, considered the most effective solution to increase efficiency of conservation activities and to reduce unnecessary duplication of efforts, as recommended by the Global Plan of Action (Leipzig, 1996). Sharing of conservation responsibilities for PGRFA in Europe was also identified by the Steering Committee as an objective for ECP/GR during Phase VI.

With reference to the article³ presented by Gass and Begemann at the European Symposium in Braunschweig (1998), the main options available are to share responsibility on an 'accession basis' (each country to take responsibility for a number of accessions) or on a 'crop-by-crop basis' (a few countries to take responsibility for entire crop collections). A third option would be to share responsibility in an integrated way on 'a subregional basis'.

Within ECP/GR, the 'crop-by-crop' option is already applied, for example under the bilateral agreement between Germany and the Netherlands, whereby CGN-Wageningen maintains the responsibility for seed-propagated potato species, while BAZ-Braunschweig takes care of the *Beta* collections. The 'accession basis' option also has been taken into

³ Gass, T. and F. Begemann. 1999. International efforts to sustain *ex situ* collections: options for a closer cooperation in Europe. Pp. 109-115 *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.

consideration by several Working Groups. The establishment of decentralized European collections was planned by the *Secale ad hoc* Group and by the Forages, Barley and *Prunus* Working Groups. These collections would comprise accessions that European genebanks would agree to maintain on behalf of all member countries of ECP/GR. Formal commitments would be taken by database managers and by curators in agreement with National Coordinators or the relevant national authority (see Report of a Workshop on *Secale* genetic resources, Poland 1996; Report of the Sixth meeting of the Forages Working Group, Norway 1997; Report of the Fifth meeting of the Barley Working Group, Germany 1997; Report of an Extraordinary meeting of the *Prunus* Working Group, Switzerland 1998).

Some of the advantages of decentralized collections would be (1) a formalized assumption of responsibility and continued access to the germplasm, (2) an equitable contribution of member countries to the system, and (3) a gradual development of all national systems encouraged. Prerequisites would be a high level of completion of the central databases and of confidence among countries regarding the quality of conservation and regeneration procedures and the continued free access to the germplasm.

The 'crop-by-crop' option would lead to the development of centres of excellence, characterized by high quality and crop specialization, to the benefit of a reliable conservation system and of a superior service to the users. However, the system would be difficult to implement when the total number of accessions in a collection was very large and difficulties would arise in the multiplication of genetic material distant from its original habitat. The responsibility to share accessions and to offer services would rest with the individual institution and not be under the control of a multilateral agreement.

This introduction was concluded with a reminder that the Steering Committee had encouraged the Working Groups to analyze the advantages and disadvantages of the various options for sharing responsibilities for their respective crop, including the technical conditions to be fulfilled.

Discussion

In the discussion following, B. Desprez identified probable difficulties in the implementation of a central system, since it would be more expensive to establish a central genebank than to make use of the existing national systems. Also, problems would likely emerge in the regeneration of the material. He also highlighted the benefits of relying on several people in different countries and on their varied expertise, rather than concentrating all the work in the hands of a few. Interest from a multiple range of stakeholders was also seen as being able to more effectively influence the governmental level with funding requests. He also pointed out the importance of *in situ* conservation, which cannot be centralized, together with the *ex situ* responsibility for the given crop.

L. Frese expressed his favour for the development of an increasingly efficient decentralized system, but he also considered that small collections could be transferred to genebanks offering their availability to take responsibility for their maintenance on behalf of the other countries. Smaller collections of various genera could be exchanged reciprocally between countries according to national priorities and specific interest. He clarified that Braunschweig would be open to consider this kind of arrangements, provided that these collections were suitable for multiplication in the central European habitat. The responsibility for *ex situ* conservation of specific material should stay with the institution having the best possible (natural) conditions and/or capacities. If genebanks could focus their capacities and expertise on specific genera this would contribute to more efficient management of genebank holdings.

Recommendations

The Group agreed on the usefulness of finding an acceptable mechanism whereby responsibility could be accepted for the maintenance of the Most Original Samples (MOS) identified in the IDBB. The completion of this exercise would allow all the collections holding duplicates to safely reduce their commitment for the maintenance of redundant samples.

The proposed mechanism is the following:

By the end of March 2000, the Database manager of the IDBB will provide the database in DBase format to all the Beta Network curators. All accessions will be marked as either MOS or probable duplicates. Curators will be asked to check the validity of these categories and to provide comments and corrections by the end of October 2000.

Whenever the MOS status is accepted, curators will also be requested to accept the accompanying responsibility for the maintenance of those accessions. Specific responsibilities for the MOS maintainer, the Database manager and the genebank hosting safety-duplicates are agreed as follows:

The responsibility of the maintainer of a MOS is defined as follows:

- *ensure that the accession is maintained under long-term conservation conditions in compliance with the international standards and the quality standard procedures agreed within the WBN;*
- *ensure that an appropriate safety-duplicate is deposited in a genebank, preferably within another WBN country;*
- *provide unrestricted access to the accessions to bona fide users from the WBN;*
- *in case of impossibility of honouring the commitment for long-term conservation and regeneration, inform the database manager.*

The responsibility of the IDBB manager would be:

- *facilitate the repatriation of material by distributing relevant information about accessions conserved in countries other than the country of origin;*
- *update the database when informed of changes by the national information systems and make the database available to the collection holders, both as a searchable and downloadable database on the Internet, and as a diskette upon request;*
- *forward to MOS maintainers any request for seeds;*
- *provide the collection holders and the WBN with information about the degree of safety-duplication of the collection.*

The responsibility of the genebank hosting safety-duplicates would be:

- *maintain a sufficient quantity of safety-duplicated germplasm in long-term storage in compliance with international standards and under a 'black-box' arrangement;*
- *not distribute the germplasm and the related information;*
- *immediately notify the MOS maintainer in case of any problem with the safety-duplicate;*
- *not carry out viability tests;*
- *not regenerate the safety-duplicated germplasm.*

Genebank quality standards

The WBN Secretary proposed to develop quality standards for the management of Beta holdings. He informed the Group that a discussion on the establishment of quality standards was held at a meeting of the Dutch-German Board for Plant Genetic Resources on the initiative of CGN at Wageningen, The Netherlands, in 1997. The development and

implementation of quality standards is considered as a prerequisite for further task-sharing and exchange of collections within the German-Dutch cooperative programme. In 1998 the ECP/GR *Avena* Working Group discussed different options for quality standards.

The main objectives of quality standards would be: to guarantee proper conservation of *Beta* genetic resources, to build trust in each other's competence and techniques, and to improve service for genebank users.

Two options for the development and implementation of quality standards were then described, referring to a discussion held by the ECP/GR *Avena* Working Group in 1998. On that occasion a proposal was made to establish a voluntary peer review system. A committee of Group members was supposed to visit member genebanks with the objective of assessing the degree of implementation of quality standards agreed by the Group and to discuss possible improvements. A second option would follow the principles of the ISO 9000 standards, based on the following procedures:

- development of a quality concept
- development of a model for production quality
- development of a model for quality control
- implementation of a quality control system in the database
- assessment of the function of system elements and development of technical guidelines.

Elements of a production quality concept would be:

- description of basic collection management aspects (is the collection divided into a base, active and security collection, etc.
- description of technical equipment (seed drying procedures, storage temperatures, etc.).

Elements of the technical guidelines could be:

- technical guidelines for seed increase procedures for each species
- development of regeneration passports for documentation of key data during the seed production process (fertilization, type of isolation applied, population size, etc.).

It was noted that genebanks would not be forced to follow a fixed concept. The principle of the ISO 9000 concept is rather: "Describe what you are doing, and prove that you are doing it!"

Recommendation

It was recommended that genebanks develop a pamphlet on seed-increase procedures on the basis of a draft written by L. Frese, which was distributed to the Working Group before the meeting. It was also recommended that the genebanks cooperating with the WBN accept the principles of the ISO 9000 and that they develop their own quality guidelines for Beta collections and publish them.

Genebanks who have already developed internal protocols are encouraged to send copies to L. Frese, to be used for further distribution and discussion within the Network.

Opportunities for *in situ* conservation of wild beet species

Ayfer Tan explained that the Aegean Agricultural Research Institute, Turkey is involved in two *in situ* conservation projects. The first one is focused on wild relatives and wild tree species and the second is the global project coordinated by IPGRI, aiming at strengthening the scientific basis for on-farm conservation.

She explained that the Gene Management Zones identified during the projects include the areas of distribution of the wild relatives of *Beta*, section *Beta* and section *Corollinae*.

Ecosystem-based surveys and species-specific inventories were made and management plans are under development, whereby *ex situ* and *in situ* conservation strategies are integrated.

An output of the project which is already available is the physical and ecological description of the selected areas.

The Group expressed its appreciation for the development of *in situ* conservation projects within the area of distribution of the wild *Beta* species. A matter of specific concern was identified for *B. macrocarpa* in southern Spain and Portugal, where the populations are potentially endangered by the reduction of their habitat, due to changes in the agricultural systems. Rare populations of *B. nana* in Greece are also considered probably under pressure.

Recommendation

The Group recommended that the wild relatives of Beta, and especially B. macrocarpa Guss. and B. nana Boiss. et Heldr. and possibly species from section Procumbentes, be included in in situ conservation projects by the respective countries and that international agencies such as the Council of Europe pay a close look at the monitoring of populations under potential danger.

Collecting activities

L. Frese described the results of two plant explorations in the Caucasus area (Armenia, Georgia and Daghestan-Russia) in 1990 and 1991. There is an overall impression that a lot of material from *Corollinae* section was lost in this area. L. Frese noted that another mission will start in Azerbaijan next week with the objective of searching for populations of *B. lomatogona* and to verify historical reports on the occurrence of inland forms of *B. vulgaris* L. subsp. *maritima* (L.) Arcang.

L. Panella mentioned preliminary negotiation with the Greek Gene Bank. It is intended to revisit collecting sites of *B. nana* in Greece and to collect seeds. A collecting mission would also be required to assess the degree of genetic erosion within *B. nana* and to recommend *in situ* conservation measures.

Presentation and adoption of the report

The Section *Discussion and Recommendations* of the report was presented to the participants and the report was adopted with few modifications. It was agreed to publish the technical report, selected papers and abstracts of all papers and posters presented during the meeting as an ECP/GR *Beta* Working Group report. Full papers will be published in a reviewed journal (*Journal of Sugar Beet Research*).

Election of the Working Group and Vice-Chair, and definition of the Beta Coordinating Committee

The proposal was made that L. Frese, permanent Secretary of the WBN, establish a strong linkage with ECP/GR by becoming the Chair of the Working Group on *Beta*. The Group approved the proposal. L. Frese accepted with pleasure on the condition that he would not continue to act as the Chair for many years. B. Desprez was proposed as the Vice-Chair and he accepted with pleasure. L. Frese reminded all that the ECP/GR *Beta* Working Group is an integral element of the WBN. He suggested electing, as in previous years, members of the *Beta* Coordinating Committee and requested participants from the USA and Asian countries to volunteer. M. McGrath (USA) was proposed, elected by the Group and he accepted with pleasure. The Asian region had been represented by India (2

turns) and China (1 turn). Participants from Iran had intended to join the fifth WBN meeting but met difficulties at the very last moment. It was proposed to ask M. Nasser Arjmand from the Sugar Beet Seed Institute at Karaj (I.R. of Iran) whether he would be available for this function. On 30 September 1999 Mr M. Nasser Arjmand thanked the Working Group for the trust shown and accepted the offer on the condition that he could be replaced by another Iranian scientist if the need arose.

The following persons will serve the ECP/GR and WBN for a term of 3 years:

- L. Frese (ECP/GR Chair, IDBB manager, Germany)
- B. Desprez (ECP/GR Vice-Chair, BCC member, France)
- M. McGrath (WBN, BCC member, USA)
- M.N. Arjmand (WBN, BCC member, Iran)

The Group recommends that the delegates from Italy and Poland inquire within their countries about the possibility of hosting the next ECP/GR and WBN meeting in the year 2002.

Closing remarks

A tour was made of some of the related research activities taking place in the laboratories and field plots at Broom's Barn, including a visit to the site where testing of *Beta* spp. for powdery mildew resistance was in progress.

On behalf of the participants, the Chairman warmly thanked the Director Dr J. Pidgeon for the splendid hospitality which contributed to an agreeable and productive mood during the meeting. Special thanks were addressed to Dr Asher as well as to Melanie Allison and all the staff involved in the organization of the meetings. Their commitment and excellent organizational work was appreciated by all participants. L. Frese thanked the members of the previous *Beta* Coordinating Committee (Dr M. Asher, Dr L. Panella and Prof. Sun Yi Chu) for their commitment, advice and continued support of the WBN Acting Secretary during the past 3 years. He also expressed his gratitude to L. Maggioni (representing the ECP/GR) for the financial support, his contributions to the meeting and valuable guidance. On behalf of the participants, Dr H.M. Srivastava expressed his gratitude to breeding companies and the sugar industry for their financial support which enabled the organizers to again convene beet experts from all geographic regions relevant to the crop.

Part II A. National collections

Beta genetic resources in Armenia

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According to the information available (archeological, literary, linguistic) beets have been cultivated in Armenia since ancient times. Armenian types typically have the general ancient external shape but with short or round roots. Crop types such as *Beta vulgaris* L. are characterized by great polymorphism. Unfortunately, most of the old cultivars disappeared for different reasons and the local genepool of cultivated beets is now impoverished.

It is considered that where the plant is regarded as an ancient, indigenous culture, it has its specific name. The ancient Armenian names of beet are *bazuk*, *baskik*, *chukuntur*, *banjar-klmpoz*, *machar*, *tsimel*, *silkh-chapary* and later it was called *chakndekh* (Srvandztyan 1876; Menevishean 1897; Bedevian 1936; Gabikean 1968).

The first name *basuk* is regarded as an original Armenian word, while the second has a common root with Persian names (*chugundur*) and the old Georgian *chakundeli*. This proves the local cultivation of beets and also that they were borrowed from the above-mentioned countries. According to Alishan (1895), wild and mountainous beets were used by the inhabitants to prepare different dishes with specific names: *silkh chapary*, *silkh pary*, *chaltar*, *chikundur* (similar to the Georgian *charkhaly*). In this respect, three varieties of wild beets are distinguished.

The existing Armenian name *zilk* probably refers to wild types. It has a common origin with the Arabic *zilkh*, *silkh* and is similar to the ancient name *silk* in the east, related to the shape of the leaves. In 1184 the Armenian healer Mkhitar Heratsy recommended beet, cut in slices, to his patients. This shows that beetroots were well known in Armenia at that time. Beet leaves are rich in mineral salts and vitamins (C: 60 mg%, A: 4 mg%); dry matter content is 12.5%; protein content is 24.4%. They also can be a valuable feed source. Prospects for cultivating wild crops are increasing, owing to several positive characters: early maturing (even earlier than spinach), ability to develop abundant foliage in spring and late fall, and ability to produce rich green biomass for animal feed in summer. Trials on beet seedbed preparation and cultivation practices were conducted and developed.

Wild beets in Armenia

Populations of mountainous beets (*Corollinae*) originated as a result of the Quaternary climatic change in the Transcaucasus mountains.

At present three species can be found which are widely popular in Armenia:

- *B. macrorhiza* Stev. is a large-rooted species. This species grows as a weed in sparsely distributed populations common at high altitudes (2000-2200 m above sea level).
- *B. lomatozona* F. et M. is the only species with monoseed fruit clusters, and grows as a weed in poorly vegetated regions.
- *B. corolliflora* Zoss., a tetraploid species, grows in wet climate in the highlands (2000-2700 m asl).

These three species have a common feature despite their morphological and anatomical differences: the hard pericarp, which prevents moisture penetration. The treatment of seeds with compressed nitrogen has not proved effective to induce germination. In case of mechanical damage of the seed coat, germination occurs in 5-7 days at a temperature of 20–29°C. The seed coat is damaged when they are kept in H₂SO₄ for 30 minutes and in

0.5% NaOH for 4 hours.

It should be mentioned that natural conditions (combination of temperature and humidity) influence the level of germination of the fruit clusters from September to March.

Anatomical research has established that *B. macrorhiza* is the closest to the cultivated beet variety which does not have mechanical tissues. Leaves and leaf stems are relatively larger than those of the other two species. Roots of *B. lomatogona* species are very rigid and stiff. The mechanical tissues are far more developed in the roots of *B. corolliflora* than in those of *B. lomatogona*. The leaf blades of *B. corolliflora* are significantly thicker than those of cultivated beets.

The study of wild varieties of beets reveals a number of valuable selection features:

- autumn seeding time
- cold-resistance
- large seeds, sprouts and roots
- drought resistance
- resistance to some leaf diseases.

The monoseed nature of *B. lomatogona* is particularly important.

These valuable features can be utilized only through distant hybridization of wild *Beta* L. varieties and forms with cultivated species.

Data referring to the use of wild varieties for breeding are available in the literature; detailed information can be found in the works of Burenin (1983).

Wild species also have negative features:

- excessively deep penetration of roots into the soil
- stick-shaped roots
- stiffness
- excessively early growth
- bolting during the first year, which reduces the thickening of the roots and the sugar content.

For the creation of distant hybrids in beets, the following must be taken into consideration: (1) the presence of useful characters in the wild species, and (2) the level of fertility in crossings between wild and cultivated species.

In interbreeding it is very important to take into consideration the appropriateness of the hereditary characters, because an undesirable combination is not excluded.

Beta lomatogona is known as a monogerm seed and drought-resistant species. Its hybrids are valuable for obtaining monogerm beets. Intercrossing of *B. lomatogona* with cultivated species is very difficult and requires amphyploid hybrids. The monogerm character is recessive in this species, therefore its successful introgression to cultivated species is not likely for the near future.

The intercrossing of two wild species is of great interest within the *Corollinae* section (Burenin 1983):

B. macrorhiza Stev. ($2n=18$) \times *B. lomatogona* ($2n=18$): hybridization is very difficult; few hybrids can be obtained, and great meiosis disorders are observed.

B. macrorhiza ($2n=18$) \times *B. corolliflora* ($2n=36$): hybridization is very difficult; few hybrids can be obtained because of reduction fission disorders.

B. corolliflora ($2n=36$) \times *B. lomatogona* ($2n=18$): hybridization is easy; hybrids are tetraploid, self-fertile and productive.

B. macrorhiza ($2n=18$) \times *B. vulgaris* ($2n=18$): hybridization is easy; hybrids are productive, they are valuable for the obtention of big sprouts of beets which are cold and winter resistant.

B. vulgaris ($2n=18$) \times *B. lomatogona* ($2n=18$): hybridization is difficult: hybrids are not fertile.

Given the high potential use and the endangered status of wild *Beta* germplasm in Armenia, it is recommended that collaborative collecting missions be organized in the near future in this country.

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Sugar beet in Azerbaijan

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Azerbaijan is a unique country from the natural history and biodiversity perspectives (Vavilov 1966). Caucasus, including Azerbaijan, together with Mediterranean countries, presents a remarkable specific and varietal diversity of beet (*Beta*). Four beet species out of 12 distributed in the world are found here: *Beta perennis* (L.) Freyn, *B. vulgaris* L., *B. lomatogona* F. et M. and *B. macrorhiza* Stev. Each of these four species is a distinctive ecogeographical type, characterized by certain natural habitat and biological specificities.

Long-term experiments conducted in various agro-ecological conditions showed that Azerbaijan is very favourable for sugar beet cultivation and is considered a potentially high-yielding region. Among the agronomical problems of sugar beet cultivation, methods of direct seed sowing without transplanting were studied in more detail. In experiments conducted over many years, a good harvest was obtained even in heavy clayey gray soils with spring sowings (50-70 t/ha), as opposed to post-harvest sowing yields as low as 2.5-3.5 t/ha. The sugar content in the roots reached up to 17.5% (Aliev 1974, 1984, 1988).

In spite of this, sugar beet was not systematically cultivated in Azerbaijan as a traditional crop. It was cultivated in collective and state farms and in households in a small area during World War II when people were faced with food and sugar shortages. After the war, problems of food and sugar shortages were eliminated and there was no need to cultivate sugar beet for sugar production. However, sugar beet has been cultivated as a valuable fodder crop since then (Aliev 1991).

After the downfall of the former Soviet Union and the achievement of Azerbaijan's independence, some difficulties arose in providing the population with sugar and this spurred the cultivation of local sugar beet.

In spite of favourable conditions, local breeding and seed production were not developed, and only introduced varieties were grown. Sugar beet's importance is increasing in Azerbaijan and its cultivated area increases regularly, from 2000 ha in 1992 to 10 000 ha at present. But yield and sugar production have not increased, for various reasons.

Local varieties and sugar-processing factories are not available in the country. Sugar-processing factories are now under construction. Therefore the promotion of breeding activities with the purpose of developing local varieties tolerant to biotic and abiotic factors, and organization of the seed production are required.

There are currently no working collections in the country, but about 20 varieties of various origins are used. Along with these, large-rooted and multi-rooted beets are found in Azerbaijan, especially in the upper and medium mountain belts on stony and dry slopes; at weedy and ruderal sites in brushwoods, wild species can be found with useful traits for potential breeding (Anonymous 1952). The most interesting area for collecting lies within the bounds of the country's eastern and western slopes of the Talysch mountains, where still undescribed wild beet forms can be found.

New material collected in collecting missions may provide genetic resources not only for disease resistance but also for other agronomic valuable characters.

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Germplasm collections in Belarus

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A high level of interdependency exists between the Republic of Belarus and other European countries with regard to genetic resources of major crops. We are interested in making genetic collections readily usable by our breeders, and confirm that it is impossible for one country to maintain and exploit them effectively.

Belarus does not have a National Programme for the conservation and use of genetic resources. However, such basic principles were developed by the National Academy of Sciences. A Special Project was planned, due to start in 1997, but for budgetary reasons it was delayed. Its main objectives were:

- to organize the maintenance and analysis of the existing collections of plant genetic resources in the Republic of Belarus
- to develop a system of passport and characterization description
- to collect and preserve information concerning genetic and breeding value of the material
- to build a catalogue of the existing national plant genetic resources and organize their regeneration
- to make genetic collections, including donors of useful traits accessible to the institutions interested in their utilization, to obtain access to relevant information from the international centres of biodiversity and promote information exchange between national and international centres.

The project was planned for a 3-year period. It was also planned to establish the National Coordinating Centre at the Institute of Genetics and Cytology, with additional staff from the Research and Breeding Institutions involved in this project. However, restrictions in the funding of agricultural research had a negative impact on the budget plans of the Breeding and Research Institutes.

In recent years close collaboration was established between east European institutions, including from Belarus, and other relevant institutions of the same profile, through participation in joint projects (INTAS, Copernicus) and attendance at scientific conferences, meetings and courses, providing personal contacts and material exchange.

Breeding activities in our country are mainly carried out by the public sector. Genetic collections of cereals (wheat, rye, barley, triticale), potato, flax, beets, tomatoes are maintained in the Institute of Genetics and Cytology, Institute of Experimental Botany, Botanical Garden (all part of the National Academy of Sciences); the Institute of Forestry, Institute of Farming and Fodder Crops, Belorussian Institute of Potato Research, Institute of Horticulture, Institute of Greengrocery, Institute for Plant Protection, and in Breeding stations as seeds and *in vitro* collections. Each Breeding and Research institution is responsible for conservation of the genetic material originated, collected, bred or selected within its territory of competence and is responsible for maintaining its viability.

Parts of germplasm collections in Belarus are safety-duplicated within the country, in the Russian Federation and in the Ukraine. We are willing to establish a cooperative and integrated system for conservation and use of plant genetic resources for food and agriculture in Europe, to facilitate different forms of regional cooperation and to participate in developing a global network of base collections.

Status of the *Beta* collection in the Czech Republic

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History

Plant genetic resources (PGR) including sugar, fodder and garden beet were originally gathered in the last century at breeding stations with the aim of utilizing them in breeding programmes. Systematic work on plant genetic resources in former Czechoslovakia and in the Czech Republic developed step by step since the beginning of the 1950s. Genetic resources (GR) of sugar and fodder beet were gathered, maintained, evaluated and utilized at the former Breeding Station Sem.ice. Garden beet accessions have been gathered as part of the vegetable collection at the former Research Institute for Vegetables in Olomouc, now a branch of the Czech Gene Bank. Both institutions were responsible, as cooperators on PGR, for the collections mentioned above.

In the field of documentation, computerization of passport data started in the country in the mid-1970s. Passport data of *Beta* genetic resources submitted by both cooperators were introduced into the national documentation system EVIGEZ.

Cooperators taking part in the national PGR network were responsible for maintenance of PGR until 1989 when the facility for long-term storage of seed samples at the Research Institute of Crop Production (RICP) in Prague was built. Since then the cooperators started to regenerate seed-propagated PGR, including *Beta* GR, and transfer them into the genebank storage facility. The process continued until the privatization of the Breeding station Sem.ice. The Research Institute for Vegetables was abolished in the beginning of the 1990s, but fortunately the GR unit was saved and joined with the genebank in the RICP as the workplace specialized in vegetable genetic resources.

Current status of *Beta* subcollections

Sugar and fodder beet subcollections are conserved in the genebank (29 accessions of sugar beet and 28 of fodder beet). All of these are of Czechoslovak or Czech origin. Passport data collected in the past are available for 319 and 107 accessions respectively (Table 1). These subcollections have not been increased recently because newly released cultivars are exclusively hybrids. The subcollections were evaluated partly in the framework of GENRES CT95-42 at the Breeding station Kostelec u Krizku on the basis of agreements.

The garden beet subcollection consists of 113 accessions of salad beet and 17 Swiss chard accessions. They include 13 salad beet and 1 Swiss chard accession of Czechoslovak or Czech origin. Passport data are available in the documentation system for 135 and 31 accessions respectively. The collection is systematically multiplied, regenerated under technical isolation and evaluated. Evaluation data are submitted to the documentation system and seed samples to the genebank facility.

Passport data on Czech *Beta* genetic resources are available on the Internet at the following URL: <<http://genbank.vurv.cz/genetic/resources/>>.

Table 1. Survey of *Beta* genetic resources in the Czech database and genebank

Species/varieties	No. of accessions
Total <i>Beta</i>	
Passport data	596
Accessions available	190
accessions of Czech or Czechoslovak origin	71
seed samples stored in genebank	96
<i>Beta vulgaris</i> var. <i>altissima</i>	
Passport data	319
Accessions available	29
accessions of Czech or Czechoslovak origin	29
seed samples stored in genebank	29
<i>Beta vulgaris</i> var. <i>rapacea</i>	
Passport data	107
Accessions available	28
accessions of Czech or Czechoslovak origin	28
seed samples stored in genebank	28
<i>Beta vulgaris</i> var. <i>vulgaris</i>	
Passport data	135
Accessions available	113
accessions of Czech or Czechoslovak origin	13
seed samples stored in genebank	34
<i>Beta vulgaris</i> var. <i>cicla</i>	
Passport data	31
Accessions available	17
accessions of Czech or Czechoslovak origin	1
seed samples stored in genebank	2
<i>Beta</i> - wild species	
Passport data	4
Accessions available	3
accessions of Czech or Czechoslovak origin	0
seed samples stored in genebank	3

Conditions of Beta seed samples maintenance in the Czech genebank

Seed samples received from the cooperator must be in good health, with required level of germination, this being the cooperators' responsibility. In the genebank the seed samples are dried down to 6–7% moisture content under a maximum temperature of 25°C. At least 12 000 seeds per accession are stored in glass jars with vapour-proof lids. The seed samples in the active collection are kept under a temperature of –5°C.

Possibilities of safety-duplication of the Czech Beta collection

After the construction of the new genebank at the Research Institute of Crop Production in Piesňany in the Slovak Republic, the agreement on safety-duplication was settled. This agreement is a good base for a system of mutual safety-duplication of the most valuable parts of PGR collections, including the *Beta* collection.

Formation of the Beta 'core' collection

The Czech genebank is willing and prepared to provide data and seed samples of the accessions suitable for the core collection preparation. Special evaluation of garden beet accessions can be carried out in the genebank station at Olomouc.

Possible use of molecular techniques for the core collection preparation can be discussed with the Department of Molecular Biology at RICP Prague.

The French Network for *Beta* genetic resources

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In France, management of beet genetic resources has been carried out through a cooperative network of different partners from state organizations (Ministry of Agriculture, CTPS, GEVES, INRA, University of Lille), professional organizations (GNIS, ITB, FNAMS) and private breeding companies. The coordinator of the network is BRG (Bureau des Ressources Génétiques = Genetic Resources Board). Network members agree on a common pool, on maintaining, evaluating and distributing the genetic resources. A Steering Committee manages the Network, assisted by a Coordination Section in charge of activities and technical organization (see Desprez 1998).

The French *Beta* Network is defined in regards to (as a part of) the already existing World *Beta* Network. The material which is introduced into the collection ("National collection") as a priority is that for which France will assume responsibility.

Considered part of the National collection are:

- the French cultivars arising from the French catalogue (A and B lists)
- the populations and the old cultivars with a French origin (e.g. diploid populations stored at INRA)
- the wild material arising from prospections on the French territory (*in situ* conservation)
- the material well known for the presence of identified genes
- the material arising from the dynamic management programme, which associates wild and cultivated beets (programme initiated at IIRB).

Since the first working group meeting in 1994, a charter was signed in November 1997. A copy of this charter was given to L. Frese, Secretary of WBN and Chair of the ECP/GR Working Group on *Beta*. An internal "manual" was also jointly prepared by the members, in particular to describe the common standard for multiplication and seed storage.

INRA was supposed to be in charge of finding a network coordinator, but unfortunately they decided not to be involved any more in sugar beet breeding and improvement, and therefore the network and its evaluation programme are currently in a "standby" situation. However INRA is proceeding with its own evaluation programme before stopping its activities on beet, and a meeting should be held soon to find a network coordinator.

Everything will be done to enhance this programme and especially to keep in good shape the wild material collected from France by Devon Doney and Henry Laby.

Concerning the dynamic management programme (buffer population programme), the first prebreeding material was produced from wild *B. maritima* (which often carries Rhizomania-resistant genes), and has been distributed among the participants. Considering the success of this first establishment of a common buffer population, a second programme is being implemented. The latter uses some of the well-characterized accessions arising from the EC project led by L. Frese. In collaboration with him a group of accessions showing resistance genes to *Erysiphe*, yellows virus, Rhizomania, etc. were shared with some participants in 1999 to enhance a new buffer population programme, in principle identical to the previous one. All these buffer programmes are presented under the IIRB Genetic and Breeding group. Everyone can participate.

Another programme could be launched under the French Network system together with German colleagues, based upon a similar system of buffer populations, choosing from the EC project accessions carrying resistance genes to *Cercospora beticola*, an important and complex disease (four or more genes are involved and only one source of resistance is

currently commercially used).

For further information on the French *Beta* Network, the following persons should be contacted:

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Reference

Desprez, B. 1998. Towards a French Network for beet genetic resources. P. 82 in International *Beta* Genetic Resources Network. A report on 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 (L. Frese, L. Panella, H.M. Srivastava and W. Lange, eds.). International Crop Network Series. 12. International Plant Genetic Resources Institute, Rome.

Beta genetic resources in Georgia

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Georgia is a country of ancient agriculture characterized by a great diversity of endemic and indigenous crop varieties. The country deserves attention as a "breeding ground" of species and subspecies. The importance of the Georgian endemic species and indigenous varieties of crops is determined not only by their historical role, but also by the great role they play in creating crop varieties of a new type, characterized by high productivity and resistance to pests as well as to stressful climatic conditions. These qualities are especially characteristic of the varieties of wheat, corn, barley, fruit and grape created by Georgian scientists.

In Georgia the development of industrial beet production began at the end of the 19th century, when highly productive beet varieties intended for different purposes were introduced. *Beta vulgaris* var. *cicla* has been used in our country for the preparation of different kinds of so-called *pkhali* – a dish of dressed boiled vegetables – since time immemorial, this dish still being the centrepiece of the Georgian table nowadays.

Although beet is a popular product in Georgia, the conservation and use of its genetic resources need improvement. Selective work for the development of new highly productive and disease-resistant varieties is not being carried out. Although *B. maritima*, according to literature, is spread in the region of the Black and Caspian Sea, wild relatives of beet have not been studied. The conservation and multiplication of beet varieties, both *ex situ* and *in situ*, are not in good condition. Attending this meeting will enable us to establish close links with developed countries and specialized scientists, and give us an opportunity to obtain high-quality seeds and information on their production and storage.

Currently available beet resources

Four beet types are produced: leaf beet (mangold), table beet, fodder beet and sugar beet. The first three are produced by small farmers on their small plots. Sugar beet is produced by large companies on large-scale farms, about 5000 ha area. There is also a working sugar factory which uses sugar beet imported from the Ukraine.

Research work on beet is carried out mainly at the Institute of Agriculture (Georgian Academy of Agricultural Science) where agrotechnical measures have been developed for sugar and table beet. At the same institute a scant collection of beet genetic resources is kept under poor conditions. The selection of better beet varieties for Georgian conditions is being studied by the Department of Vegetable Crops at the Agrarian University.

The Institute of Plant Protection has studied the pests, diseases and weeds and has developed effective control measures. These measures have been adopted by farmers.

At present in Georgia the following varieties of different beet forms are distributed:

- table beet: 'Bordeaux 237', 'Gori Efrut', 'Odnorostkovaya', 'Dvusemiannaya', and the local variety 'Digomi' characterized by good flavour and long-term storability. The rest of the varieties are imported. For the last 3-4 years the Institute of Agriculture has studied the imported varieties and hybrids; outstanding among them is the Dutch variety 'Bikures' which can be profitably grown under local conditions.
- leaf beet (mangold): 'Chankutela', 'Sotelia', 'Tsiteli pkhali', 'Lukulisi', 'Giganti', 'Lomi', which are local varieties.
- fodder beet: 'Bares', 'Pobeditel', 'Eckendorf yellow' (all imported).
- sugar beet: 'Paltushkovskaya', 'Raminskaya', 'Odnosemiannaya' (all imported).

In Georgia beet pests and diseases are widespread. The most important are miner moths, aphids, fleas, bugs, cercosporosis, *Oidium*, *Phomopsis* and rust.

Status report on *Beta* genetic resources activities in Germany

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Introduction

The sugar beet is one of the most important cash crops in Germany. It is grown on 505 000 ha (1997/98). While breeding for higher root and sugar yield, improved sugar quality and characters facilitating the production of the crop such as monogerm seeds have always played an important role in variety development. For several years breeders also have been increasing their efforts in the field of breeding for plant diseases, pest and environmental stress resistance. Breeders are systematically supplementing their working collections with germplasm required to meet the needs for ongoing and future breeding work. Researchers working in the private or public sector in Germany acquire *Beta* germplasm from different sources, among them the national *Beta* germplasm holdings. In particular the Gene Bank of the Federal Centre for Breeding Research on Cultivated Plants (BAZ) is used by researchers in the private and public sector as an intermediary for the request of specific germplasm held by other genebanks of the World *Beta* Network.

Genebank holdings

Beta genetic resources collections are maintained by two institutions. The BAZ Gene Bank is located at Braunschweig. The BAZ is part of the research sector of the Ministry of Food, Agriculture and Forestry (BML). The *Beta* collection at Braunschweig is managed as the joint German-Dutch *Beta* collection within the framework of an agreement signed by the German and Dutch Ministries for Agriculture in 1984. The Institute of Plant Genetics and Crop Plant Research (IPK), with its genebank, operates under the Ministry of Education, Science, Research and Technology (BMBF).

Collecting

There is a tendency to focus collecting activities on species that match national interests. Germplasm is only collected and added to the national holdings to fill in specific gaps. Since the last WBN meeting in 1996 (Izmir, Turkey), the BAZ Gene Bank and IPK Genebank have collected only a few new *Beta* accessions during multicrop collecting missions. Today the total national *Beta* genetic resources holding consists of 2202 accessions (Table 1). On the basis of seed quantity and quality, 55% of the BAZ Gene Bank's collection and 87% of the IPK Genebank's collection are currently available.

Seed multiplication and processing

Isolation greenhouses, hemp isolation fields or spatial isolation are used at both locations to multiply *Beta* accessions. Biennial material is sown in October and vernalized in a cold greenhouse during winter. Depending on the length of the sowing to bolting period, annual types are sown between late January and late March in the greenhouse in peat pots and transplanted to the isolation greenhouse or hemp isolation plot. Pericarp caps of fruit balls of *Corollinae* and *Procumbentes* species are removed manually, sown in the greenhouse in April to May, cultivated further and transplanted to 10-L pots in late summer. These plants survive the winter in Germany under a rain and wind shelter without any problems. About 60-70 plants of each accession are grown to avoid losses.

Table 1. *Beta* genebank holdings in Germany

Botanical name	BAZ Gene Bank			IPK Gene Bank		
	Available	Seed regeneration required [†]	Total holding	Available	Seed regeneration required	Total holding
<i>Beta</i> sp.	2	17	19	10	8	18
<i>B. macrocarpa</i>	21	17	38	4	0	4
<i>B. patula</i>	0	5	5	0	0	0
<i>B. vulgaris</i> subsp. <i>adanensis</i>	29	4	33	0	0	0
<i>B. vulgaris</i> subsp. <i>maritima</i>	273	92	365	48	7	55
<i>B. vulgaris</i>	56	64	120	42	27	69
<i>B. vulgaris</i> subsp. <i>vulgaris</i>	40	12	52	7	0	7
<i>B. vulgaris</i> subsp. <i>vulgaris</i> Leaf Beet group	111	26	137	64	1	65
<i>B. vulgaris</i> subsp. <i>vulgaris</i> Garden Beet group	168	35	203	65	1	66
<i>B. vulgaris</i> subsp. <i>vulgaris</i> Fodder Beet group	97	40	137	60	2	62
<i>B. vulgaris</i> subsp. <i>vulgaris</i> Sugar Beet group	195	25	220	14	0	14
<i>B. corolliflora</i>	26	57	83	1	0	1
<i>B. macrorhiza</i>	10	25	35	0	0	0
<i>B. lomatogona</i>	22	73	95	1	0	1
<i>B. intermedia</i>	87	124	211	0	0	0
<i>B. trigyna</i>	11	14	25	0	1	1
<i>B. nana</i>	0	14	14	0	0	0
<i>B. procumbens</i>	5	2	7	0	0	0
<i>B. webbiana</i>	3	0	3	0	0	0
<i>B. patellaris</i>	29	6	35	2	0	2
Total	1185	652	1837	318	47	365

[†] As computed by GENSTORE, the storage and information management system of the BAZ Gene Bank (Bücken and Frese, Zeitschrift für Agrar informatik, in press). If the number of viable seeds in the storage container is less than a threshold level, the accession is automatically defined as 'not available'. In the case of hard-seeded species no germination data are available. Seed availability depends solely on the amount of spare seed in the container.

Hemp barriers and isolation greenhouses have different advantages and disadvantages for seed production. As temperatures in the isolation greenhouse may rise during the day in summer up to 45°C, we prefer to multiply late-bolting, biennial material in hemp isolation, although there is always the risk of slow growth of hemp plants and insufficient isolation.

Fast-bolting species adapted to warmer spring temperature like *B. macrocarpa*, *B. patula*, *B. vulgaris* subsp. *adanensis*, early bolting subsp. *maritima* and all species of section *Procumbentes* can be multiplied in the isolation greenhouse without problems. Because of very early flowering, often in mid-March, *B. macrorhiza* can only be regenerated in isolation greenhouses. *Beta corolliflora*, *B. intermedia* and *B. trigyna* can be successfully grown in the isolation greenhouse as well. During humid springs, however, seed set can be insufficient in cool and damp growing conditions. These species, in particular *B. lomatogona*, are less adapted to the growing conditions in the field and greenhouse at the Braunschweig location. Without special efforts, i.e. cultivation in expensive growth chambers, seed production of *B. nana* is impossible at Braunschweig.

In general seeds are harvested as bulk on 50-60 plants per accession. In particular in hot summers, seed plants are removed from the isolation greenhouses as early as possible to avoid adverse effects of high temperatures on the seed viability. Seed stalks are dried in the larger temperature-controlled greenhouses or in a drying chamber at 25°C (Braunschweig). The seeds are then threshed with a Hege threshing machine, sieved and roughly sorted with a wind sorter machine. For several years a belt sorter and the polishing machine at the Dieckmann company have been used for the final seed processing. A small proportion of the polished seeds is then taken for the germination test. The remaining part of each sample is dried within a period of 3 weeks in a drying chamber at 25°C and 3% air humidity to a seed moisture content of 5-6%.

Germination tests

The *Beta* collection at the BAZ Gene Bank is tested according to a modified ISTA (International Seed Testing Association) method whereby 8 × 25 seeds are placed on round filter papers in Petri dishes. The germination temperature is 20°C (8 h light/16 h dark). After 7 days, the seedlings are counted. A seed ball producing one healthy seedling is considered to be fully viable.

Hard-seeded species are not tested.

Seed storage

About 200-250 g of carefully dried seeds are stored in an airtight sealed tin plate container at -10°C (active collection sample, large storage room). If the accession is new, a second 10-g sample (base collection) is vacuum-sealed in an aluminium foil bag and stored at -18°C in a refrigerator, and a third one sealed in an aluminium foil bag is sent as security-duplicate to the CPRO-DLO CGN at Wageningen, The Netherlands. To date, 1460 base collection samples have been packaged and stored in a separate compartment at Braunschweig and 1202 *Beta* security samples were sent to the CGN.

Two hundred and thirteen (213) *Beta* accessions have been received from other genebanks like the Czech, Russian and Iranian genebanks and are being kept as 'black-box' security duplicates sealed in aluminium foil bags at -18°C.

Data documentation

All passport, characterization, evaluation and seed stock management data are documented in GENSTORE, the storage and information management system of the BAZ Gene Bank. The system is currently running under the ORACLE 6.0 DBMS software. *Beta* evaluation data are kept in a database structure different from the main system (see C. Germeier, this volume, p. 55).

Distribution of germplasm and information

Information and seed samples are distributed freely. In 1998, 1086 *Beta* samples were sent by the BAZ Gene Bank to users.

Germplasm characterization and evaluation

During seed increase each accession is described according to a standard minimal descriptors list derived from the IPGRI Descriptors for *Beta*. Evaluation of germplasm is only conducted by the BAZ Gene Bank in exceptional cases. Mostly, evaluation work is implemented by breeding companies and research institutes in Germany, by members of the International Institute for Sugar Beet Research (IIRB), or through the EU project GENRES CT95 42 (see also abstract, this volume, p. 90).

Research

Beta genetic resources are used in Germany in different research contexts:

- investigation of species relationships and evolutionary aspects
- risk assessment studies and potential geneflow between sugar beet and wild species
- genetic problems related to utilization of germplasm and, more recently
- investigation of the *Beta* genome.

Project proposals can be submitted to a number of funding agencies by any researcher. A specific coordination mechanism is provided by the GFP (Association for the Promotion of German Plant Breeding). The annual meeting of the GFP is often the starting point for new research initiatives and projects. The meeting may be used by researchers to harmonize a proposal with the interests and needs of the breeding companies. Generally, a short research project draft is discussed between researchers and the GFP member companies during the annual meeting of the GFP before a full project proposal is submitted to funding bodies. These projects are then implemented in cooperation with GFP member companies.

International cooperation

Since sugar beet breeding has become an international activity with many players in the northern hemisphere cooperating with the few sugar beet breeding companies, genebanks obviously have to maintain working relationships at the national and international levels. There is therefore no longer a strict separation between national, European or international activities. In the field of evaluation the BAZ Gene Bank has been cooperating with institutions within Europe, in Iran, India and China.

Current status of *Beta* genetic resources in Greece

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The Greek Gene Bank today holds 746 accessions of *Beta*. Almost all the material has been collected through IBPGR-supported expeditions in Greece and other Mediterranean countries in the period 1979-86. The focal points for the collections in Greece were the Hellenic Sugarbeet Industry (HSI) and the Greek Gene Bank. The Greek Gene Bank has been assigned regional responsibility by IBPGR for maintaining this germplasm. Collecting expeditions, countries and areas explored and number of accessions collected are listed in Table 1.

Table 1. Origin of the *Beta* germplasm maintained in the Greek Gene Bank

Year	Collector	Country	Accessions	Collected area
1979	IBPGR	Greece	83	Eastern Aegean islands
1980	IBPGR	Greece	86	Ionian islands, Peloponnese
1981	GBRBIRM-PBI	–	54	
1981	GRCHSI	Greece	8	Halkidiki, Thessaloniki
1981	IBPGR	Greece	96	Peloponnese, Sterea Hellas, mountains for <i>Beta nana</i>
1981	IBPGR	Italy	107	Sicily
1982	GBRBIRM-PBI	Algeria	25	
1982	IBPGR	Greece	48	Creta island
1983	GBRBIRM-PBI	–	7	
1983	IBPGR	Greece	62	Makedonia – Thessalia
1983	GRCTOBIN	Greece	4	Eastern Makedonia
1984	IBPGR	Tynesia	22	
1985	GRCGGB	Greece	32	Central Greece, Evia
1986	IBPGR	Cyprus	39	
1986	IBPGR	Israel	62	
1988	GRCGGB	Greece	1	Peloponnese
1988	IBPGR	Syria	10	
		Total	746	

The collection consists of seven species, of which the most predominant and representative of Greece and the region are *B. vulgaris*, *B. maritima* and *B. nana*. The other species are represented by a limited number of accessions, which were provided by the Birmingham Gene Bank (United Kingdom), as reference material. The species representation in the Greek Gene Bank appears in Table 2. Of the 746 accessions, 420 were collected in Greece (*B. vulgaris*, *B. maritima* and *B. nana*) and 326 in other countries, mainly Mediterranean.

The majority of the accessions are conserved under medium-term conditions (0-5°C, 25-30% storage room air humidity) with the expectation of a timely regeneration-multiplication to produce adequate seed for subsequent storage in the long-term base collection. About 100 accessions, multiplied between 1985 and 1987 by the Hellenic Sugar Industry, were deposited under long-term storage conditions (-19 to -21°C, hermetic packaging in tin cans).

Table 2. *Beta* species, respective accessions and country of origin of the *Beta* collection at the Greek Gene Bank

Species	Accessions	Country of origin – Collection
<i>Beta macrocarpa</i>	7	1 Algeria, 1 Cyprus, 5 Tunisia
<i>Beta maritima</i>	272	
<i>Beta nana</i>	28	mountains of Mainland Greece and Peloponnese
<i>Beta patellaris</i>	5	from Birmingham collection
<i>Beta procumbens</i>	1	from Birmingham collection
<i>Beta vulgaris</i>	432	
<i>Beta webbii</i>	1	from Birmingham collection
Total	746	

A new opportunity for regeneration was provided by the EU GENRES CT95-42 programme on *Beta* Genetic Resources, funded in the framework of EU Regulation 1467. The programme has a 5-year duration (1996-2001) and aims at the regeneration and multiplication of threatened *Beta* genetic resources, the replenishment of national and European base collections, the establishment of national and European core collections, the identification of duplicates, and the agronomic and molecular evaluation of this germplasm for various important agronomic characteristics and for resistance to stress factors and diseases. Despite certain administrative and biological difficulties encountered owing to the diverse genetic composition, particularly of the wild germplasm, the programme is very successful. Preliminary results obtained so far show that promising genes for resistance to many menacing *Beta* diseases and stress factors exist in this germplasm and there is expectation for a promising contribution to the European *Beta* breeding industry.

Under the GENRES CT95-42 programme the Greek Gene Bank has multiplied about 200 accessions in the first 4 years. Only part of these accessions produced adequate seeds for distribution to the partners in the programme for further evaluation. A limiting factor was the very early bolting of *B. maritima* accessions which produced seeds before their full vegetative growth, even in the propagation pots. Therefore their seed production was very limited.

In parallel, significant screening work on indigenous wild and cultivated *Beta* germplasm has been underway for many years at the Genetics and Breeding Section of the Hellenic Sugar Industry, aiming at the identification and utilization of useful genes conferring resistance to a number of pathogens menacing the sugar beet crop in Greece.

The Greek *Beta* collection has certain geographical gaps, which need to be filled in the near future. The central Aegean, the region of Epirus and Corfu island and Thrace are promising areas, which have never been explored.

Regarding the geographical distribution of *Beta* species in Greece, the explorations have shown that:

- *B. maritima* has its highest concentration in two regions, the central-eastern part of Greece and the Ionian islands, and the eastern Aegean islands
- *B. vulgaris* has a homogeneous distribution throughout Greece
- *B. nana* has small threatened populations in the mountains of mainland Greece.

Genetic erosion of *Beta* germplasm is progressing at an alarming pace in Greece. The habitats of *B. maritima* (coastal areas) are destroyed by human pressure for summer resort development in these areas. On the other hand, traditional varieties and local populations of *B. vulgaris* are constantly reduced by the pressure and demands of modern agriculture. Recent visits to known *Beta* habitats on the occasion of expeditions targeted to other species revealed that trend, and proved the need for urgent rescue action, in the framework of our national programme which is expected to be in effect next year and covers not only beets, but all crops and wild relatives in Greece.

Beta genetic resources activities in India: current status and future prospects

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Introduction

Sugar beet (*Beta vulgaris* L.) and sugarcane (*Saccharum* sp.) are the two important sugar crops cultivated in many countries in the world. India, Pakistan, Iran, Iraq, Turkey, China, Japan, Egypt, Morocco and the USA produce sugar from sugarcane as well as from beet. Sugar beet was introduced in India as a supplementary sugar crop to augment sugar production in hot summer months, from mid-March to May (75 days) when sugar recoveries from sugarcane show a steep declining trend. At present we have a cane-cum-beet sugar factory at Sriganaganagar (Rajasthan), which processes sugarcane from November to mid-March and then shifts to sugar beet processing. This factory has additional equipments like a washer, slicer and diffuser to process sugar beet.

The genus *Beta* comprises many cultivated types (sugar beet hybrids, open-pollinated genotypes), breeders' lines, other germplasm lines, as well as leaf beets, fodder beets, table beets, and many wild and weedy genotypes and landraces (Letschert *et al.* 1994; Frese 1992, 1994; Frese *et al.* 1998; Srivastava 1995, 1998; Srivastava *et al.* 1992). The World *Beta* Network (WBN) during its first and second meetings held at Wageningen, The Netherlands (1989) and Braunschweig, Germany (1991), summarized the main objectives of WBN as follows: to rationalize *Beta* genetic resources activities, to enhance access of germplasm to all potential users, to stimulate use of germplasm in breeding research programmes and to exchange information on various aspects of *Beta*. The WBN also suggested that each member country of WBN should present a national report about the *Beta* genetic resources activity. This paper summarizes the current *Beta* genetic resources activities undertaken at the Indian Institute of Sugarcane Research, Lucknow and at the national level from 1996 to 1999, under five major headings: (1) national germplasm system, (2) *Beta* collections and accessions obtained, (3) germplasm conservation, (4) evaluation of *Beta* germplasm for productivity, abiotic and biotic stresses, and (5) documentation, enhancement and utilization, etc.

National Germplasm System

In India the Indian Institute of Sugarcane Research under the ICAR, Ministry of Agriculture Govt. of India, is responsible for *Beta* genetic resources work.

Beta accessions obtained

During the period 1996-99 about 70 accessions of *Beta* were obtained from the BGRC collection in Braunschweig (Germany). Further, some breeders' lines, commercial and semi-commercial varieties were obtained from the USA, Sweden, Denmark, France and Iran for evaluation in multi-location testing of a coordinated Project of ICAR.

Germplasm conservation

The germplasm received is kept at IISR in air-conditioned rooms. Facilities for medium- and long-term conservation are available at the National Gene Bank at New Delhi, at the National Bureau of Plant Genetic Resources. Most of the inbred lines developed by IISR and open-pollinated diploid varieties and selections are now being multiplied in the hills for long-term storage at NBPGR.

Evaluation of *Beta* germplasm

About 37 *Beta* accessions from BGRC were evaluated for quantitative traits, total sugar content and tolerance to high-temperature conditions at late harvest in the hot summer months of May and June. Twenty other germplasm lines and landraces were evaluated for different morphological and agronomic attributes. Cytogenetic work on some genotypes has been undertaken.

Documentation

Beta accessions obtained are documented as per the WBN IDBB (International Database for *Beta*) System. The diploid germplasm lines and open-pollinated genotypes received from abroad have been studied for various morphological attributes and also used in the breeding programme. Two promising high-temperature varieties, 'Viz LS-6' and 'IISR Group-I', were developed and released for commercial cultivation in India.

Future workplan

In the coming years we propose to take up the following activities:

- evaluation of new accessions for morphological, quantitative traits and tolerance to drought and high temperature
- joint collecting mission in Iran – subject to availability of funds from IPGRI/FAO with the recommendation from WBN
- continuation of cytological studies on *Beta* sp.

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Beta genetic resources in Italy

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Beta germplasm in Italy is mainly concentrated at the Istituto del Germoplasma (CNR) in Bari, and at the peripheric section of the Istituto Sperimentale per le Colture Industriali (ISCI) located in Rovigo, northern Italy.

The ISCI sugar beet seed collection is exclusively composed of sugar beet germplasm constituted by the Rovigo Section of ISCI. This germplasm is composed of 109 diploid plurigerm families, 17 monogerm O-Type lines, and 27 tetraploid plurigerm families. Consequently, the germplasm stored at ISCI has a presumably quite narrow genetic base, but on the other hand has unique characteristics and cannot be present anywhere else in the world. Some of the oldest breeding lines, which can be traced back to the activity of Ottavio Munerati in the first half of this century, could be endowed with valuable traits and are source of known genetic resistance to some important diseases (e.g. *Cercospora*).

The seeds constituting the collection are stored at the Rovigo Section of the Institute, in a cold room (temperature between 5 and 7°C), and at low humidity (about 25%). These conditions allow the Institute to maintain for as long as possible the seed germinability. However, planning the field reproduction of these materials is becoming a necessity. This reproduction should of course be carried out in strict isolation conditions, and probably will have to be staggered over a prolonged period, given the impossibility of creating so many different isolation centres, involving all the Sections and experimental fields of the Institute. Every family is coded with a progressive number, and in most cases the seed availability is good.

Presently, the only traits for which the stored germplasm has been characterized are the M trait (multi or monogerm; the families are mostly multigerm, except the 17 O-Type lines), the ploidy level (27 are tetraploid and the remaining are diploid), some morphological characteristics of the leaf apparatus (erect, semi-erect or expanded habit; smooth or irregular leaf surface; leaf edge, smooth or pleated) and of the root (more or less elongated shape, and root size).

As stated above, the stored material could enclose useful traits such as resistance to diseases unknown in the period of the Constitution, such as Rhizomania, or not considered of strategic relevance on the basis of the old diffusion area of the culture, such as for instance drought or cold resistance; these traits are now considered of the highest priority for sugar beet culture. A thorough characterization of the ISCI collection for these traits in the future would be very advisable.

Beta genetic resources in Latvia

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Three cultivar groups of *Beta vulgaris* subsp. *vulgaris* are cultivated in Latvia: sugar beets, fodder beets, and vegetable red beets. There are no species of *Beta* in the wild flora of Latvia (Gavrilova and Šulcs 1999). Local varieties of cultivated beets were created at different times for sugar and fodder beets. Only varieties of foreign origin of red beets were used in Latvia.

Fodder beets have been grown in Latvia since the beginning of the 19th century (Holms and Kalniņš 1992). Nevertheless, local breeding started only in the 1930s in the Meņotne Plant Breeding Station. Variety 'Meņotnes Sarkan-s' was created there in 1940. Since 1946 fodder beet breeding was continued at the Lejaskurzeme Plant Breeding Station, where varieties 'Balt-s Puscukurbietes' and 'Lejaskurzemes' were developed. Since 1983 fodder beet breeding at the Lejaskurzeme Plant Breeding Station was closed, and at the beginning of the 1990s seed production of fodder beet was also terminated. Unfortunately, at the moment no accessions of fodder beet of Latvian origin are represented either in the Latvian Gene Bank or in another working collection in Latvia.

Sugar beets have been grown in Latvia since the second half of the 19th century, but on a large, industrial scale only since the 1920s (Holms 1992). Local sugar beet breeding first started at the Stende Plant Breeding Station, and after a few years it was moved to the Meņotne Plant Breeding Station.

To our knowledge Latvia is the northernmost area of industrial sugar beet growing in Europe. The purpose of breeding is to develop varieties adapted to the local growing conditions which are colder and wetter, and with a shorter vegetation period than other areas.

Some multigerm synthetic varieties were developed by the hybridization of the best western and eastern varieties and following mass and individual selection ('M2', 'Meņotnes 070', 'Meņotnes 080', 'Meņotnes 104'). Later on a monogerm synthetic variety was created ('Meņotnes Viensklas 7').

Since the mid-1960s the main direction of the sugarbeet breeding in Latvia was the creation of hybrid monogerm varieties based on cytoplasmic male sterility (CMS). CMS (Owen's cytoplasm) from multigerm breeding lines of Danish origin was transferred to the best Latvian monogerm lines. Corresponding 0-type lines were created by topcrosses and selection. CMS lines were used at the Meņotne Plant Breeding Station to develop monogerm hybrids 'Meņotnes Hibr&ds 9' and 'Meņotnes Hibr&ds 18', which were recommended for commercial growing respectively in 1977 and 1983. In the following years some promising hybrids were created. Nevertheless, after privatization, plant breeding at the former Meņotne Plant Breeding Station was interrupted since the beginning of 1998.

All the best accessions of sugar beet of Latvian origin available at that moment were moved to the Latvian Gene Bank located at the Institute of Biology of the University of Latvia in Salaspils (Rashal 1999).

The transferred material included 'Meņotnes Hibr&ds 18' and three other promising hybrids. In their turn each hybrid is derived from 6-37 different monogerm lines, including the sterile lines and their 0-type maintainer. Additionally, the 30 best multigerm pollinator lines selected for their combining ability were also transferred to the Latvian Gene Bank. Altogether 98 accessions of sugar beet of Latvian origin are included in the Gene Bank.

About 5000-15 000 seeds per accession were received. Seeds were dried and put in

long-term storage in aluminium bags in refrigerators at -18°C . Seeds are available upon request.

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Beta genetic resources activities in Lithuania

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The National Plant Genetic Resources Programme for cultivated plants was initiated in Lithuania in 1994. Eight research and educational institutions which had earlier been involved in the conservation of genetic resources joined the Programme (Bādvityt• 1998).

The first steps in *Beta* genetic resources conservation in Lithuania were made in 1993. All activities are under the control of the Industrial Crop (sugar and fodder beets) and Vegetables (red beets) groups.

Two research institutions are responsible for the national *Beta* collection: the Lithuanian Institute of Horticulture (LIH) and the Lithuanian Institute of Agriculture (LIA). The long-term storage facilities are based at the LIA.

The collection of red beet (*Beta vulgaris* L. subsp. *vulgaris* var. *atrorubra*) is located at LIH (26 most important accessions). Currently 5 accessions are kept in the long-term storage (Lithuanian varieties), and the rest are maintained in the working collections.

Four of five Lithuanian red beet varieties were described in the Catalogue of Lithuanian Plant Genetic Resources (Bādvityt• *et al.* 1997). The majority of accessions maintained in the working collections are breeder's lines (14 accessions), which have valuable traits such as high yield, earliness and bigermy (Armolaitiene and Petroniene 1998). Foreign varieties (6 accessions) are also valuable as donors of earliness, root type, monogerm seed, etc. The single accession of red beet landrace was collected in 1996 near Vilnius in the village 40 Totoriu. It is a very interesting local variety with large roots, excellent storage qualities, good health and disease resistance. Seed stalks are productive and of good shape.

The responsibilities for collecting, evaluating, utilizing and storing genetic resources of sugar beets (*B. vulgaris* subsp. *vulgaris* var. *saccharifera*) and fodder beets (*B. vulgaris* subsp. *vulgaris* var. *crassa*) are based at the LIA. The collection consists of the old varieties, breeding material and cultivated or wild *Beta* species received from abroad (Tamosiuniene 1998). Currently seven accessions are kept in the long-term storage; others are maintained in the working collections.

Nine Lithuanian fodder beet varieties were described in the Catalogue of Lithuanian Plant Genetic Resources. All these varieties are fodder (4 accessions) and semi-sugar beets (5 accessions). Sugar beet varieties were included in the genebank collection in 1998, when it was decided to recover the only remaining monogerm Lithuanian sugar beet hybrid. Working collections of fodder and sugar beets are different from year to year, because of stocktaking of old seed samples kept in conventional storage.

The evaluation of collections is carried out according to IPGRI descriptors for *Beta* in both institutes. Documentation of accessions' passport data has recently started.

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The *Beta* collection in Poland

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The *Beta* collection is located in the Institute's Department in Bydgoszcz as a unit of the Centre for Plant Genetic Resources, Plant Breeding and Acclimatization Institute (IHAR) Radzików. The Centre coordinates, finances and provides storage facilities for crop genetic resources in Poland.

Focus is set on the collecting, maintenance, evaluation and documentation of wild species and cultivated beets.

The collection contains wild species of sections *Beta*, *Corollinae* and *Procumbentes*. Species of the *Corollinae* section (perennial species) are maintained in the field. Male sterile ecotypes of subsp. *maritima* are kept as *in vitro* cultures.

Other wild species and cultivated forms are stored as seed samples. Seed samples are kept in glass jars at -15°C and 5-8% moisture content in the Gene Bank of the Institute in Radzików. Part of the material is stored in Bydgoszcz under medium-term storage ($0-4^{\circ}\text{C}$).

Accessions have been obtained from national breeding institutions and on exchange basis from foreign collections and institutions. During the last 3 years new accessions were obtained from expeditions to Ukraine, Slovakia and Moldavia.

The number of accessions stored at present amounts to 26 accessions of wild species and 236 accessions of cultivated beets (108 sugar beets and 138 fodder beets).

Safety-duplication will be implemented in the near future.

For evaluation, the IPGRI Descriptor List for *Beta* was chosen. Germplasm evaluation and seed multiplication are done at Bydgoszcz (wild species) and at the Experimental Station in Koźczewice (cultivated beets). Evaluation of cultivated beets is done on 10-m^2 plots in two replications with standard check varieties in a 2-year cycle. About 25 accessions are evaluated each year. Both morphological and agronomic features are evaluated. The collected and evaluated germplasm is being utilized in sugar and fodder beet breeding and in several research programmes.

Status of the beet collection preserved at the Vavilov Institute

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In the main catalogue 1598 accessions are listed, including table beet (278 accessions), fodder beet (291), leaf beet (43), sugar beet (965), primitive (transitional) forms (10) and wild species (11).

The first *Beta* accessions were brought to VIR by N.I. Vavilov from Afghanistan (1924), Mediterranean countries (1926-27) and Indochina (1929).

Beta seed from the collection undergo regeneration once in 7-9 years. Collection accessions are maintained *in vivo* at five experimental stations of VIR: Maikop Station (Krasnodar Region), Volgograd Station (Volgograd Province), Moscow Division (Moscow Province), Daghestan Station (Republic of Daghestan) and Pushkin Laboratories (Leningrad Province).

Part of the collection is placed under controlled conditions for long-term storage: 600 accessions in the National Seed Store at Kuban (storage temperature -4 to -6°C), and 710 accessions in the freezers at Pushkin Laboratories of VIR (storage temp. -18 to -20°C). The working collection (1598 accessions) is preserved at room temperature in the premises of the Institute in St. Petersburg.

The core collection contains 351 accessions, including sugar beet (88), fodder beet (119), table beet (114), and leaf beet (30). The collection is annually increased by 10 to 50 accessions.

From 70 to 75 accessions are planted annually at three experimental stations for ecogeographical studies. Evaluation for resistance to bolting is performed at the Polar Experiment Station of VIR (Murmansk Province) and involves 50-60 accessions each year.

To ensure safety of the accessions the following measures are taken: (1) individual accessions are planted simultaneously at two stations with the purpose of seed multiplication; (2) accessions with a small number of seed are maintained *in vivo*, planted in a hotbed or glasshouse at Pushkin Laboratories; (3) accessions placed for long-term storage are duplicated at Kuban and Pushkin facilities (especially those with quick loss of germination ability).

Since 1995, a bilingual comprehensive passport database has been available for 1598 accessions.

Review of sugar beet genetic resources in Slovakia

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Sugar beet can be grown successfully in Slovakia on nearly all soil types, besides salty and stony soils. The most suitable soil type is chernozem, the most productive soil for agriculture.

The area cultivated to sugar beet in Slovakia in 1999 is 33 810 ha. There are 63 registered varieties of sugar beet (three of Slovak origin, among which the two varieties 'Monriz' and 'Rizoma', bred in cooperation with KWS, Germany, are resistant to Rhizomania) and eight varieties of fodder beet (four varieties of domestic origin: 'Bu..ianský ňltý valec', 'Ema', 'Aja', and 'Bela').

Genetic resources of sugar and fodder beet are studied and preserved in SELEKT, Research and Breeding Institute Bu..any, since 1992 under the coordination of the Research Institute of Plant Production Piešťany (RIPP). Great attention is given to this topic and RIPP tries to obtain enough financial support for this activity.

The village Bu..any is situated at 48°26'N, 17°41'E, 155 m above sea level. According to total rainfall and temperature Bu..any belongs to the maize region, but in reality Bu..any belongs to an intermediate area (maize and sugar beet region).

Genetic resources are maintained and multiplied by the breeders. The collection currently contains 78 accessions of sugar beet and 48 of fodder beet.

Table 1. Overview of genetic resources of sugar and fodder beet

Species	No. of samples	Type of samples [†]				
		AC	GS	CU	OL	BL
<i>Beta vulgaris</i> var. <i>altissima</i>	78	3	–	45	23	7
<i>Beta vulgaris</i> var. <i>crassa</i>	48	3	5	38	2	

[†] AC=registered varieties; GS=genetic stock; CU=cultivated material; BL=breeding lines; OL=old varieties.

The structure of the passport data follows the principles of the FAO/IPGRI Multicrop Passport Descriptor List adopted after the workshop on Central Crop Databases held in Budapest, Hungary, 1996, with some additional descriptors.

Morphological, biological and economic characters of beet are evaluated according to the morphological descriptor list developed on the basis of IPGRI, UKSUP and EVIGEZ Descriptor Lists. Thirty-two morphological characters are currently studied.

The RIPP Genebank has operated since 1997. Beet accessions are stored in the base collection at –17°C with a 10-year cycle of germination monitoring (11 accessions, 8 of sugar beet and 3 of fodder beet). The base collection is safety-duplicated.

The active collection contains 48 accessions (18 of fodder beet and 30 of sugar beet). This collection serves for breeding and research purposes, regeneration of material, evaluation and documentation. The samples are stored at a temperature of 0-2°C for 10–15 years depending on the stock of seed.

Other genetic resources are in the working collection, which serves the purposes of breeders and is not stored in the Genebank.

The genepool of sugar and fodder beet provides the base for the choice of parental lines for crosses with the aim to create more variable genetic material for the breeding of new varieties.

Important results have been obtained. We started in Bu..any with breeding of biological material for tolerance to Rhizomania after 1990, when the occurrence of this disease was confirmed in Slovakia. The best way for breeding such material was crossing domestic male lines with female tolerant CMS lines from foreign countries, obtained from firms which had more experience in creating tolerant materials and earlier had started such breeding. This cooperation led to the breeding of the varieties 'Monriz' and 'Rizoma'.

In fodder beet breeding, accession code 14 was used as male parent and an MS line of sugar beet SL-63 was used as female for the breeding of variety 'Ema'. Accession 59 was used as the female parent for the breeding of fodder beet 'Aja'. Accession SL-64 was used as female and accession 19 as male in the breeding of variety 'Bela'.

During 1995-98 in SELEKT Bu..any a scientific and technical project focused on the research of sugar beet genetic resources tolerance against Rhizomania. The susceptibility to Rhizomania of the parent lines was tested. Diploid and tetraploid multigermlines of pollinators were grown in artificial conditions, which were optimal for the development of the pathogen, on soil heavily infected with BNYVV (Beet Necrotic Yellow Vein Virus). The susceptibility of tested materials was checked with a serologic test. Materials for which the test confirmed that they have lower susceptibility to BNYVV were used after multiplication in test crossing with less susceptible CMS lines from domestic breeding and with tolerant foreign lines.

Three-year observations confirmed the plasticity of the tested components in behaviour in the BNYVV-infected environment. This first result is encouraging to continue with further breeding experiments with some selected materials. Some lines apparently differed from the others in their strength and at the same time a low concentration of the virus was found in laboratory and field conditions. Therefore they are considered promising for future breeding research. It is expected that their thorough genotypic characterization will lead to obtaining material with even higher tolerance.

Three hybrids tolerant to Rhizomania obtained through international exchange surpassed the control varieties in all the tested traits: E 632 and 641 (Desprez) and 4A0092×15078 (KWS). The last of them was included in the state variety trials in 1998 where it reached the third position in refined sugar yield under the indication BU 6003.

In the years 1995-98 an investigation of the incidence of sugar beet Rhizomania was carried out. Beet samples presenting symptoms of the disease taken from the field during vegetation were examined for presence of BNYVV virus using a serological test. The aim of the investigation was to map incidence and spread of the disease in our country and to reduce damages as much as possible. The result of this investigation carried out in 1995-98 is a database of tested plots chosen on the basis of the location of sugar factories.

Owing to the favourable results of the previous project a new scientific and technical project was undertaken in 1999 focusing on the complex system of integrated protection of sugar beet in the presence of BNYVV in the soil. It is divided into four activities:

- development of biological materials with increased tolerance to BNYVV
- investigation of occurrence of BNYVV in Slovakia
- effect of a new generation of liquid fertilizers on sugar beet yield and quality
- optimization of the protection of sugar beet with different tolerance to BNYVV and the use of effective herbicides against weeds.

Status of *Beta* genetic resources in Switzerland

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The Swiss Federal Station for Plant Production of Changins started the establishment of a vegetable collection in 1980. This collection has been set up after the introduction of more and more F₁ hybrid varieties, to avoid loss of local varieties and landraces. These types of varieties have been collected in Switzerland and 400 accessions of some 48 different species are now stored in our genebank.

Particular attention was paid to some species for which a breeding programme was carried out. One of these species was Swiss chard (*Beta vulgaris* subsp. *cicla* var. *flavescens*) and at the moment 62 accessions of Swiss chard are conserved in our genebank including 33 accessions of Swiss origin, 9 from the Netherlands, 8 from France, 6 from Italy, 2 from Denmark, 1 from Sweden and 3 of unknown origin. Ten accessions of *B. vulgaris* subsp. *cicla* var. *cicla* and 13 of *B. vulgaris* var. *conditiva* are also conserved in our genebank.

Safety-duplication is carried out in collaboration with the Federal Center for Breeding Research on Cultivated Plants (BAZ) in Braunschweig, Germany, where 62 accessions are stored currently. For the 23 accessions for which no safety-duplication exists, 21 still have to be regenerated, which will be carried out in the coming years. All accessions are stored in aluminium laminated sealed bags at -20°C.

Status of *Beta* genetic resources in Turkey

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Introduction

Turkey is one of the centres of origin of beet. Species of two sections, sect. *Beta* and sect. *Corollinae*, are found in Turkey (Table 1) with wide distribution (Tan 1992, 1993a; Doney *et al.* 1995). The habitats of those species are described in Table 2. Studies on *Beta* collections from Turkey show continuous variation in most of the characteristics resulting from the geneflows between wild and cultivated forms (Ford-Lloyd and Williams 1975; Buttler 1977; Ford-Lloyd 1991; Letschert 1993; Tan 1994a). 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 are conducted within the framework of the National Plant Genetic Resources Research 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. The Aegean Agricultural Research Institute (AARI) has been designated as Coordination Centre for the National Programme (Tan 1992, 1998; Firat and Tan 1995).

Table 1. *Beta* species found in Turkey

Beta Section Beta

Wild species

Beta vulgaris subsp. *adanensis*

Beta vulgaris subsp. *maritima*

Beta vulgaris subsp. *maritima* var. *trojona*

Beta vulgaris subsp. *Provulgaris*

Cultivated species

Sugar beet

Leaf beets

Garden beets

Beta Section Corollinae

B. macrorhiza

B. lomatogona

B. intermedia

B. trigyna

B. corolliflora

B. foliosa ?

Table 2. Habitats of *Beta* species in Turkey

Beta Section Beta

Sea level to 700 m

Mainly in coastal areas but found at inland habitats influenced from littoral regions

Weeds in cultivated fields

Field borders

Roadsides

Beta Section Corollinae

550 to 2300 m

Inland mountainous areas

Field borders

Weeds in cultivated fields

Roadsides

In vegetation of woody perennials

Quercus woodlands

In vegetation of herbaceous and woody perennials

Beta genetic resources activities

Survey and collecting

The first step in beet genetic resources activities is collecting – sampling the maximum variation and determination of the interspecific, agro-ecological 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 and weedy forms are considered in the group for *ex situ* conservation. Surveying and collecting *Beta* species were systematically initiated in the late 1960s. The distribution and habitats of the species found in Turkey were revised (Tan 1992). The herbarium species are also collected during the survey to maintain the specimens at AARI herbarium as the reference of the beet collection and for further identification.

***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 foil is 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 material.

***In situ* conservation**

The recent establishment of the *In Situ* Conservation Project of Turkey aims to maintain wild crop genetic resources in their natural habitats. This project is the first of its kind to consider 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 the establishment of *in situ* Gene Management Zones (GMZs) in selected pilot areas that are rich in target crop wild relatives. Highest priorities have been given to globally significant non-woody crop species which are in the first gene pool of cereals as well as important woody species and selected forest species. 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 has also aimed at integrating *in situ* conservation with the existing *ex situ* conservation programme of Turkey. 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 National Plan for *in situ* conservation.

Another ongoing project formulated in 1995 by IPGRI together with national programmes in nine countries is the global project to strengthen the scientific basis of *in situ* conservation of agricultural biodiversity. The nine countries involved in the project are Burkino Faso, Ethiopia, Nepal, Vietnam, Peru, Mexico, Morocco, Turkey and Hungary. The main objectives of the project are: (1) to support the development of a framework of knowledge on farmer decision-making processes that influences *in situ* conservation of agricultural biodiversity, (2) to strengthen national institutions for the planning of new implementation of conservation programmes for agricultural biodiversity, and (3) to broaden the use of agricultural biodiversity and participation in its conservation by farming communities and other groups. As a project member, Turkey has initiated a

project on “*In situ* on-farm conservation of landraces from transitional zone in Turkey”. This project is involved in the *in situ* (on-farm) conservation of local crops, cultivar (or landraces) with active participation of farmers. The socioeconomic and ecogeographical surveys will be conducted in the northwestern Transitional Zone adjusting to western, northwestern Black Sea and central Anatolian Regions to determine the distribution of landraces and socioeconomic status of landrace cultivation. A database of the information compiled from the surveys will be established. During the surveys, existing landraces will be collected and maintained *ex situ* which will be complementary to *in situ* conservation. The landrace(s) will be selected as target species and genetic variation analyses will be conducted. The candidate Gene Management Zones (GMZs) will be determined for the possibility of *in situ* (on-farm) conservation of target species. Data compiled from surveys and genetic analysis will be loaded onto Geographical Information Systems (GIS) following the data analyses, interpretation and mapping prepared to better understand the ecogeographic variation of targeted landraces throughout the region for the possibility of *in situ* conservation on-farm. Since beet landraces are cultivated in the region where the project will be conducted, the inventory of beet landraces will be identified within the framework of the project.

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 (geneflow) 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. The germination procedure was followed in accordance with the result of the study on seed morphology and germination of beet species found in Turkey (Tan 1993b).

Evaluation and characterization

Characterization and 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 cooperates with evaluation/characterization programmes aiming at using this valuable material for breeding.

Characterization and evaluation activities started recently for beet species. IBPGR/IPGRI descriptors are used with some modifications (IBPGR/CGN 1991). Some characterization results are given in Tables 3 and 4 (Tan 1994b).

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 (Tan and Tan 1998a,

1998b). *Beta* genetic resources data from survey, collecting and characterization activities are documented using the central NPGRRP Database Management System.

Table 3. Characterization results of *Beta* Section *Beta*

Beta* Section *Beta

Continuous and high variation within and between populations
Lack of local and geographical isolation
Microevolution of wild beets
Gene flow
Morphological relationships of species
Variants of *Beta vulgaris*
Primitive farming system
Populations that should be considered as infraspecific in *B. vulgaris*:
 Beta vulgaris subsp. *adanensis*
 Beta vulgaris subsp. *maritima*
 Beta vulgaris subsp. *maritima* var. *trojona*
 Beta vulgaris subsp. *provulgaris*

Table 4. Characterization results of *Beta* section *Corollinae*

Beta* Section *Corollinae

Basic species, cytotypes, hybrids, apomictic forms
High variation between populations
Continuous variation between some *B. lomatogona* populations
Populations that should be considered as intraspecific
 B. lomatogona: 2x, 4x, 6x
 B. intermedia
 B. trigyna
 B. corolliflora
 B. macrorhiza
 B. foliosa ?

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 the UK

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There is no single collection of *Beta* germplasm in the UK, but germplasm is divided principally between three institutes:

1. The Millenium Genebank at Wakehurst Place holds a small number of wild beet samples, most of which represent duplicate samples deposited after USDA germplasm collecting activities within the UK.
2. The Vegetable Genebank at HRI, Wellesbourne holds a small number of leaf and garden beet accessions.
3. At the University of Birmingham (School of Biosciences) there is a larger working collection of nearly 1000 accessions that includes material of all *Beta* species, as well as the full range of cultivated beets.

While the germplasm in the Millenium Genebank and the Vegetable Genebank is stored under long-term storage conditions, the Birmingham collection is only maintained under low moisture content storage conditions at 4°C.

Although generally unable to undertake seed regeneration or evaluation, the University of Birmingham actively collaborates within the EU GENRES CT95-42 project, where both seed increase and evaluation of Birmingham germplasm have been possible. Otherwise, the University of Birmingham is involved in various research activities on beet germplasm, which largely involve the development and use of molecular markers for studying genetic variation.

Beet germplasm research and evaluation also takes place at IACR-Broom's Barn, an institute which is also involved in the EU GENRES project referred to above. Specific interest in terms of research involves screening and evaluation of germplasm for disease and abiotic stress tolerance (contact: Dr M. Asher).

The Institute of Terrestrial Ecology at Furzebrook in Dorset also undertakes research on wild beet populations within the UK, and has focused upon the analysis of gene flow between and within populations (contact: Dr A. Raybould).

Beta genetic resources: North American activities

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Introduction

There were approximately 606 670 ha of sugar beets grown in North America in 1998. Production in the US is still centered in five main regions of the country. These regions include the Great Lakes (72 211 ha), Red River Valley (292 815 ha), Great Plains (95 701 ha), Mountain States (104 611 ha) and California (41 310 ha). Canada has 20 452 ha in production. Each region has a different climate and a different mix of disease problems. The USDA-ARS has established five sugar beet research programmes: Beltsville, Maryland; East Lansing, Michigan; Fargo, North Dakota; Fort Collins, Colorado; Salinas, California. A number of universities also conduct research on sugar beet, but genetic resources research and pre-breeding activities are conducted only by four of the USDA-ARS programmes (the Beltsville programme is strictly molecular genetics). In addition to the germplasm projects of the ARS programmes, a number of sugar beet seed companies have research and breeding programmes throughout the United States.

The 1997-98 sugar beet crop was estimated at 32.66 million tons (4.225 million short tons, raw value) by the National Agricultural Statistics Service, with national yield at 22 tons per acre. However, white sugar yield per acre was nearly 7% below expectations. Some of this was due to the effect of a mild winter on storage piles, but disease pressure, especially from *Cercospora* leaf spot, reduced percent sugar concentration in growing areas across the US, and exacerbated storage problems.

National Plant Germplasm System (NPGS) and beet conservation

The NPGS is a cooperative effort by public (Federal and State) and private organizations to preserve the genetic diversity of plants. Support from the federal level is from the Agricultural Research Service (ARS) and the Cooperative State Research, Education and Extension Service (CSREES) of the USDA. State level support comes from the state agricultural experiment stations. With the understanding that scientists must have access to genetic diversity to help bring forth new varieties that can resist pests, diseases and environmental stresses, the NPGS aids the scientists and the need for genetic diversity by acquiring, preserving, evaluating, documenting and distributing crop germplasm. Research also plays an integral role in germplasm conservation by the NPGS.

Since *Beta* species originate outside the United States, the first steps toward developing diversity in the crop are acquisition and introduction. New germplasm (accessions) enter NPGS through collecting, donation by foreign cooperators or international germplasm collections. An identifying number such as the Plant Introduction number (PI number) is assigned to each accession. The accession is then evaluated, maintained and made available for distribution.

A significant activity of the NPGS is to facilitate the Crop Germplasm Committees (CGC) which are comprised of public and private scientists. These committees provide advice and counsel to the collection curators, and help to set germplasm evaluation priorities. The Sugar Beet CGC was established in 1983 as a committee associated with the American Society of Sugar Beet Technologists (ASSBT). All geographical sugar beet growing regions of the USA are represented on this committee.

USDA Beta germplasm collection

The USDA-ARS *Beta* 'active' collection is maintained at the Western Regional Plant Introduction Station, in Pullman, WA (W-6). This collection was transferred to Pullman from the North Central Regional Plant Introduction Station at Ames, Iowa in 1994. There are over 2200 accessions in the active collection, with more than 1600 of them backed up at the National Seed Storage Laboratory (NSSL) at Fort Collins, Colorado. This is the reserve collection. New accessions, when acquired and if there is enough seed, are split between the Pullman station and NSSL. Storage at Pullman is maintained at 4°C and 30% relative humidity. Storage at NSSL is kept at -18°C and seed is packeted in airtight, sealed foil packets.

Acquisition

There are currently 12 species of *Beta* in the Pullman collection, but the largest part of the collection is the *Beta vulgaris* germplasm. There are 569 accessions of the subspecies *B. vulgaris* subsp. *maritima*, which are the wild beets from Europe and North Africa. In the last two years over 100 new accessions of wild *Beta* have been added to the Pullman collection from the European collection. New breeding lines of *B. vulgaris* are constantly being added to the collection from research programmes in the United States. Of the *Beta* at Pullman, 1410 accessions are available for distribution to researchers worldwide. An active collecting programme also has been carried out with collaborators from around the world (Table 1).

Table 1. *Beta* exploration and collecting trips in collaboration with scientists from each country and other *Beta* researchers

Country	Year	Species
Southern Italy, Sardinia, Corsica	1985	subsp. <i>B. maritima</i>
England, Wales, Ireland	1987	subsp. <i>B. maritima</i>
France, Belgium, Denmark	1989	subsp. <i>B. maritima</i>
Armenia, Daghestan	1990	<i>B. corolliflora</i> , <i>B. macrorhiza</i>
Egypt	1992	subsp. <i>B. maritima</i>

Multiplication

The purpose of the Pullman collection is to provide germplasm as an active genebank. Therefore, the seed must be kept in sufficient quantity and quality so that it can be distributed and used by researchers. A seed increase programme is in place at the Plant Introduction Station to make as many of the accessions available for distribution as possible (Table 2). It is essential that the seed be increased from a sufficient number of individuals to maintain the genetic variability of the parent population. As *Beta* is wind-pollinated, isolation and/or control of pollination is necessary.

Germplasm increase is conducted year round. Accessions are chosen for seed increase when the viable seed number is below 1000. Accessions with very low seed number are increased in growth chambers or in the greenhouse where there is good control of the environment; 100-200 seeds per accession are soaked overnight with aeration in 0.3% hydrogen peroxide and then planted in vermiculite into 6-inch-diameter pots at 100 seed per pot. Upon germination and emergence, seedlings are transplanted to 'Rootainer' plant trays which contain an artificial soil media mix. Seedlings are grown in the trays to the six-to-eight leaf stage. Accessions that show no sign of bolting are vernalized in the trays in a growth chamber at 4°C under low incandescent light at a photoperiod of 8 hours. Plants are then transplanted into 2-gallon pots or planted in the field. All accessions are isolated when flowering in greenhouse rooms, growth rooms or in pollen-proof tents in the field.

Table 2. *Beta* increase activity at W-6 in the years 1995-1998

Location	Year	Started	Germinated	Harvested	Carried over
W-6	1995	94	9	27	
W-6	1996	62	5	66	
W-6	1997	92	5	59	
Europe	1997	16		16	
W-6	1998	83	7	85	74
Europe	1998	80			80
US	1998	16			16
Total		443	26	253	170

Plants are usually given normal pesticide applications during their life cycles. Pollination is enhanced by agitating the plants during the time of pollen shedding. The harvest technique varies with the accession. Some plants can be dried and bulk-harvested, while others must be carefully harvested while still green because of seed ball dehiscence from the inflorescence. Seed is cleaned at the PI Station seed-cleaning facility. Accessions that produce few seed or have just a few plants producing seed are put back into the increase cycle.

In a survey conducted in 1997 by the US Government Accounting Office of the Crop Germplasm Committees and associated public and private crop specialists, germplasm maintenance priorities were established for each crop. For sugar beets, the top priority was evaluation. Following that, the next most important activities were enhancement (breeding), germplasm acquisition, characterization and regeneration of germplasm.

W-6 has established an excellent working relationship with the IDBB for exchanging and increasing *Beta* germplasm. Approximately 200 PI accessions are being included in the IDBB *Beta* synthetic core collection. A number of PIs have been increased in Europe as part of the EU-sponsored GENRES CT95-42 Project. We have received 16 of these that were on our increase priority list. We also received 47 wild beet accessions from Europe which have been given PI numbers. In the 1998 crop year, 80 PIs will be increased in Europe; 13 of these are on our increase priority list. We also have had great support from sugar beet industry companies in the United States through the BSDF. In 1998, 16 beet accessions will be increased by US companies. This help is greatly appreciated. There are now 469 *Beta* accessions on the increase priority list. This is down from 537 in 1997. There are 20 accessions in our inventory that we have not been able to germinate. Sixteen of these are probably lost from the collection.

Evaluations

In 1983 the Sugar Beet Crop Germplasm Committee identified enhancing the commercial sugar beet germplasm pool as a high priority. This has led to aggressive evaluation of the NPGS *Beta* collection, coordinated by the Sugarbeet CGC. Since 1985 these composite evaluations have generated over 20 000 data points, more than 3000 of which describe levels of resistance to 10 major disease and insect pests of sugarbeet (Table 3). All diseases evaluated have a serious impact on sugar beets grown in the US and in many other countries. Evaluations are conducted yearly with the support of the NPGS through a competitive grant proposal system. Accessions are evaluated in single-year trials, which, the Sugar Beet CGC has found, is an adequate evaluation of the germplasm.

The Sugar Beet CGC coordinates the evaluations by researchers throughout the United States (Table 4), and the resulting data is sent to the chairman who formats it and sends it to the Western Regional Plant Introduction Station, in Pullman, WA.

Table 3. Number of accessions evaluated or being evaluated since 1985 for resistance to 10 important US sugar beet diseases

Disease	No. of accessions
<i>Aphanomyces</i>	345
Beet cyst nematode	385
Beet Western Yellows Virus	306
<i>Cercospora</i> leaf spot	565
Curly top virus	331
<i>Erwinia</i>	221
<i>Polymyxa</i>	39
<i>Rhizoctonia</i> root rot	578
Rhizomania	402
Root aphids	148
Total	3320

Table 4. The Sugar Beet CGC coordinates and evaluation effort by scientists from across the US to evaluate the NPGS *Beta* collections for resistance to important diseases and other traits

Evaluator	Agency	Location	Descriptor
R. Lewellen	USDA-ARS	Salinas, CA	Rhizomania
L. Panella	USDA-ARS	Fort Collins, CO	<i>Cercospora</i>
L. Panella	USDA-ARS	Fort Collins, CO	<i>Rhizoctonia</i>
R. Dregseth	North Dakota State University	Fargo, ND	root maggot
C. Rush	Texas A & M University	Bushland, TX	Fusarium
C. Rush	Texas A & M University	Bushland, TX	<i>Aphanomyces</i>
J. Michels	Texas A & M University	Bushland, TX	root aphids
S. Hafez	University of Idaho	Parma, ID	Nematode
R. Lewellen	USDA-ARS	Salinas, CA	Yellowing viruses
R. Lewellen	USDA-ARS	Salinas, CA	Morphological
L. Tunland	Novartis Seeds, Inc.	Longmont, CO	Agronomic
T. Brown	BSDF	Twin Falls, ID	Curly top virus

Data received from evaluation of Plant Introduction germplasm are routinely entered into the Germplasm Resources Information Network (GRIN) of the NPGS. Currently, there are data for a total of 114 characters or descriptors of beets in the GRIN database. The more complete data sets are found in the groups labeled morphology, disease, insect, chemical and cytologic. The other four categories have good data as well. This information can be found in GRIN at the NPGS World Wide Web home page of <<http://www.ars-grin.gov/npgs/>> and the specific site of the *Beta* germplasm descriptors is at <<http://www.ars-grin.gov/cgi-bin/npgs/html/crop.pl?49>>.

Documentation of the collection on GRIN is critical to the utilization of the germplasm. GRIN was created to develop and maintain an automated data retrieval system for the collection and dissemination of germplasm information, and to provide data expertise in support of the production database consisting of over 450 000 discrete accessions of plants. There are also additional records for the animal, microbial, insect and forest tree programmes. This system will serve the needs of scientists and other agricultural researchers by providing accurate taxonomy, passport, geographic, evaluation, inventory and cooperator information.

The Database Management Unit is located at:
USDA, ARS, BA, PSI, NGRL
Bldg. 003, Rm: 407, BARC-West
10300 Baltimore Avenue
Beltsville, MD 20705-2350

Pre-breeding

USDA-ARS scientists have been using these evaluation data to develop enhanced germplasm through the various sugar beet pre-breeding projects of the different USDA-ARS Sugar Beet Programmes. Almost half of the sugar beet germplasm registered in the last 5 years of *Crop Science* journal (Table 5) have a genetic contribution from accessions of the NPGS *Beta* collection. Incorporation of this germplasm into commercial hybrids by industry breeders should provide a broadening of the commercial sugar beet genepool.

Table 5. Sugar beet germplasm released and registered with *Crop Science* between 1993 and 1997 (almost half have some germplasm from the NPGS *Beta* PI collection in their pedigree)

Year	Number of <i>Crop Science</i> registrations	
	Total	with PIs
1993	3	3
1994	0	0
1995	23	9
1996	4	2
1997	17	9
	47	23

Beta Core Collection

In 1999 as a response to the Sugarbeet Crop Germplasm Committee and the other beet researchers in North America, a *Beta* Core Collection was developed from the Plant Introduction collection as a first attempt to develop a usable subset for evaluation and phylogenetic research purposes. The *Beta* core collection was derived from *Beta vulgaris* subsp. *vulgaris* and *Beta vulgaris* subsp. *maritima* only. Two separate *Beta* core collections were derived, one from *Beta vulgaris* subsp. *vulgaris* and one from *Beta vulgaris* subsp. *maritima*. In the development of these cores two different sets of selection criteria were used to stratify the accessions within these taxa.

Beta vulgaris* subsp. *maritima

1. Breakdown by ecogeographical region (Table 6).
 - A. Mediterranean
 - B. Northern European
 - C. Transition Zone (France)
2. Random selections were made from each of these regions to achieve the 10% target representation.

Table 6. The *Beta* Core Collection containing *Beta vulgaris* subsp. *maritima* germplasm is comprised of germplasm representing the countries below

Country	Number of accessions		Country	Number of accessions	
	in NPGS <i>Beta</i> collection	in <i>Beta</i> Core collection		in NPGS <i>Beta</i> collection	in <i>Beta</i> Core collection
Belgium	3	1	Israel	1	1
China	1	1	Italy	101	10
Cyprus	1	1	Netherlands	2	1
Denmark	24	2	Poland	1	1
Egypt	26	3	Portugal	6	1
FSU	1	1	Spain	12	1
France	148	15	Tunisia	1	1
Germany	3	1	Turkey	4	1
Greece	50	5	UK	115	12
India	1	1	USA	20	2
Ireland	46	5	Yugoslavia	1	1
Total		36			32

***Beta vulgaris* subsp. *vulgaris* – *Beta* Core Collection**

1. First breakdown was by beet type or use type (Table 7).
 - A. Sugar Beet
 - B. Leaf Beet
 - C. Fodder Beet
 - D. Table Beet
2. Secondly, for those accessions from outside the US, within each type, breakdown was by ecogeographical region (Table 6).
 - A. Mediterranean
 - B. Northern European
 - C. Transition Zone (France)
3. Random selections were made from each of these regions to achieve the 10% target representation.

Table 7. Core collection of *Beta vulgaris* subsp. *vulgaris*. Selected from the collection at the Western Regional Plant Introduction Station, Pullman, WA

End use	Number of accessions [†]	
	in NPGS <i>Beta</i> collection	in <i>Beta</i> Core collection
Leaf vegetable	78	8
Root vegetable	61	6
Root/leaf vegetable	24	2
Fodder	105	11
Sugar extraction	134	13
Biomass	15	2
Total	417	42

[†] A large portion of the collection is composed of germplasm developed by US breeders and deposited into the GRIN system. A coordinated effort is being made to develop a scheme to weight the US genepool using known pedigree information because this group is heavily represented in the sugar beet germplasm.

Part IIB. Scientific and technical papers

The International Database for *Beta* – state of the art

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Introduction

The establishment of the International Database for *Beta* (IDBB) was one of the first joint actions of the World *Beta* Network, beginning in 1989. The database now holds information on 10 535 accessions from 28 genetic resources collections.

The IDBB was set up by Th. van Hintum and L. Frese at the CPRO-DLO Centre for Genetic Resources (CGN) at Wageningen, The Netherlands, on an Oracle RDMS, Version 5.0. During 1991-92 it was transferred from Oracle 5.0 to Oracle 6.0 at the Institute of Crop Science (FAL) in Braunschweig. The Oracle Server in a HP-UX environment on a HP9000 workstation has been accessible with Oracle DOS-Tools SQL*Forms and SQL*Report and later on also by Access 2.0 frontends via ODBC (Table 1). Most of these tools are now outdated and Year-2000 compliance enforces another change this year for the IDBB as well as for the other documentation systems at our institute. This leads to considering the enlargement and modernization of the database architecture.

Table 1. Technical background for further development of the IDBB

Present situation	Intended situation after 01.01.2000	Desired situation medium-term
Server: HP-UX 8.07: Oracle 6.0.Server	Server: WinNT: Oracle 8.05 Server	Server: Linux Oracle 8I Server
Frontends: DOS: Oracle*Forms, Oracle*Reports Win3.11: Access 2.0 via ODBC	Frontends: Win9x/NT: MS Access97 via ODBC Win9x/NT: Oracle Developer 2000	Frontends: Win9x/NT: Oracle Developer 2000 Win9x/NT: MS Access97 via ODBC Win9x/NT: MS Access2000 via ODBC
Internet-Access: Off-line (downloadable): Downloadable DBase files indigo3.dv.fal.de/bgrc/bgrc-e.html	Internet Access: Off-line (downloadable): Access97 Backend + Frontend	Internet Access: Off-line (downloadable): Access 97/2000: Backend + Frontend
On-line searching: Off-line version (Dbase) imported to BASIS Web Server at ZADI www.dainet.de/genres/Beta/	On-line searching: Off-line version imported to BASIS Web Server at ZADI	On-line searching: Oracle 8I / Oracle Web Server

The IDBB on the Internet

Since 1997, the IDBB has been present on the Internet as an on-line version provided on a BASIS Web Server at the German Centre for Documentation and Information in Agriculture, ZADI (<<http://www.dainet.de/genres/Beta/>>) and at a Web Server located at the Federal Agricultural Research Centre, FAL (<<http://indigo3.dv.fal.de/bgrc/bgrc->

e.html>), as a downloadable off-line version, which consists of three DBase files (PASSPORT.DBF, COUNTRY.DBF, ADDRESS.DBF). The on-line version also resides on these DBase files, which are sent to ZADI at regular intervals. Thus, until now, only passport data are available on the Web. Representation of taxa and most important countries of origin are shown in Table 2, on-line search criteria in Table 3. A field list with decoding tables can be accessed at the sites.

Table 2. Accessions in the on-line IDBB

Docs.	Terms	Subspecies		Country of origin (12 countries with highest representation)		
		Docs.	Terms	Docs.	Terms	
110	COROLLIFLORA	65	ADANENSIS	1098	TUR	TURKEY
267	INTERMEDIA	4207	BEET	920	GRC	GREECE
237	LOMATOGONA	809	FODDER	634	ITA	ITALY
89	MACROCARPA	737	GARDEN	528	SUN	RUSSIA
67	MACRORHIZA	578	LEAF	439	USA	UNITED STATES
44	NANA	1823	MARITIMA	435	ESP	SPAIN
115	PATELLARIS	2083	SUGAR	405	DEU, BRD	GERMANY
12	PATULA	4721	VULGARIS	367	FRA	FRANCE
61	PROCUMBENS			366	GBR	UNITED KINGDOM
106	TRIGYNA			272	NLD	NETHERLANDS
8235	VULGARIS			267	IRN	IRAN
30	WEBBIANA			184	POL	POLAND

Table 3. Search criteria in the on-line IDBB

Primary search criteria	Further search criteria
IDBB unique identification	Origin of sample
Date of record entry to the IDBB	Collection number
Donor address	Plant number
Country of the donor	Origin date
Donor number	Origin country
Species	District
Subspecies	Collecting site
Use of the material	Longitude, Latitude, Altitude
Sample name	Status of sample
Most original address of sample	Sample category
	Most original sample
	Remarks
	Core collection

Modernization aspects

The IDBB was set up by Th. van Hintum as a relational database in 1989. Thus the basic concepts are still up-to-date and resemble the GRIN architecture in major respects. Nevertheless some modifications are needed, primarily related to the following aspects:

- Development of a universal database architecture for the IDBB, EADB (European *Avena* Database) and BGRC (Braunschweig Genetic Resources Collection) databases.
- Implementation of a human design (Table 4) avoiding codes and abbreviations (at least as far as they are not internationally standardized and accepted).
- Expansion of the relational architecture of the database.
- Improvement of passport and evaluation tables architecture; enlarging the descriptive base of evaluation experiments (additional information on projects, experimental sites, agronomic and experimental measures).

- Implementation of a bibliographic database providing scientific literature references for all major aspects of passport and evaluation data. A database was created in 1998 in cooperation with KWS and Assoc. Prof. Ma Yahuai, Institute of Sugar Beet, Chinese Academy of Agricultural Science.
- Consistent implementation of IPGRI Multicrop Passport Descriptors and FAO WIEWS descriptors.
- Development of an MS-Access 97/2000 frontend for data input and information retrieval.
- Development of import routines for MS-Office applications (especially Excel spreadsheet files from evaluation experiments).

Future vision

- Development of MS-Access 97/2000 update tools for authorized users
- Development of Java frontends (JDBC, Java SQL) for Internet on-line access.

Table 4. The ten commandments of humane database design (Koch and Loney 1995)

-
- 1 Include users. Put them on the project team, and teach them the relational model and SQL.
 - 2 Name tables, columns, keys and data jointly with the users. Develop an application thesaurus to assure name consistency.
 - 3 Use English words that are meaningful, memorable, descriptive, short and singular. Use underline consistently or not at all.
 - 4 Don't mix levels in naming.
 - 5 Avoid codes and abbreviations.
 - 6 Use meaningful keys where possible.
 - 7 Decompose overloaded keys.
 - 8 Analyze and design from the tasks, not just the data. Remember that normalization is not design.
 - 9 Move tasks from users to the machine. It is profitable to spend cycles and storage to gain ease of use.
 - 10 Don't be seduced by development speed. Take time and care in analysis, design, testing and tuning.
-

Database architecture

Passport Data

General considerations

Entries for the IDBB, as for other international databases on crop genetic resources, are documents on accessions provided by different genebanks. Primary entries are passport data representing origin, collecting information relating to a genotype and accession information relating to an accession in a certain genebank, which may be duplicated by accessions in other genebanks.

These two aspects have to be stored in different tables according to the relational database normalizing theory, because multiple accessions for each genotype are to be expected by duplication (intentional safety- and working-duplication as well as unintentional duplication). Resulting major passport tables are the ACCESSION table with information on accessions in different genebanks and the ORIGIN table with information on genotypes representing a whole duplication group (taxonomy, collecting information, etc.). This new architecture may also provide a solution to the problem of inconsistency in collection of information from different genebanks, arising from different kinds of codification and abbreviation. Updating original information is prone to criticism, as the administrators of international databases do not really know the national genebank holdings. Still worse, the need for the same corrections would arise on the same entries

again with each new delivery of data by the various genebanks.

In the new concept all passport information provided by the original genebanks (the table PASSPORT of the present version of IDBB) is kept unaltered in the ACCESSION table where it is referenced to the providing genebank. Changes in the original genebank documentation can be detected by comparing entries of this table with newly delivered data. Standardizing modifications and new scientific results (e.g. related to taxonomy) regarding the genetic entities (collected wild forms, cultivars) are made by the administrator in the ORIGIN table. Thus information provided to the user by this table uses standardized terminology, while original information by genebanks resides in the background and can be retrieved in cases of special interest.

Reevaluation of the sample category concept

Identification of duplication is one of the primary objectives of international crop databases. Since the beginning of the IDBB L. Frese carried out extensive search for duplicates. He introduced the concept of the most original samples (MOS), and IDBBNR (as MON-IDBBNR) was chosen as a key to duplication groups (Frese and van Hintum 1989). In the future this will still be the primary key for the ORIGIN table. Concepts for categorizing duplication as indicated in Table 5 were presented by Knüpffer *et al.* (1997), for activity of accessions and responsibility of genebanks by Bücken and Frese (1999).

Table 5. Categories of duplication and activity/responsibility in genebank accessions

DUPLICATION (Knüpffer <i>et al.</i> 1997)	
IDD	Identical duplication: genetically identical genebank accessions
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	Duplication indicated by identical or similar passport data
ACTIVITY/RESPONSIBILITY (modified after Bücken and Frese 1999)	
NEW	New accessions
ACO	Active (accessible) collection
PRO	Project samples
TOC	Temporarily not accessible collection (e.g. due to classification problems)
BAS	Base collection (not accessible/safety-duplicates)

Besides accessions still present in genebanks, international databases will also have to cope with accessions not in and no longer present in genebanks. In such cases, activities of NOG (not under genebank responsibility in the case of hybrid cultivars) and NOC (no longer in collection) should be added to the activity categories listed in Table 5.

Until now information on duplication, activity and responsibility of accessions is recorded in a field called SAM_CAT (sample category) (Frese and van Hintum 1989; Frese 1992, 1994). Confusion of these types of information led to serious restrictions in applicability of the sample categories. For example, the duplicate status of NOC samples could not be clarified; in case of probable duplicates (PRD) it is not possible to enter information on their activity and the responsibility of the holding genebank without losing the information about their duplicate status. In the case of safety-duplicates this problem was recognized early. For organizational reasons, for example, safety-duplicates of the Greek Gene Bank stored at the BAZ Gene Bank had to be activated, which led to the introduction of sample categories SDA (safety-duplicate in active collection) and SDS (safety-duplicate sample). Technically the problem has been solved by the BAZ Gene Bank by splitting the security-duplication samples of the Greek Gene Bank into an active sample and a passive security-duplicate sample where the seed amount allowed doing so. Strictly speaking it has not been correct to call the active samples safety-duplicates. Is SDS (safety-duplicate sample) another duplicate type or an activity category (identical to BAS)?

Further discussion on the legal (CBD, FAO Undertaking) and pragmatic aspects (seed availability) of security-duplication appears necessary (see section on *Sharing of responsibilities for conservation*, Part I of this report). To overcome some of these problems in the database, it is suggested to untangle the information in the SAM_CAT field into two fields representing duplicate type and activity as shown in Table 6.

Table 6. Transformation of SAM_CAT into Duplicate Type and Activity

SAM_CAT		Duplicate Type	Activity
MOS	Most original sample	MOS	All possible
NOC	No longer in the collection	All possible	NOC
NOG	Not within genebank responsibility	All possible	NOG
PRD	Probable duplicate	PRD	All possible
SDA	Security-duplication sample, in active collection	SDS or COD?	ACO
SDS	Security-duplication sample, not in active collection	SDS or COD?	BAS

Broadening accession information

Early this year (ecpgr_list@ngb.se, 11.02.99) M. Hulden pointed out the discrimination between the collector, the donor (which normally is a genebank providing accessions) and the collecting source, which is the habitat, farm or market, in which a collector originally found the accession. Thus an institute or research organization can never be a collecting source, but may be a donor. In the case of international databases a further distinction is to be made between the genebank holding the actual accession (identified here as 'holder') and the institute or person it came from (identified as 'donor'). Unfortunately until now the holders of accessions are identified as 'donors' in the IDBB, because the information about accessions was 'donated' by them to the IDBB. Nevertheless the way to the IDBB proposed here would open the possibility to track back the genetic entities through the institutions data available in the ACCESSION table. Table 7, which is adapted from the primary form for entering passport data in the new IDBB frontend, may clarify these possibilities.

Table 7. Example presented in the Passport form of the new IDBB frontend

MONIDBBNR		1335		TAXONOMY ZONE					
Accession name				Species Subspecies		Vulgaris Vulgaris			
COLLECTOR ZONE				COLLECTING SITE ZONE					
Institute	BIRDBP	Date	xx.07.74						
ADDRESS – Subform									
Person	D.Visser								
Collecting- Number	Sample- status	Collecting- source	Plant- number						
GENE BANK ZONE (subform representing the ACCESSION table linked by MONIDBBNR)									
IDBBNR	IDBB-Date	Duplicate Type	Core- Collection	Donor	Accession	Holder	Reception -Date	Accession	Activity
1335	12.02.88	MOS		BIRDPB		BIRDBPB	xx.07.74	B0281	ACO
2582	12.02.88	COD/SDS	+	BIRDPB	B0281	NEDBEG	?	10157	BAS
6853	12.01.89	PRD		?	?	NVRS	?	6856	ACO

--	--	--	--	--	--	--	--	--	--

? This information will have to be additionally provided by genebanks holding the accessions.

No further attempt will be made to provide information on seed availability as was proposed with the seeds table in older versions. Such information needs too much updating to be meaningful in an international off-line database.

Revision of ORIGIN TYPE descriptor, as adaptation to the Multicrop Passport Descriptors

Entries in the origin type decoding table correspond to the Multicrop Passport Descriptor collecting source (COLLSRC). For compliance with this standard some modifications have to be made, which are shown in Table 8. Criticism by M. Hulden regarding collecting source ID 4 (institute/research organization) has already been mentioned. To comply with the MCP, this descriptor will be provided, but it is recommended to enter genebanks or research institutions as donors into the ACCESSION table.

Table 8. Revision of ORIGIN TYPE corresponding to the Multicrop Passport Descriptors

Old IDBB: O_TYPE		New IDBB: COLLECTINGSOURCE	
O_TYPE	N_O_TYPE	CollectingSourceID	CollectingSource
1	WILD HABITAT	1	Wild habitat
		1.1	Forest/woodland
		1.2.	Shrubland
		1.3.	Grassland
		1.4.	Desert/tundra
3	FARM FIELD	2	Farm
		2.1	Field
		2.2.	Orchard
		2.3	Garden
		2.4	Fallow
5	BACKYARD	2.5.	Pasture
		2.6	Store
2	RUDERAL	3	Market
		3.1.	Town
		3.2	Village
		3.3	Urban
4	FARM STORE/THRESHING PL.	3.4.	Other exchange system
		4	Institute/Research organization
7	COMM.MARKET/SEED TRADE	99	
6	LOCAL MARKET		
8	INST/GENE BANK/BREED.COM		
9	OTHER		

Table 9 and Figure 1 give a summary of passport tables in the present and the suggested new version of IDBB.

Table 9. Tables for passport data in the IDBB

Old IDBB			New concept (preliminary)		
Table	No. of tuples	Decoding tables	Table	No. of tuples	Decoding tables
PASSPORT	10535	SAM_CAT O_TYPE SAM_STAT END_USE	Accession	10535	DuplicateType Activity
			Origin	7572	CollectingSource SampleStatus EndUse
			Taxon	19	
			Site	2792	
ADDRESS	1253	COUNTRY	Address	1253	
					Country

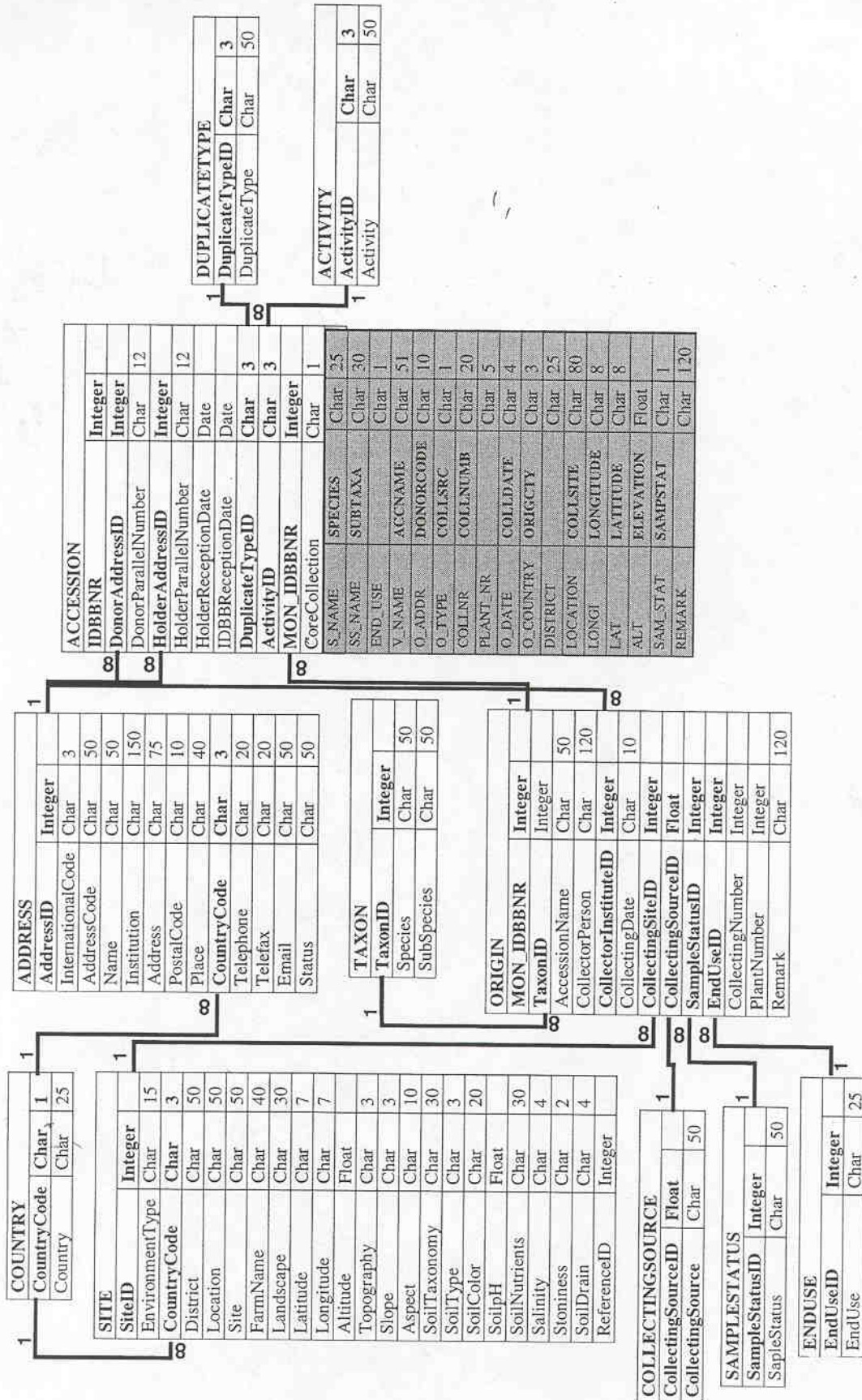


Fig. 1. Tables for passport data.

New concepts for characterization and evaluation data

Documentation of characterization and evaluation data is a much more complicated and difficult task. We will not deal with it in detail at the present stage, but just show some basic concepts, which are presently under development. *Beta* evaluation data until 1991 were held by L. Frese in the CGN documentation system. Th. van Hintum has implemented there a table architecture, which likewise can be found in the GRIN system. This table is suitable to receive the heterogeneous information deriving from evaluation experiments. It is characterized by a SCORE table (corresponding to OBRCD.DBF in PCGRIN) collecting all evaluation data in one tuple, which is surrounded by descriptive tables for experiments, descriptors, evaluation methods etc.

By transferring the *Beta* data to the genebank documentation system at Braunschweig, L. Frese developed the evaluation tables of the German-Dutch *Beta* Collection into the IDBB, which now can be taken as the foundation stone for further evaluation documentation in the IDBB. Table 10 and Figure 2 may give an impression of the preliminary architecture for evaluation data in further IDBB versions.

Table 10. Tables proposed for characterization and evaluation data in the IDBB

Old IDBB	New concept (preliminary)		
Tables	Tables	No. of tuples	Decoding tables
	Tables characterizing methodology		
TRAIT CHAR/EVAL	Trait		Generic terms for descriptors
	Descriptor	66	IBPGR-Descriptors
	Descriptor Synonym		Synonyms for IBPGR-Descriptors
METHODOLOGY	Method	67	Methods used evaluating the descriptors
	Key	93	Units of measurements and rating keys
	Evaluation Standard		Links descriptors and methods Standard cultivars
	Tables characterizing research projects		
	Project ProjectAdmini stration		Important chairpersons for the project
	Tables characterizing experiments		
EXPERIMENT	Experiment	66	Characterizes experimental design
	Site		Characterizes experimental sites
	Treatment		Treatments of experiments
	Operation		Cultivation Agronomic measures in experiments
	Intervention		Lists times of agronomic interventions
	Tables characterizing evaluation results for accessions		
	Measurement		Links methodological and experiment information
SCORE	Score	16671	Observations and descriptive statistics
ADDRESS	Address	1253	Country

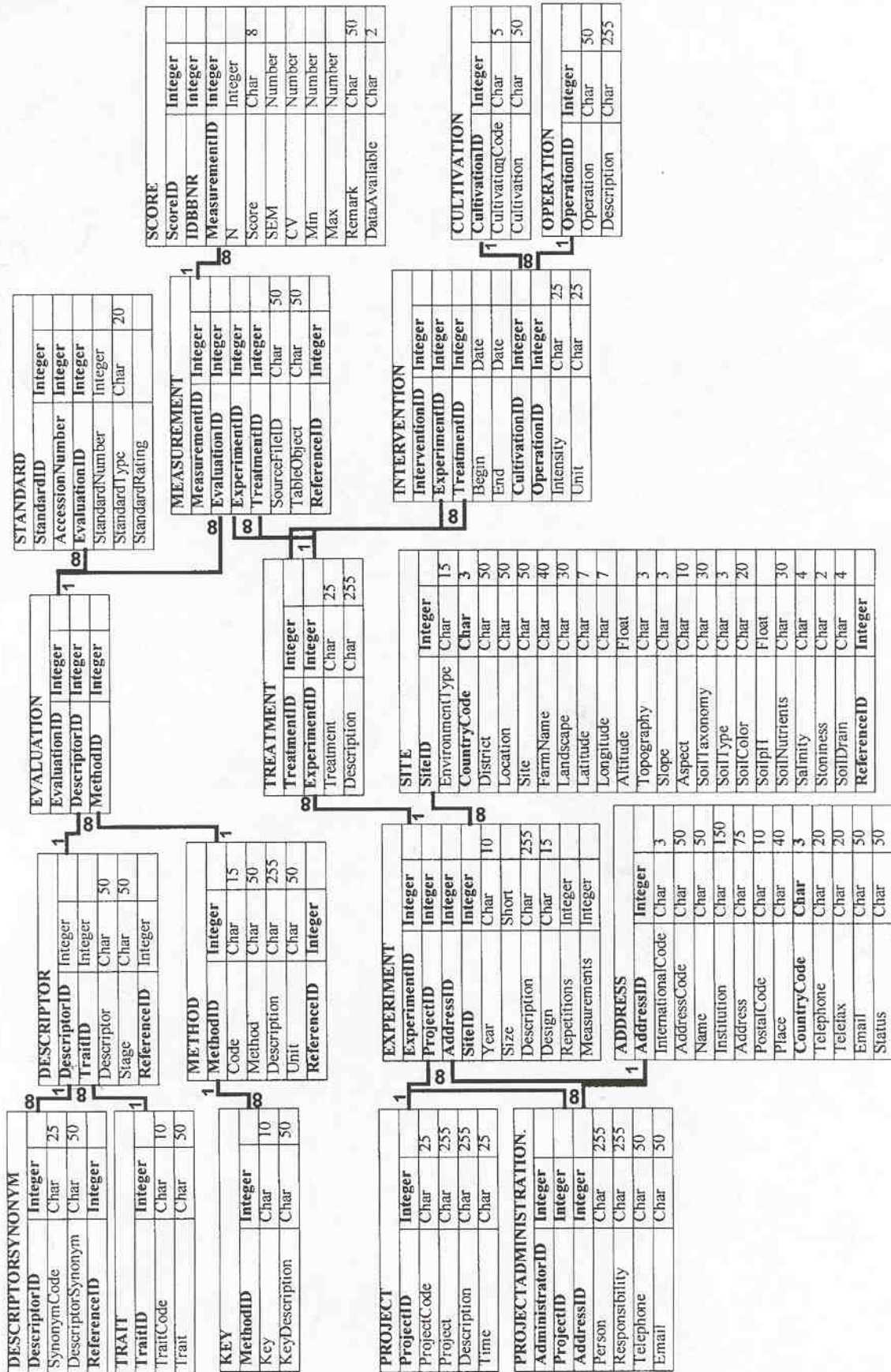


Fig. 2. Tables for evaluation and characterization data.

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Study on the relationship between Chinese and East Mediterranean *Beta vulgaris* L. subsp. *vulgaris* (leaf beet group) accessions

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Introduction

In China, leaf beet has been cultivated for about 2500 years. Only Chinese leaf beet germplasm is widely distributed in central China in the Yangtze River and Yellow River Valleys. In 1883 Ge Yan Qing described the differences between leaf beet and sugar beet by means of isozymes at our institute. Wang Ji Zhi (1989) observed distant relationships between *B. patula* and *B. vulgaris*, close relationships between *B. vulgaris* subsp. *cicla* [according to Lange *et al.* (1999) *B. vulgaris* subsp. *vulgaris* leaf beet group] and *B. vulgaris* by description and analysis of their hybrid progenies. Recently in China leaf beets were distinguished into five different types: white leaf beet, green leaf beet, “four seasons” leaf beet, curly leaf beet and red leaf beet.

Frese (1991) conducted a field experiment with 74 leaf beet accessions from various parts of Europe and described 17 morphological and agronomic characters. Classification of the taxa proved to be difficult because of the lack of sufficiently delineated taxonomic entities.

In this study, we employed RAPD genetic markers to study genetic diversity in leaf beet and we also used 18 morphological characters according to the IPGRI Descriptors for *Beta* to describe the material. In this paper, we discuss the diversity and relationships between accessions by analysis of morphological characters and RAPD data.

Morphological characterization

Twenty-five leaf beet accessions collected in China, Greece and Turkey were measured at different stages of plant development in the field (Table 1). Three characters, i.e. flowering start, flowering end and fruit ball position showed no significant differences. The leaf rosette attitude of most accessions was open (~65°), only accession BGRC58263 was erect (~85°), two accessions (BGRC45000, BC006) are prostrate (~30°), other accessions are semi-prostrate (~45°). The leaf colour of almost half of the 25 accessions was green, the others were all yellow/light green. Only in BGRC32657 a few plants with green petioles were found, in two accessions pink and red petiole colour was observed, white and light green petiole colour was found in most accessions. All the accessions grown in the experiment were annual. Growth habit in BGRC45000 was procumbent, others all belonged to the erect or procumbent type of plants. Three classes of stem colour were recorded: white, green and yellow/light green. White-coloured stem occurred in a few plants only, more plants with yellow/light green stems were observed, while the highest number of plants showed white stems. Only BGRC58263 had no stem pigmentation, entirely red stem pigmentation was moderately represented, red-striped plants prevailed. Particularly leaf rosette diameter, leaf rosette height, leaf number, leaf length, petiole length and petiole width had significant differences between and among 25 accessions as was shown by a variance analysis (not presented here). Clustering analysis of these six characters was processed by the method of the longest distances; most of Chinese leaf beet clustered into one group. They are presumably more closely related. A few accessions were grouped into other groups.

Table 1. Origin and designation of the experimental entries

Reference No. (Fig. 1)	IDBBNR	Donor Parallel No.	Species	Subspecific name	Variety name	Country of origin	Region of origin	District
1	3062	10130	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet		TUR		Adana
2	2675	32393	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Seskoulo	GRC		Peloponnes e
3	3107	32645	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Seskulo Or Ghoules	GRC		Crete
4	3119	32657	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Lakhano Or Lakhari	GRC		Crete
5	3379	45494	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Seskoulo	GRC		C. Greece
6	3382	45497	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Seskoulo	GRC		C. Greece
7	3385	45500	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Seskoulo	GRC		Macedonia
8	3403	45518	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Pazia	GRC		Magnissias
9	6927	56746	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Panzaria	GRC		Kos
10	8439	58263	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Pazi	TUR		Hatay
11	8461	61201	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet		TUR		Mugla
12	9046	BC003	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Lu Niupicai	CHN	SW CHINA	Sichuan
13	9047	BC004	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Lian Shui	CHN	SE CHINA	Jiansu
14	9048	BC005	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Wu Han Hong	CHN	N CHINA	Wuchang
15	9049	BC006	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Hong Niupicai	CHN	S CHINA	Fuijiang
16	9050	BC017	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Chong Qing Hong	CHN	SW CHINA	Sichuan
17	9051	BC018	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Yuan Jiang Lu	CHN	NE CHINA	Hulan
18	9052	BC019	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Bi Jie Hong	CHN	S CHINA	Guizhou
19	9053	BC020	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Rong Cheng	CHN	S CHINA	Henan
20	9054	BC021	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Qinggan Niupicai	CHN	SW CHINA	Sichuan
21	9055	BC022	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Hong Niupicai	CHN	S CHINA	Guizhou
22	9056	BC023	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Shang Yao	CHN	S CHINA	Jiangxi
23	9089	BC027	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Hong Zhou Bai	CHN	E CHINA	Zhejiang
24		BC033	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	"Four Seasons"	CHN	SW CHINA	Sichuan
25		BC035	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Xin Ren Bai	CHN	S CHINA	Guizhou
26	3633	49716	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Bleda	ESP		Valencia
27	6934	56753	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Spinach Beet Perpetual Spinach			
28	9059	BC026	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Jundacai	CHN	S CHINA	Hunan
29		BC032	<i>vulgaris</i>	<i>vulgaris</i> Leaf Beet	Gui Zhou Bai	CHN	S CHINA	Guizhou
30			<i>vulgaris</i>	<i>vulgaris</i> Sugar Beet	Tian Yan-7	CHN	NE CHINA	Heilongjiang

RAPD analysis

Total DNA was isolated using a slightly modified phenol/chloroform method: approximately 25 mg fresh young flower buds were collected from plants of 30 accessions, including those described in the field experiment and the sugar beet variety Tian Yan 7 (see Table 1), and suspended in 400 µl buffer containing 0.5% SDS. Plant DNA purity and concentration were detected by spectrophotometer and 0.5% agarose gel.

PCR was performed in a 0.5-ml tube of 25 µl volume consisting of 100 ng genomic DNA, 5 pmol primer, 2.5 µl 10 × buffer 50 mmol MgCl₂, 5 mol dNTP, 1.5 Utaq DNA polymerase. The reaction mixture was overlaid with a drop of mineral oil. The following primers were used: OPB06, OPB08, OPB17, OPB18, OPB20, OPG09 (Fig. 1), OPG10, OPG14, OPN06, OPN07, OPN20. Amplification was carried out in a DNA Thermal Cycler PTC 200 programmed for an initial 1 min denaturation at 94°C, followed by 45 cycles of 15 sec at 95°C, 45 sec at 37°C and 1 min at 72°C, at last 5 min at 72°C for extension. The total time was 2-3 hours, shorter than before.

The amplified DNA products were separated on 1.4% agarose gel. RAPD data were recorded as presence (1) or absence (0) of amplification fragments (Fig. 1). The data were processed with cluster analysis using the unweighted pair group method with arithmetic mean (UPGMA) and then plotted as cluster diagramme (Fig. 2).

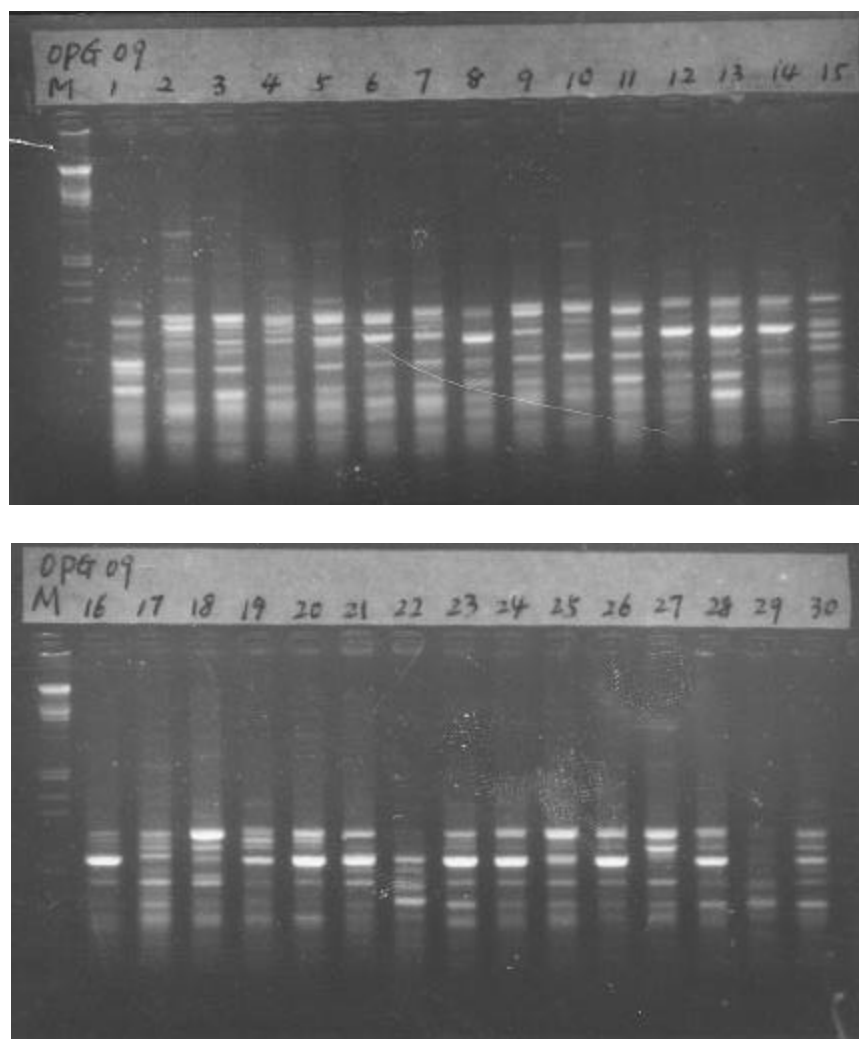


Fig. 1. RAPD of the 30 entries. Primer OPG09 was used.

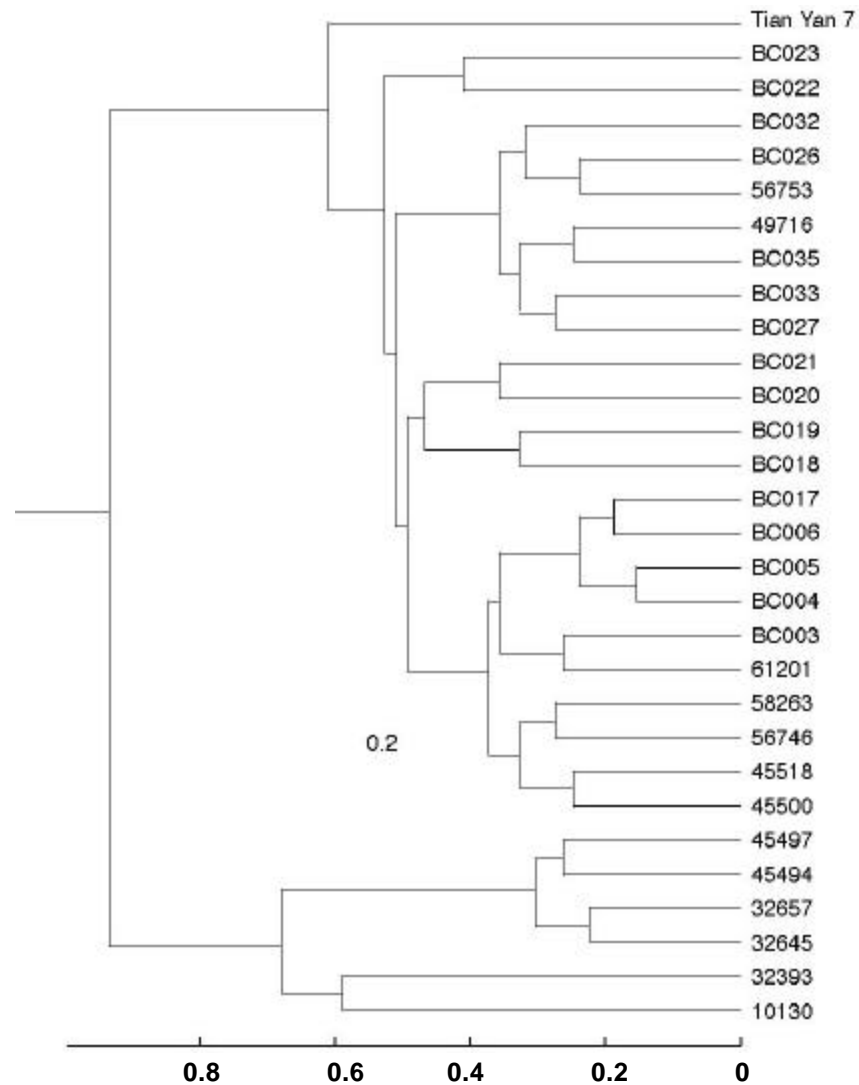


Fig. 2. Results of the cluster analysis based on RAPD.

RAPD analysis showed much polymorphism among the 30 entries. Twelve random primers detected 110 amplified fragments, the polymorphic fragments produced 101 bands, the polymorphic frequencies was 91.81%, average 9.17 bands of each primer. The range of genetic distance was 0.1500-0.6712. The closest relationship was found between BC004 and BC005, the largest difference was observed between BC027 and Tian-Yan 7.

If the cluster diagramme is cut at the distance measure of 0.8 the accessions form two clusters. The larger cluster (A) contains all accessions from China, accessions from Turkey, Greece, Spain and the sugar beet accession Tian Yan 7. In the smaller cluster (B) only accessions from Turkey and Greece are represented. Within the larger cluster accessions from Turkey and Greece are grouped together in a subcluster (BGRC58263, 56746, 45518, 45500).

Discussion

This is the first report of the use of RAPD markers to study variation in leaf beet accessions. There were some differences in cluster results between RAPD analysis and the analysis of the morphological traits which requires further investigation. The differences may have been caused by a stronger environmental influence on morphological traits which is not the case with RAPD.

The RAPD results have shown that all the Chinese leaf beet grouped into one group. There was a closer relationship between all accessions from China. BGRC56753 (origin country unknown), BGRC49716 from Spain and BGRC61201 from Turkey, as well as the sugar beet Tian Yan 7 were also grouped together with Chinese material, indicating a similarity between these and the Chinese material at the level of RAPD markers. Cluster A contained East Mediterranean accessions mainly grouped together in a subcluster close to cluster B.

It can be assumed that the leaf beet was introduced to China by two different routes: first, Arab traders may have brought the crop from Iran to China; second, leaf beet may have been introduced on the Si Chou road or by sea. Leaf beets were probably initially grown in China in areas with growing conditions similar to their place of origin and then started to spread throughout the country.

The results of this paper support the hypothesis that, after the introduction of the crop to China, the Chinese and East Mediterranean leaf beet genepool became genetically different owing to the adaptation of the crop to Chinese growing conditions and farmers' selection. The Chinese accessions were collected in provinces with significant environmental differences (Table 1), causing considerable differentiation in the Chinese leaf beet germplasm.

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Variation in beet resources collected in Ukraine and Slovak Carpathian mountains

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The National Centre for Plant Genetic Resources in Poland organized in 1996, 1997 and 1998 international expeditions in Ukraine, Slovakia and Moldova to collect the local populations of cultivated plants still existing there.

The expeditions were conducted in the East Carpathian Mountains in Slovakia and Ukraine, Piedmont region (valley of the Dniestr river) and in lowland area. A small part of Moldova was also explored in 1998. The collecting area is shown on the map (Fig. 1).

Among different seed samples, 77 beet accessions of garden and fodder beets were obtained from small farmers in 30 villages and provided to the *Beta* Collection in Bydgoszcz.

The evaluation of morphological, biological and some agronomic features was carried out on the field plots. An average 60-80 roots per accession were grown except for 12 accessions with low seed numbers or poor germination. After harvesting, beets were left for maintenance in isolation and evaluation in the second year of growth.

Great variation was found both between and within the populations. Most of the accessions were a mixture of fodder beets of different shapes and colours, garden beets and hybrids between fodder and garden beets. Only 20% of accessions were fodder or table beets, uniform in shape and colour.

The range of variation in morphological traits is presented in Figure 2a-f. Dry matter content varied from 6.2 to 13.4% and average root mass from 240 to 1850 g. Three accessions showed high bolting susceptibility.

Cytological analyses revealed that the accessions studied were diploids, except for four from lowland Ukraine (UKR/97-73, 103, 208 and 232) which were anisoploids (mixture of $2 \times 3 \times 4 \times$). One monogerm population was found in the material from Slovakia (SLO/97-74). The remaining accessions were multigerm with two-three germs/ball.

Among all the accessions multiplied, 10 plants were tested for self-fertility in isolation bags. In each accession highly self-compatible plants were found. These results explain the different segregation ratios in mixed populations which are not in agreement with the results concerning inheritance patterns for colour and shape in fodder beets (Kajanus 1913; Schlösser 1949; Knapp and Mundler 1957). Self-compatibility allows different types to coexist in one sample and fix the new variation which occurs during multiplication done by farmers themselves. The evaluation revealed that in those countries in small farms it is common practice to cultivate beets as a mixture.

According to information obtained during the expedition, the oldest populations are from the Carpathian Mountain region and surroundings (before World War II).

After multiplication these accessions will be tested for resistance to beet diseases.

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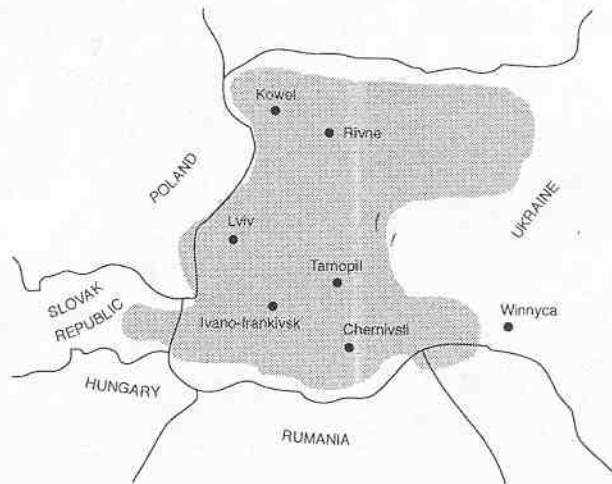
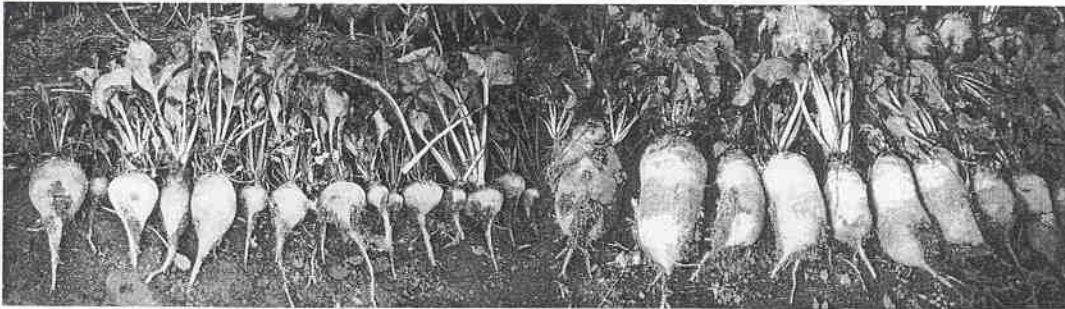
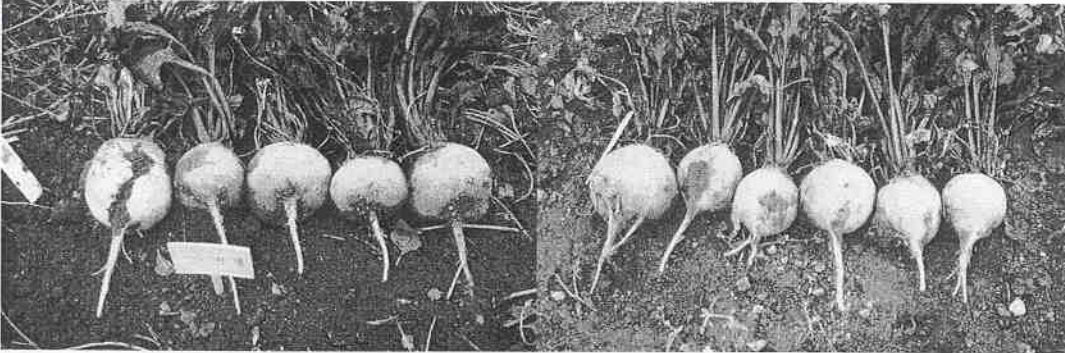


Fig. 1. Regions of *Beta* accession collecting in 1996, 1997 and 1998.



a

b



c

d



e

f

Fig. 2. Various morphological traits exhibited by *Beta* accessions: (a) UKR/96-81, Sloboda Bolechivsk, Ivano Frank; (b) UKR/97-164, Novoselki, Vladymir; (c) UKR/96-50, Vytvycja, Ivano Frank; (d) UKR/96-99, Lipa, Ivano Frank; (e) SLO/96-401, Inovce, Vychodoslov; (f) SLO/97-74, Vielkie Rovne, Zabladiе.

Part III. WBN meeting abstracts

Papers

Estimating geneflow among sea beet populations using molecular markers

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Restricted dispersal of seed and pollen will limit geneflow in all plants to some extent. Estimates of the spatial scale of geneflow can help design strategies for efficient sampling of genetic resources. In addition, some wild relatives such as sea beet are the potential recipients of transgenes from genetically modified crops. In these cases, estimates of geneflow can help to inform environmental risk assessments by predicting the rate of spread and local frequencies of transgenes in natural populations. In this paper, we describe methods for estimating geneflow from the spatial distribution of variation in allele frequencies at molecular marker loci. When geneflow is estimated between all pairs of populations, a significant negative correlation between geneflow and the geographical distance between populations indicates that geneflow is spatially restricted (isolation by distance) at the scale of the sampling. Regressions of geneflow and distance can be used to derive estimates of, say, the distance at which geneflow drops below a critical value. This is not simple, however, as regressions use matrices of pairwise data rather than independent points. Using isozyme and RFLP data from sea beet populations in Dorset (UK), we describe methods for the correct testing of differences between such regression slopes, and derivation of confidence intervals of estimates of parameter values from the regression slope. We show that estimates of the rate of change of geneflow with distance from RFLPs and isozymes are significantly different, and examine the sensitivity of this result to the effects of single loci.

Impact of geneflow from cultivated beet on genetic diversity of wild sea beet populations

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Geneflow and introgression from cultivated plants may have important consequences for the conservation of wild plant populations. Cultivated beets (sugar beet, garden beet and leaf beet: *Beta vulgaris* subsp. *vulgaris*) are of particular concern because they are cross-compatible with the wild taxon, sea beet (*B. vulgaris* subsp. *maritima*). Cultivated beet seed production areas are sometimes adjacent to sea beet populations; the numbers of flowering individuals in the former typically outnumber those in the populations of the latter. In such situations, geneflow from cultivated beets has the potential to alter the genetic composition of the nearby wild populations. In this study we measured isozyme allele frequencies of 11 polymorphic loci in 26 accessions of cultivated beet, in 20 sea beet accessions growing near a cultivated beet seed production region in northeastern Italy, and 19 wild beet accessions growing far from seed production areas. We found one allele

that is specific to sugar beet relative to other cultivated types and a second that is in much higher frequency in Swiss chard and red beet than in sugar beet. Both alleles are typically rare in sea beet populations that are distant from seed production areas, but both are common in those that are near the Italian cultivated beet seed production region – supporting the contention that geneflow from the crop to the wild species can be substantial when both grow in proximity. Interestingly, the introgressed populations have higher genetic diversity than those that are isolated from the crop. The crop-to-wild geneflow rates are unknown, as are the fitness consequences of such alleles in the wild. Thus, we are unable to assess the long-term impact of such introgression. However, it is clear that geneflow from a crop to a wild taxon does not necessarily result in a decrease in the genetic diversity of the native plant.

Genetic diversity and genetic variability in *Beta vulgaris* subsp. *maritima* under subtropical climates of India

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Beta vulgaris subsp. *maritima* is generally a self-incompatible, cross-pollinated perennial species. It grows from Mediterranean coasts to European Atlantic coasts. This subspecies grows along sea coasts and is, therefore, salt-tolerant. *Beta vulgaris* subsp. *maritima* as a source of CMS has been reported in different accessions collected by various scientists from Turkey, Greece, Morocco, Tunisia, England and France. Thirty-seven accessions of *B. vulgaris* subsp. *maritima*, obtained from the BAZ Gene Bank located at Braunschweig, Germany, were evaluated for 14 quantitative and quality traits at the Indian Institute of Sugarcane Research, Lucknow under the subtropical climate of North India. The important characters studied were: root characters (root weight, root length, crown size, number of rings, shape and colour); leaf characters (leaf length, leaf width, petiole length, etc.); flowering characters; Brix %, and tolerance to high temperatures (40°C and above). This experiment was sown in November 1996 and harvested in May-June 97. Genetic diversity was studied and compared by the Mahalanobis D² and Spark methods. The relationship of genotypes to geographic origin, on the basis of all the traits studied, the contribution of each character to genetic diversity and the most important attribute which contributed to diversity were also studied. Inter- and intra-clustering was done and six clusters were constituted by the Mahalanobis D² method. Genetic variability, heritability, and genetic advance for quantitative traits were studied by Fisher's method. This paper presents the results obtained, and the utilization of genotypes from each cluster for use in breeding programmes is described and discussed in detail.

Genetic diversity among and between beet landraces in Iran

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Cultivation of beet landraces is prevalent in most provinces of Iran. Seed samples of 175 beet landraces have been collected in the *Beta* Gene Bank of the SBSI. Characters such as 1000-seed weight, germination, ploidy level, hypocotyl colour and annuality of the genetic material have been identified. Morphological characteristics, such as foliage characters, root shape, and root colour of 18 accessions were evaluated in 1998. Morphological characteristics vary among and between the accessions. Yield and technological characteristics of the genetic material were determined and the differences in root quality are presented.

Localization of a second monogerm gene in sugar beet using RFLP markers

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Only one gene, *M-m*, controlling the multi/monogerm phenotype has been described and mapped into linkage group No. 2. In our experiments a second new monogerm gene, designated *m2*, was analyzed in F_2 segregating populations from crosses between monogerm and multigerm lines of Russian origin (S22 and No. 14, respectively). The *m2* gene was localized using RFLP markers already mapped on the sugar beet genome. Finally, 17 RFLP probes were selected and 56 plants of an F_2 population were examined. As a result, nine RFLP markers located in eight linkage groups (excluding No. 2) were found to segregate independently from the monogerm trait. Another eight RFLP probes were located in linkage group No. 2 and demonstrated an association with monogermity. The linear order of these markers was identical to those described earlier. Some RFLP markers differed in localization distance when compared with previously published data. The *m2* gene was distantly mapped in the same linkage group (No. 2) as the *m* gene. The localization distance between the *m-m2* genes was determined as 32.2 cM. These results on the localization of a second monogerm gene *m2* using the RFLP method confirm our previous genetic analysis where individuals with the heterozygous genotype *m/m2* can have a bi-germ phenotype.

Towards a map of functional genes focused on carbohydrate metabolism

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Complex physiological traits are the result of action and interaction of specific genes. In our project we want to assign role and relevance to some of the genetic components determining sugar quality and yield. The work is based on an F₂ population deriving from a cross between two parental genotypes with different sugar yield parameters. Each progeny of F₂ plants will be evaluated in a QTL analysis. At the molecular level, candidate genes will be considered to be associated with major QTL effects. We have developed degenerate primers to conserved regions of genes potentially relevant to carbohydrate metabolism, and the corresponding PCR fragments from sugar beet genomic DNA or cDNA have been cloned. The metabolic pathways considered include the Calvin cycle, synthesis of transient starch, glycolysis, sucrose synthesis and transport, the citrate cycle, nitrate reduction, amino acid synthesis and osmoprotection. So far, the sugar beet homologues of more than 50 genes have been analyzed. Most alleles differ by very few nucleotides and this requires sensitive techniques for the detection of polymorphisms. We use RFLP, CAPS, SSCP and Heteroduplex analysis for mapping. At present 38 of the genes have been ascribed to linkage groups. A new preliminary functional map will be presented.

Beet gynogenetic lines: induction, flow cytometry and technological estimation

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More than 70 gynogenetic lines were induced in *in vitro* culture of unfertilized ovules from plants of the most common Belarus sugar beet cultivars ('Ganusovskaya 55', 'Belorusskaya 69', 'Yanash A3', 'Verkhnyachskaya 103' and 'Belotserkovskaya 40'). Regenerants developed through organogenesis and embryogenesis on the MS induction medium supplemented with BAP and high sucrose content. Clonal micropropagation techniques were used for their maintenance. For overcoming difficulties during the adaptation period, ion-exchange substrates of a defined content were successfully applied. In early subcultures all ovule-derived lines were cytologically tested. Doubled haploids were obtained by colchicine treatment and by spontaneous polyploidization after long-term cultivation of haploids. In addition to light microscopy, flow cytometry (Partec PAS II) was used for screening ploidy level in 50 cultured *in vitro* sugar beet samples of different origin and age. The majority of regenerants from diploid donors were mixoploids (n+2n) and the rate of spontaneous polyploidization differed among them. A few lines originating from cells with unreduced chromosome numbers, and thus heterozygous, were found. In the case of tetraploid donor plants the gynogenetic regenerants showed diploidy. A reduction of ploidy level in cells of control shoots has never occurred. Mixoploidy in doubled haploids could be overcome by recultivation of regenerated plants

using apical meristems of generative shoots. Field trials (1995-98) demonstrated the difference in productivity traits between recultured gynogenetic lines and primary regenerants. Estimation of root weight and sugar content in 1-year vegetative plants of some gynogenetic lines, and their hybrids with a Red tester and two male-sterile forms, allowed selection of the best ones.

The Synthetic *Beta* Core Collection – state of the art

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The high costs for evaluation projects call for a rational use of germplasm collections in screening programmes. For the efficient exploitation of a large collection, subsets should be selected that represent a maximum of genetic diversity of a given genepool in a minimum set of accessions. Such subset is called a core collection. If the entities of this core collection are composed of material donated by several genebanks, it is called a synthetic core collection. Within the GENRES CT95-42 project a Synthetic *Beta* Core Collection (SBCC) has been developed, which is being evaluated by project partners for resistance to biotic and abiotic stress agents. A preliminary survey of the evaluation data has shown that most of the low disease resistance scores have been reported to occur in *B. vulgaris* subsp. *maritima* accessions.

Two methods can be distinguished for the selection of accessions for a core collection. Branching methods are based on passport data combined with knowledge of, and assumptions about, the structure of a genepool. In the case of *Beta*, the whole genus is considered as the genepool. The core collection has been composed using knowledge on the evolution and domestication of the species, their potential usefulness for breeding, and the geographic distribution of particular accessions. Accessions numbers have been chosen and earmarked in the International Database for *Beta* (IDBB). In total 674 accessions have been selected. *Beta* section *Beta* accessions represent 88% of the collection while sections *Corollinae* and *Procumbentes* represent 10% and 2% respectively. Eighty-nine percent of the material is of European and West Asian origin while other areas altogether are represented with 11%.

It has been suggested that 200 accessions of section *Beta* would sufficiently represent the genetic diversity of this section. Under this assumption the fraction of section *Beta* germplasm in the SBCC may be too large. During the GENRES CT95-42 project, characterization and evaluation data are generated that can be applied for clustering, the second method for core collection development. By analyzing the data, redundancy can be detected and the core collection be rationalized. In the case of a small part of the 'garden beet' core collection, first attempts towards improvement of the core collection by cluster analysis based on morphological characters, yield and chemical components have been made.

Disease resistance in populations of *Beta* species

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As part of a pan-European effort to improve the utilization of *Beta* germplasm in sugar beet production, approximately 600 *Beta* accessions are being evaluated at IACR-Broom's Barn for resistance to several economically important diseases of sugar beet. These include two yellows virus diseases, beet mild yellowing virus (BMV) and beet yellows virus (BYV), two seedling damping-off diseases caused by the fungi *Aphanomyces cochlioides* and *Pythium ultimum*, and powdery mildew (*Erysiphe betae*). A wide range of *Beta* material is being evaluated; most are related cultivated varieties (fodder beets, garden beets, leaf beets, sugar beets – 60% of total) or *B. vulgaris* subsp. *maritima* (25%), but other *Beta* accessions of the sections *Beta* (10%), *Procumbentes* (2%) and *Corollinae* (2%) are included.

Available results indicate a wide range of reactions to each disease within the *Beta* germplasm collection. Importantly, there is a significant number of accessions with very low levels of disease. To date testing has shown that, for each character, approximately 1-6% of accessions exhibit apparently high levels of resistance; for BMV and powdery mildew promising accessions have been retested and, in most cases, resistance has been confirmed. For the remaining characters confirmatory tests are in progress. When resistance is confirmed individual plants are vernalized (where necessary) and either selfed or inter-crossed, depending on their self-compatibility, to generate seed. From this it is planned to assess the heritability of the character and the genetic control of the resistance; limited testing with seed produced from BMV-resistant plants has shown that the resistance identified so far is heritable.

Exploiting novel sources of disease resistance in *Beta* germplasm using molecular markers

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Breeding disease-resistant sugar beet cultivars is of paramount importance in the move toward reducing pesticide inputs in sugar beet production. To be durable in the field, disease resistance may need to be based on highly effective genes from different sources with different modes of action. Novel sources of resistance derived from wild *Beta* species are likely to be a good source of the genes required. However, before such sources can be used efficiently in breeding programmes, it is necessary to determine how many genes control resistance in a particular source and whether they are the same as currently used genes. By developing molecular markers linked to novel disease resistance genes, many of these questions can be addressed. Marker-assisted selection (MAS) can then be employed to speed up the introgression of new genes into suitable germplasm and ensure they are not lost during a breeding programme. In our preliminary studies, we have developed amplified fragment length polymorphism (AFLP) markers linked to the BNYVV resistance gene *Rz* and markers linked to quantitative trait loci (QTL) for powdery mildew resistance. The markers linked to *Rz* have been used in comparative studies of different sources of BNYVV resistance and have highlighted similarities and differences between the 'Holly' source, which contains *Rz*, and other non-Holly sources of resistance.

Beta breeding and genetics at East Lansing: molecular methods, genetic diversity and trait elucidation

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The USDA-ARS has maintained a sugar beet breeding programme at East Lansing for over 60 years in support of the sugar beet industry in Michigan. For most of this time, variety development and release has been the main goal, with successive progress made in developing resistance to *Aphanomyces* seedling disease, *Cercospora* leaf spot tolerance, low-tare genotypes and *Rhizoctonia* root rot tolerance. Current emphasis continues on these aspects, as well as examining field emergence *in vitro* and *in situ*. With the exception of tissue culture activities, little of this work has involved a laboratory component. Currently, we are building a programme involving high-throughput genotyping technologies to gain the ability to survey a wide range of germplasm and begin to correlate molecular markers with agronomic and morphological traits. The programme is at an early stage. To date, we have created hybrids between sugar beet (represented by a California breeding line susceptible to the suite of diseases encountered in Michigan, which carries the dominant self-fertility allele and segregates for genetic male sterility) and representatives of the major *Beta* crop groups (fodder beet, garden beet, leaf and wild beet) as well as sugar beet varieties adapted to Michigan. A number of these have been selfed; thus segregating populations are available for genetic analysis. A project to develop Expressed Sequence Tags (ESTs) as markers is just beginning. Clones from a leaf cDNA library are in hand, and will be simultaneously used as RFLP markers and sequenced to identify putative functions as identified in nucleotide sequence databases. An analysis of genetic diversity among US germplasm sources was conducted with RAPD markers, showing a trend toward greater homozygosity in more recent releases. Genomic subtraction has been successful in reducing polymorphic complexity between male-fertile and male-sterile pools from a single population. However, the fragments recovered have not yet been tested for their predictive potential in segregating populations. The tools for molecular genotyping have been acquired and are in place. Agronomic evaluations may be facilitated via testing for correlated traits.

Twenty years of screening sugar beets for resistance to

Rhizoctonia solani

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Each year, an artificial *Rhizoctonia* root rot epiphytotic is established in the field by the USDA-ARS Sugar Beet Research Unit (SBRU) located at Fort Collins, Colorado, to evaluate sugar beet resistance to this disease. In this nursery, the SBRU has used cyclic mass selection, recurrent selection and progeny testing in the breeding programme to develop sugar beet germplasm resistant to *Rhizoctonia solani* AG2-2. In the last 30 years over 40 *Rhizoctonia* root rot-resistant germplasm have been released from this programme. Additionally, this nursery has been used to evaluate the resistance of sugar beet hybrids and experimental breeding lines submitted by Beet Sugar Development Foundation member companies and public sugar beet breeders. There has also been a programme for more than 10 years that uses this nursery to screen the US National Plant Germplasm Systems *Beta* Plant Introductions. The current SBRU breeding programme continues to utilize this nursery and, to produce reliable results, adequate epiphytotics must be

developed under varied environmental conditions. Manipulation of the micro-environment in the field has allowed maintenance of the consistency of disease intensity in resistant and susceptible controls across experiments and years. Data obtained from this nursery over the past 15 years illustrate this consistency. The influence of interplot interference, which could be a problem in small plot work, has been examined because significant interference might cause erroneous results resulting in lower relative resistance ratings in experiments in which the majority of the lines were susceptible. We are confident that field techniques developed by the SBRU provide the consistent epiphytotics necessary to continue selecting *Rhizoctonia* root rot-resistant germplasms and to test the resistance of sugar beet lines to this disease.

Genetic variation for drought stress in sugar beet

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In semi-arid regions of the world, fluctuation in sugar beet (*Beta vulgaris* L.) yield can largely be attributed to differences in duration and intensity of drought stress. In the current study, 49 diverse breeding materials of sugar beet were evaluated for root yield (RY), sugar content (SC), sugar yield (SY), and white sugar yield (WSY) under irrigated condition and two types of drought conditions at the two locations of Karadj and Mashhad in 1996, 1997 and 1998. A randomized complete block design with two replications was laid out for each irrigation treatment. Different breeding materials were evaluated in each year but some common lines were used as controls in all cases. Water stresses started at about the six-leaf stage of plants. Severe stress continued throughout the growing season in Karadj and irrigation was applied when the TDR probes recorded 15% soil water content at depths of 0-60 cm. In Mashhad, the field was under stress for a period of 50 days only by withholding water after the six-leaf stage. Stress tolerance indicators such as the stress susceptibility index (SSI), stress tolerance (TOL), stress tolerance index (STI), yield stability index (YSI) and potential yield productivity (MP) were estimated for each genotype to distinguish the high-yielding genotypes both in the stressed and non-stressed experiments. Root yield and its related characters (SY and WSY) exhibited the largest differential genotypic responses to drought conditions. Stress applied for either a limited period (Mashhad) or continuously for the whole growing season (Karadj) gave similar results, but the effects of the continuous stress were more pronounced. Under the severely stressed conditions, total mean values of RY, SY and WSY decreased to 59.13%, 59.07% and 60.02%, respectively, compared with the controlled experiment whereas SC had an increase of 5.70%. Total mean values for characters such as RY, SY, WSY and SC decreased in the drought conditions of Mashhad to 71.59%, 67.42%, 64.91 and 94.64% of the well-watered control, respectively. Comparing the indexes for screening drought-tolerant sugar beets, the stress tolerance index (STI) can be used effectively to distinguish the high-yielding genotypes both in stressed and non-stressed environments. A breeding strategy is suggested that involves selection, mainly based on root yield in contrasting environments, to ensure broad adaptation of sugar beet genotypes.

Posters

Adaptogenesis in *Beta L.*

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Adaptogenesis, or formation of new adaptive characters and functions, is based on polymorphism resulting from differentiation in populations. Three types of adaptogenesis have been described for *Beta L.*, namely phylogenetical, populational and ontogenetical (Burenin 1996). The intrapopulational adaptogenesis involves different groups of biotypes, including mutants. A pattern of microevolution has been elaborated, based on the example of two mutant beet forms. Adaptive functions in ontogenesis reveal themselves in the liability of transition from the vegetative to generative phase and the variability of interphase periods in different cultivars, forms and lines.

The beet collection includes 400 accessions of table, 600 fodder, 900 sugar and 50 leaf beets. In terms of ploidy, diploids make up 74%, anisoploids 19%, and tetraploids 7% of the collection (Burenin and Gavrilyuk 1994). By means of active and passive screening, 350 accessions have been tested for resistance to bolting, 418 for resistance to black root, 233 accessions for resistance to storage rot, 110 for monogermicity, 150 for salt and drought tolerance; chemical composition has been studied in 630 accessions. Genetic diversity has been examined for characters controlled by major genes identified in beet: 22 for vegetative organ characters, 6 for vegetative organs and 2 for resistance to diseases (Burenin and Shevtsov 1990). As a result, a genetical collection comprising 142 accessions has been formed to include 26 monogerm lines, 3 self-fertile types, 5 annual types and 59 CMS biotypes. The core collection includes 136 accessions of sugar, 118 of fodder, 114 of table and 31 of leaf beet (Burenin 1998).

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The linkage disequilibrium between cpDNA and mtDNA haplotypes in *Beta vulgaris* subsp. *maritima* (L.) and its consequences on the origin of male-sterile cytoplasm

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The structure and evolution of the plant mitochondrial genome may allow the recurrent appearance of the same mitochondrial variants in different populations. Whether a mitochondrial variant is distributed by migration or appears recurrently by mutation (creating homoplasmy) in different populations is an important question with regard to the use of these markers for population genetic analyses. The genetic association observed between chloroplasts and mitochondria (i.e. two maternally inherited cytoplasmic genomes) may indicate whether or not homoplasmy occurs in the mitochondrial genome. Four hundred and fourteen individuals sampled in wild populations of beets from France and Spain were screened for their mitochondrial and chloroplast polymorphisms. Mitochondrial DNA (mtDNA) polymorphism was investigated with RFLP and chloroplast DNA (cpDNA) with PCR-RFLP, using universal primers for the amplification. Twenty and 13 variants for mtDNA and cpDNA were observed respectively. Most of them exhibited a widespread geographical distribution. As a very strong linkage disequilibrium was estimated between mtDNA and cpDNA haplotypes, a high rate of recurrent mutation was excluded for the mitochondrial genome of beets. Identical mitochondrial variants found in populations from different regions were more likely to be due to migration than to recurrent mutation.

Variation in beet resources collected in the Ukraine and Slovak Carpathian mountains

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In 1996, 1997 and 1998 the National Centre for Plant Genetic Resources, Poland, organized international expeditions in the Ukraine and Slovak Carpathian mountain regions and in Moldova in order to collect the local populations of cultivated plants which still exist there. Among different samples, 77 multigerm beet accessions of garden and fodder beets were collected from individual small farmers (Podyma, Nowosielska, Hauptvogel and Boguslavskij) and provided to the *Beta* Collection in Bydgoszcz.

Morphological and agronomic features of the accessions were evaluated in 1996 and 1997 on field plots by Dalke and Kudowicz. Plants of each accession were left for multiplication in isolation bags because of the small number of seeds. The accessions evaluated were composed of a mixture of fodder beets of different shape and colour and very often also table beets. Hybrids between fodder and table beets were also found. The composition of accessions in shape and colour depended on the locations (villages). Only about 20% of accessions of fodder and garden beets were uniform in shape and colour.

Dry matter content varied from 6.2% to 13.4%. These beets have been cultivated and multiplied in farmers' back gardens within small areas and can be considered as local types developed from old multigerminant varieties.

Origin and diversity of Baltic sea beet populations (*Beta vulgaris* subsp. *maritima* Arcang.) in Germany analyzed by RAPD-PCR

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There are indications that the distribution of sea beet has not reached its potential ecological peak in the Baltic Sea area and so far no systematic examination has been conducted to clarify the origin and genetic relationship between the Baltic sea beet populations. Theoretically, the establishment and spread of wild beet populations could be the result of different processes: (1) introduction of seeds from wild populations, (2) naturalization of cultivar or weedy types after introduction into wild habitats, and (3) a combination of 1 and 2 with subsequent hybridization and evolution to an intermediate genotype.

In this investigation, the distribution range of sea beet populations on the Baltic Sea coast of Germany was examined by collecting samples from the fields and performing RAPDs. German Baltic sea beets have been found mainly on the German island of Fehmarn. The relatively large number of *B. vulgaris* subsp. *maritima* on Fehmarn was unexpected, because wild beets are usually very rare in Germany and the population on Helgoland in the North Sea was regarded as the only stable one in the country. Genetic analysis suggests a close relationship between German sea beets and Danish sea beet populations.

The new sea beet populations can be found sympatrically with German agricultural areas with flowering sugar beets and weed beets, thus posing chances of gene escape from genetically modified cultivars. This is of particular concern for the risk assessment associated with gene flow of genetically modified beets.

Access to information on plant genetic resources of beets (*Beta* spp.)

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Worldwide access to information on accessions of genetic resources collections is an essential requirement for their utilization. Today the International Database for *Beta* (IDBB) holds information on 10 535 accessions stored in 28 genetic resources collections. The IDBB serves as a central information entry point within a network of decentralized collections.

Increasingly the Internet is being used to provide information on genetic resources. The user can choose between on-line searching or downloading off-line versions. In cooperation with the BAZ Gene Bank the IDBB is presented as on-line version by the Information Centre for Genetic Resources (IGR) in the German Agricultural Information Network (<<http://www.dainet.de>>). The source files are managed by the BAZ Gene Bank.

Table 1 presents some addresses and information about beet genetic resources databases on the Internet. Besides the IDBB and the US Genetic Resources Information Network, passport information can be retrieved on-line from national genebank information systems. The Russian Vavilov Institute holds about 1500 accessions.

Table 1. Databases of *Beta* genetic resources on the Internet

Database	Internet address	Provider	Data provided	Access	No. of accessions
IDBB	www.dainet.de/genres/Beta/	BAZ/ZADI	Passport	On-line	9461 [†]
	indigo3.dv.fal.de/bgrc/bgrc-e.html	BAZ	Passport	Off-line Downloadable Dbase	9469 [‡]
GRIN	www.dainet.de/genres/pgrdeu/	ZADI	Passport, Evaluation	On-line	2395
	www.ars-grin.gov/npgs/searchgrin.html	GRIN			
PCGRIN	www.ars-grin.gov/npgs/pcgrin.html	GRIN		Downloadable Frontend+Dbase	2320
VIR	www.dainet.de/genres/vir/data/dbf.htm	ZADI	Passport		1562
CGN	www.cpro.dlo.nl/cgn/database/	CPRO	Passport		205 [‡]
NGB	www.ngb.se/Databases/Accson.html	NGB	Passport		94

[†] Without samples no longer in collection (NOC).

[‡] Active duplicates of the German-Dutch *Beta* collection.

The International Database for *Beta* (IDBB) provides information on by far the greatest number of accessions. So far only passport data are on-line. The next downloadable version, in MS-Access 97, should also provide evaluation data.

The Germplasm Resources Information Network (GRIN), a service of the US National Plant Germplasm System (NPGS), provides a highly elaborated passport and evaluation database on-line and off-line on almost 2500 accessions.

Cytologic and genetic investigation of abnormal pollen development in sugar beet (*Beta vulgaris* L.)

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Plants with abnormal pollen development have been found in sugar beet (*B. vulgaris*) and wild *Beta* species (*B. macrocarpa* and *B. vulgaris* subsp. *maritima*). The majority of mutations acting in microsporogenesis in *Beta* species result in complete male sterility. Cytological observations of male-sterile forms have shown that male meiosis proceeds normally until tetrad formation, after which microspore degeneration begins before pollen wall (exine) formation.

Four sugar beet male-sterile forms of different origin were investigated. Cytological study of microsporogenesis has revealed two forms in which degradation of microspores begins after the start of pollen grain wall formation. Genetic investigation of all forms has shown that male sterility is determined by recessive nuclear genes. Cytological and genetic investigation of male-sterile forms has shown that these nuclear genes are non-allelic to each other. New nuclear genes were found which have not been described before.

Two cytological mutations "ap" (accretion pollen) and "ps" (parallel spindle) of sugar beet, which did not result in male sterility, were studied. In normal diploid sugar beet plants mutation "ps" leads to diploid pollen grain formation. The second hybrid generation segregated into two phenotypes, normal and with mutation "ps". Mutation "ap" leads to non-release of microspores in tetrads. In anthers, pollen consists of normal single pollen grains and pollen grains aggregated in tetrads. Mutation "ap" is inherited as a single recessive nuclear gene.

Molecular analysis of genetic diversity in sugar beet breeding material

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The aim of the study was to evaluate the efficiency of the RAPD method for analysis of genetic diversity in closely related breeding materials of sugar beet. The DNA polymorphism of maintainer (O-type) lines and their sublines was analyzed by the RAPD method. The 19 primers selected after screening 34 primers in a preliminary survey produced from 10 to 87 DNA bands varying between 275 and 2536 bp. The highest number of PCR products (108) was observed in lines LO8B and LO8C but only 86 bands were generated with all primers in line LO10. No single marker band was observed that enabled the discrimination of individual lines. In paired comparisons, the number of bands present in both lines was compared with bands present in only one line of the analysed pair. The genetic similarity index was calculated using Nei and Li's matching coefficient. The lowest genetic similarity coefficient (0.60) was found between LO6 and LO10 lines and the highest genetic similarity (0.92) was obtained for LO8G and LO9 lines. RAPD analysis enabled us to distinguish a separate group consisting of LO8A, LO8B, LO8C, LO8D and LO8G lines, which were discriminated from the others by high mutual genetic similarity.

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Drought tolerance in *Beta* germplasm: results from field and growth chamber screens

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Drought is the single most important factor limiting sugar beet yields in the UK and climate change models indicate that the problem will get worse. We have initiated a programme aimed at improving the drought tolerance and water-use efficiency of sugar beet. The first phase is to screen *Beta* germplasm accessions for drought tolerance. One screen evaluates material subjected to water deficit for 4 weeks in a controlled environment (CE) room. Over 200 accessions (obtained from the BAZ Gene Bank) have been screened so far. Another screen evaluates root and total dry matter yield of material planted in the field. In 1998, 16 lines representing various *Beta* types (*maritima*, fodder and sugar beet) were tested under irrigated or rain-fed conditions. Two lines performed better than the mean and are being re-tested in 1999, along with another 30 diverse sugar beet lines. The 1999 trial is being conducted under 0.4 ha of polythene covers with and without drip irrigation. Initial results suggest that the primary CE room screen is useful in selecting lines that may show promise and warrant field testing. We hope that the screening will identify sources of germplasm that have greater drought tolerance than current commercial varieties. The next step will be to develop a mapping population from parents of contrasting drought tolerance, identify QTLs associated with physiological/morphological traits conferring tolerance (the objective of related concurrent work), and ultimately isolate molecular markers associated with these QTLs for marker-assisted selection.

Mitochondrial DNA variation in maintainer lines (O-type) of sugar beet

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The reason for intensive molecular studies of the sugar beet mitochondrial genome, especially male-sterile lines of different origin, is the availability of only one source of male-sterile cytoplasm (Owen source) in breeding programmes. The variability of maintainer line (O-type) mitochondrial DNA has rarely been analyzed.

To study the possibility of mtDNA diversity in maintainer lines, we performed RFLP analysis of different male-fertile materials. Mitochondrial DNA was isolated from: (1) line LO6 and three sublines of line LO8 indexed from American monogerm populations, and (2) two sublines from each of LO9, LO10 and LO12, lines which were selected from the Russian monogerm population. Digestion of mtDNA with *EcoRI* revealed three different restriction patterns. Lines LO6 and LO8 possess typical *EcoRI*/mtDNA patterns previously described for N cytoplasm of sugar beet (*Beta vulgaris* L.). Lines LO9, LO10 and LO12 showed separate restriction profiles resembling patterns for mtDNA of fertile plants of wild beet *Beta vulgaris* subsp. *maritima* digested with *EcoRI* and classified as N₂ and N₃ types. The alterations in *EcoRI* restricted mtDNA of some maintainer lines were associated with differences in the organization of *coxII* and *atpA* genes. Probing mtDNA with *coxII* revealed a strong additional hybridization signal for only the LO9A line representing the

new type mtDNA (N_2 type of *B. vulgaris* subsp. *maritima*). Hybridization of *EcoRI* mtDNAs fragments with the *atpA* probe showed the lack of one band in a set of hybridization patterns for LO10A, LO10B₉ and LO12F lines possessing the N_3 type of cytoplasm described for *B. vulgaris* subsp. *maritima*. RFLP analyses of mtDNA disclosed mitochondrial genome diversity in male-fertile breeding material and the association between mitochondrial DNA variation and the origin of parental material used for selected O-type lines.

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Cytological and karyotypic studies in some species of genus

Beta

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The karyotype and its various components are used as a measure to decipher karyo-evolutionary trends in a given taxon. With this in view, chromosomal details of four species of the genus *Beta* were studied to determine their relationship with respect to karyotype and meiotic features and to ascertain the feasibility of their involvement in the development of interspecific hybrids and polyploids for use in sugar beet breeding programmes under subtropical climates of India.

Four species of the genus *Beta*, viz. *B. vulgaris* L., *B. vulgaris* L. subsp. *maritima*, *B. vulgaris* L. subsp. *orientalis* and *B. lomatogona* with chromosome numbers $2n=18$ were studied. Their karyotypes are basically of an asymmetric nature. Total haploid chromatin length ranged from 17.99 to 24.17 μm , whereas individual chromosome size ranged from 1.50 to 3.15 μm . According to Stebbin's class of asymmetry these species ranged from 2A to 4A via 3A, thereby confirming the evolutionary trend among the karyotypes. The karyotype of *B. vulgaris* L. var. LS-6 developed at IISR was most advanced and it fell in class 4A. The karyotypes of more than one species e.g. *B. vulgaris* subsp. *maritima* and subsp. *orientalis* were grouped in the same class. To deduce further gradations in the same class of asymmetry, a chromosome Dispersion Index (DI) of 0.592 for *B. vulgaris* L. var. LS-6 confirmed its highest karyotypic specialization.

Meiotically, all the species formed predominantly open bivalents with distal chiasma localization. Chiasma formation per bivalent decreased with the increase in the length of pairing blocks which reflected the possibility of a species-specific variable gradient of chromosome condensation, because sugar beet karyotypes are relatively constant at somatic and meiotic phases (Nakamura and Tsuchiya 1982). Detailed estimation of chiasma frequency for a constant amount of DNA per bivalent in each species will be studied to test the validity of this assumption.

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Genotype × environment interaction in sugar crops: II. Comparison of different stability models and the efficiency of the AMMI matmodel in sugar beet

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Sugar beet (*Beta vulgaris* L.) is cultivated in India as a supplementary sugar crop. In India sugar beet is sown in October-November and harvested from mid-March to the first week of June, when temperatures start rising and range between 35°C and 45°C with hot winds. Under such conditions there is generally a decline in root yield due to mortality of roots and an increase in the impurity index. In order to study the performance of genotypes for root yield, impurity index and recoverable sugar under these heterogeneous and varying environments, it is essential to study genotype × environment (G × E) interactions and identify stable genotypes for such conditions. Different biometrical models have been used to study G × E interactions and phenotypic stability. The objectives of the present study are: (1) to study G × E and stability parameters by the methods of Finlay and Wilkinson (1963), Eberhart and Russell (1966), Perkins and Jinks (1968) and the AMMI matmodel (Gauch and Furnas 1991); (2) to apply the Additive Main Effects and Multiplicative Interaction (AMMI) matmodel in sugarbeet, and (3) to compare efficiency and usefulness of different models in sugarcrops (Srivastava *et al.* 1991).

Eighteen diploid genotypes were evaluated at IISR, Lucknow, for 2 years and with two dates of harvesting, thus constituting four environments. Data on root yield, sucrose %, impurity index (i.e. Na, K and alpha-aminonitrogen), recovery and recoverable sugar/ha were recorded. G × E interactions were studied and compared by different models. Significant differences among genotypes for most of the characters was observed. Environment E + (G × E) interaction was also significant. Root yield data analyzed by the AMMI matmodel differed from the unadjusted raw data. The root yield estimates by AMMI are thus probably more accurate than raw data. Varieties 'IISR Comp-1' and 'LS-6' developed at IISR, Lucknow, were found to be more stable varieties using both the Eberhart and Russell model and the AMMI matmodel. The comparative efficiency of different stability models and the efficiency of the AMMI matmodel and its use for sugar beet will be described and discussed.

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Beta genetic resources in the Czech Republic

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There has been a long-term tradition of breeding sugar and fodder beets in the former Czechoslovakia. Relatively highly productive cultivars were released in the 1930s and 1940s. A collection of sugar and fodder beet was formed in the Semice breeding station in order to maintain, evaluate and have ready accessions for further utilization. A limited part of the collection was transferred into genebank storage in the period 1989-90. Garden beet accessions have been gathered as part of a collection of vegetables in the former Research Institute of Vegetables in Olomouc.

At present the genebank maintains 29 accessions of sugar beet and 28 of fodder beet. Most of these 57 accessions are beets of Czech or Czechoslovak origin. In total, 130 garden beet accessions are available in the Czech Republic. Among them, 113 accessions belong to *Beta vulgaris* subsp. *vulgaris*, cultivar group Garden Beet and 17 to *B. vulgaris* subsp. *vulgaris*, cultivar group Leaf Beet. Three accessions belong to other wild species.

A set of 50 accessions was selected from both sub-collections for their characterization in the framework of GENRES CT95-42. Phenological phases, leaf rosette, leaf blade and petiole characteristics, as well as susceptibility to some diseases, were evaluated during the vegetative period.

Fodder and sugar beet breeding, germplasm collection and usage in Lithuania

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The availability of germplasm, its description and knowledge of different species and forms of an individual crop is essential for a successful breeding programme. The fodder and sugar beet breeding programme in Lithuania was started in 1933. Sugar beet breeding was carried out until 1947, restarted in 1957 and closed again in 1971. Three sugar beet varieties were bred during this period, one of them monogerm. Fodder beet breeding was carried out until 1996 and during this period eight varieties were developed. The most productive work was done during the period 1972-96. Three fodder beet hybrids were created: 'Dotnuvos vienasekliai' (monogerm 2n), 'Dotnuvos geltonieji' (multigerm 3n) and 'Raudoniai' (monogerm 2n).

The *Beta* genetic resources work in Lithuania was started in 1993 and is under the control of the Industrial Crops Group. All activities concerned with collecting, evaluation, utilization and storage of *Beta* genetic resources are based at the Lithuanian Institute of Agriculture. The long-term storage facilities are also based there.

The *Beta* germplasm collection in Lithuania consists of the old local varieties, breeding material and cultivated or wild *Beta* species received from abroad. Currently, approximately 6 accessions are kept in long-term storage. Other accessions are in working collections. These are large old varieties used about 50 years ago in Lithuania. The majority of this material is fodder beets. Only one Lithuanian sugar beet variety can be recovered from an old seed sample.

Evaluation of the accessions is carried out according to the IPGRI descriptors for *Beta*.

Review of genetic resources of sugar beet in Slovakia

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Genetic resources of sugar and fodder beet have been studied and conserved at SELEKT, Research and Breeding Institute Bu..any, since 1992, under the coordination of the Research Institute of Plant Production, Piešťany. A lot of attention is focused on this topic in the Institute which tries to obtain sufficient financial resources for this programme. Genetic resources are maintained and multiplied by the breeders.

At present 78 accessions of sugar beet and 48 of fodder beet are maintained. The Gene Bank at the Research Institute of Plant Production has been running since 1996. The base collection contains 11 accessions (8 of sugar beet and 3 of fodder beet). The base collection is also stored as part of the active collection. The samples are stored at -18°C , with an expected lifespan of 50 years. The active collection contains 48 accessions (18 of fodder beet and 30 of sugar beet). This collection is used for breeding and research, regeneration of material, evaluation and documentation. The samples are stored at $0-2^{\circ}\text{C}$ for a period of 10-15 years according to the stock of seed. Other accessions are maintained in a working collection which is used for breeding and is not stored in the Gene Bank. Genetic resources of sugar and fodder beet are the basis for selection of parental components for crossing, with the aim of creating more variable biological material for breeding new varieties.

Important results have been obtained. Two accessions have been used in the breeding of sugar beet varieties recently: pollinator V38 as the male component in the hybrid variety 'Monriz', and pollinator V97 as the male component in the variety 'Rizoma'. Both varieties are tolerant to Rhizomania and were bred in cooperation with the seed company KWS. In fodder beet breeding, accession 14 has been used as the male component, and an MS line of sugar beet accession SL-63 as the female component in the breeding of variety 'Ema'. In addition, accession 59 has been used as the female component in the breeding of fodder beet variety 'Aja'.

The European *Beta* project – synopsis of results

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The project 'Evaluation and enhancement of *Beta* collections for the extensification of agricultural production' (GENRES CT95-42) is being funded for 5 years by the Commission of the European Union. Grants for complementary projects were given by IPGRI through the European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR) to stimulate co-funding by national funding bodies in the Czech Republic, Poland and Russia.

In the first and second poster the role of project partners, the objectives of all projects, the distribution of tasks and interaction between partners are described. Within the GENRES project the major objectives are: (1) improvement of germplasm conservation; (2) evaluation on resistance to eight biotic and one abiotic stress agents; (3) rationalization of the European *Beta* holdings and development of the core collection, and (4) documentation and diffusion of results. The Czech and Russian genebank partners implemented seed multiplication of accessions required by the GENRES project. Evaluation data on resistance to the black leg seedling disease in a fraction of the Synthetic *Beta* Core

Collection has been contributed by the Russian genebank. The Polish partner was engaged with the horticultural evaluation of a garden beet collection and the description of the same material using RAPD.

The third poster describes the major results of the various projects. Partners of the GENRES project detected accessions with a high level of *Rhizoctonia* resistance, a significant number of accessions with very low levels of BMV content and significant variation for BMV, *Aphanomyces*, *Pythium*, *Cercospora beticola* and Rhizomania resistance. The Russian partner provided information on interesting variation for black leg disease tolerance. The Polish partner found variation in agronomic traits useful for garden beet breeders, and using cluster analysis the partner succeeded to provide new information on the structures of genetic diversity within a set of 40 garden beet accessions.

Appendix I. Proposal for the establishment of an ECP/GR *Beta* Working Group submitted to the ECP/GR Steering Committee at its seventh meeting (Braunschweig, Germany, 29 June and 4-5 July 1999)

Background

In 1996, 34 European countries produced sugar beet (*Beta vulgaris* L. subsp. *vulgaris*) on a total of 5 585 193 ha. Within the European Union the crop is grown on 1 980 000 ha, producing a turnover of 5 006 million ECU per year for farmers. Sugar beet has become one of the most important cash crops of the northern hemisphere. Particularly in eastern European countries the species has significance as a root vegetable and a source of natural dye.

Europe is the major distribution area of the genus *Beta*. In fact, the genus and its sections (*Beta*, *Corollinae*, *Nanae* and *Procumbentes*) including the cultivated forms (leaf, garden, fodder and sugar beet) are all native to the European region and adjacent areas. Because of the narrow breeding pool the crop is genetically vulnerable and suffers from a range of pests, diseases and abiotic stress agents. There is therefore a large use of insecticides and fungicides on sugar beet. Hence, the demand for resistant varieties is increasing for both economic and ecological reasons. Breeding companies expect that the market share of resistant sugar beet varieties will be raised from about 20% in 1996 to about 40% in the year 2007 in Europe. In the case of economically significant virus diseases, genetic resources collections are the only source for novel genetic variation required for the development of resistant varieties. There are accordingly both pragmatic and political reasons (Convention on Biological Diversity) for work on *Beta*.

In 1987, an ECP/GR workshop on *Beta* was held at Wageningen, The Netherlands, with the objective of developing a cooperative programme on *Beta* genetic resources. Two years later, a workshop largely funded by IPGRI was convened again at the Centre for Genetic Resources (CPRO-DLO CGN). On this occasion, IPGRI launched the concept of 'self-sustaining networks'. The World *Beta* Network founded in 1989 at the CGN was chosen as one of the first in a series of networks to test this concept.

WBN meetings followed in 1991 (Germany), in 1993 (USA) and in 1996 (Turkey). These meetings were split into a technical, germplasm management section and a scientific section. The latter attracted more and more researchers. All meetings were partly funded through IPGRI with additional financial support from breeding companies and the sugar industry. Especially in 1993 the view was expressed by many participants that none of the other international scientific organizations would cover all beet breeding aspects in such a comprehensive way as does the WBN. The concept of 'self-sustaining networks' seemed to be successful because of the growing interest as expressed by the increasing number of participants (13 delegates in 1987, 75 in 1993).

However, the 1996 meeting revealed some shortcomings in the concept. While researchers and scientists from the public and commercial sector were mostly able to fund their participation from their own budgets, many of the curators of European *Beta* collections lacked the necessary funds. The network activities tended to shift from genepool conservation and management aspects to utilization. The growing interest in utilization as such is a positive development and actually a result of the 1989 meeting. However, while research on the genus *Beta* and the utilization of wild germplasm is progressing, the joint management of European *Beta* collections tends to lag further and further behind. The basis for germplasm utilization, i.e. a rationally managed European network of collections, is not developing at the same pace due to lack of communication opportunities for curators of collections.

Current status and achievements

- IPGRI descriptors for *Beta* fully revised in 1991.
- Establishment of the International Database for *Beta* (IDBB) in 1989.
- Foundation of the World *Beta* Network (WBN) in 1989. This has stimulated many research activities (biosystematics, diversity studies, phylogenetic relationships, evaluation and utilization of wild germplasm, and many more).
- Revision of *Beta* section *Beta* (1991) and adoption of the culton concept for cultivated *Beta vulgaris* subsp. *vulgaris* (1996).
- IDBB on-line on Internet in 1996.
- GENRES CT95-42 project approved in 1996.

Justification

According to the CBD, each country or region is responsible for the management of its own biodiversity. It is therefore suggested that Europe should play a major leading role in the safeguarding and management of this valuable native gene pool. Within Europe there are 17 national *Beta* holdings, but only four European curators attended the 1996 WBN meeting (see Table 1).

The council regulation 1467/94 offers opportunities for collaboration between some of the *Beta* curators. Since 1996, the EU project GENRES CT95-42 has been funded within the framework of this council regulation. However, activities such as the rationalization of collections through identification of duplicates, systematic security duplication and the implementation of joint seed increase programmes, as already suggested at the 1987 meeting, need the active involvement of all curators of *Beta* collections in Europe. Furthermore, the establishment of a 'Synthetic *Beta* Core Collection' as part of the GENRES CT95-42 tasks has become a top-down process, excluding partners from the decision-making process. More active discussion between project partners and those not funded by the project is required to achieve the objectives discussed since 1987 and defined by the GENRES CT94-42 project.

Proposed workplan

An ECP/GR *Beta* Working Group should focus on collection and gene pool management aspects. Evaluation and utilization aspects are well covered by WBN members. The delegates of the working group would be committed:

- to review past recommendations and its implementation status;
- to update the International Database for *Beta* (IDBB) with respect to passport, characterization and evaluation data;
- to harmonize and rationalize European *Beta* holdings based on information contained in the International Database for *Beta*;
- to organize and implement systematic safety-duplication;
- to compile jointly a seed increase and processing manual;
- to discuss and develop jointly the preliminary Synthetic *Beta* Core Collection;
- to assess the potential and regional feasibility of the *in situ* conservation concept for wild *Beta* species in Europe;
- to develop a European strategy for *Beta* germplasm conservation. This could include the development of concepts for more rational gene pool management of outcrossing species. A new molecular marker methodology that could assist this process has been developed recently for beet;
- to look for links between gene pool management and breeders' prebreeding activities and to develop concepts;
- to assess the need for further collecting missions, especially in eastern and southeastern

European countries. This may result in targeted collecting of germplasm that is still lacking in the total holding;

- to discuss problems related to germplasm ownership and benefit-sharing.

Table 1. Corresponding partners and/or partner genebanks in Europe

Country	National <i>Beta</i> collection / <i>in situ</i> conservation potential present	National delegates attending the 1996 meeting
Albania	??	No
Armenia	?/Yes!	no
Austria	??	no
Azerbaijan	?/Yes!	no
Benelux	Yes/yes	no
Bulgaria	Yes/yes	no
Cyprus	Yes/yes!	no
Denmark	NGB/yes!	no
Belarus	??	no
Estonia	??	no
Finland	NGB	no
France	Yes/yes!	(yes, French Network)
Georgia	?/yes!	no
Germany	Yes/(yes)	Yes
Bosnia Herzegovina	??	no
Greece	Yes/yes!	no
Hungary	Yes/?	no
Croatia	??	no
Ireland	yes/yes!	no
Israel	yes/yes!	no
Italy	yes/yes!	no
Latvia	??	no
Lithuania	??	no
Moldova	??	no
The Netherlands	yes/yes	through German-Dutch cooperation
Macedonia	??	no
Czech Republic	yes/no	no
Poland	yes/no	yes
Portugal	?/yes!	no
Romania	yes/yes	yes
Russian Fed.	yes/no	yes
Uzbekistan	??	no
Yugoslavia	??	no
Slovenia	?/yes?	no
Slovakia	??	no
Spain	yes/yes!	no
Sweden	NGB	no
Switzerland	yes/no	no
Turkey	yes/yes!	yes
UK	yes/yes!	no
Ukraine	yes/yes?	no

An ECP/GR *Beta* Working Group would provide the best possible forum for discussion and organization of such joint activities. It is suggested that the ECP/GR *Beta* Working Group meetings be organized as part of the ECP/GR Industrial Crops and Potato Network. Meetings could be organized in conjunction with WBN meetings every 2 to 3

years. This would allow efficient interaction between researchers and breeders from the public and commercial sector and European curators of *Beta* collections. Valuable collections are also located outside Europe in the USA, China, Egypt and Iran. Most of the responsible curators are WBN members and could join the ECP/GR *Beta* Working Group as observers.

The next WBN meeting is scheduled to take place at Broom's Barn (UK) from 8-10 September 1999.

I hope that this proposal, which I am also submitting on behalf of the WBN Coordinating Committee, will meet with your kind consideration and approval.

Yours sincerely,

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Appendix II. Agenda of the first meeting of the ECP/GR Working Group on *Beta* jointly held with WBN members

Broom's Barn, Higham, Bury St. Edmunds, United Kingdom, 9-10 September 1999

Thursday 9 September

- 08.30 Opening and introduction
Selection of the Chairman for the meeting
- 09.00 Information on Phase VI of the ECP/GR programme (*L. Maggioni*)
- 09.20 Report of the WBN secretary (*L. Frese*)
- 09.40 Information exchange
- IPGRI/FAO Multicrop passport list (*L. Maggioni*)
 - International Database for *Beta* - state of the art (*C. Germeier*)
 - Characterization and evaluation data

Discussion and recommendations

- 10.30 Coffee break
- 11.00 EU project GENRES CT95-42 (*L. Frese*)
- Identification of duplicates
 - Technical organization of the Synthetic *Beta* Core Collection (SBCC)

Discussion and recommendations

- 12.30 Lunch
- 14.00 National collections status reports
- | | | | |
|----------------|---------|--------------------|----------------|
| Azerbaijan | Germany | Lithuania | Turkey |
| Belarus | India | Poland | United Kingdom |
| Czech Republic | Iran | Russian Federation | USA |
| Georgia | Italy | Slovakia | Others |

- 15.30 Sharing of responsibilities, e.g. designation of responsible institutions for maintaining an accession, safety-duplication - *Discussion introduced by L. Maggioni*

Discussion and Recommendations

- 16.30 Coffee break
- 17.00 Genebank quality standards - *Discussion introduced by L. Frese*
- Discussion and Recommendations*

- 17.30 Opportunities for *in situ* conservation of wild beet species
- 18.00 Collecting activities

Conference dinner

Friday 10 September

- Drafting of the report
- 11.00 Discussion and approval of the report.
Selection of Working Group Chair and Vice-Chair

Appendix III. List of Participants

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Appendix IV. Abbreviations and acronyms

AARI	Aegean Agricultural Research Institute, Turkey
ASSINSEL	Association internationale des sélectionneurs, Switzerland
BAZ	Federal Centre for Breeding Research on Cultivated Plants, Germany
BGRC	Braunschweig Genetic Resources Collection, Germany
BMYV	Beet Mild Yellowing Luteovirus
BNYVV	Beet Necrotic Yellow Vein Virus
BRG	Bureau des ressources génétiques, France
BYV	Beet Yellows Closterovirus
CAAS	Chinese Academy of Agricultural Science, P.R. of China
CBD	Convention on Biological Diversity
CGN	Centre for Genetic Resources, the Netherlands
CMS	Cytoplasmic Male Sterility
CPRO-DLO	Center for Plant Breeding and Reproduction Research, the Netherlands
CTPS	Comité technique permanent de la sélection des plantes cultivées, Ministère de l'Agriculture, France
ECP/GR	European Cooperative Programme for Crop Genetic Resources Networks
FAO	Food and Agriculture Organization of the United Nations, Italy
FNAMS	Fédération Nationale des Agriculteurs Multiplicateurs de Semences, France
GEVES	Groupe d'Etude et de Contrôle des Variétés et des Semences, France
GIS	Geographic Information System
GNIS	Groupement National Interprofessionnel des Semences, Graines et Plants, France
GRIN	Genetic Resources Information Network, USA
HRI	Horticulture Research International, Wellesbourne, UK
IACR	Institute of Arable Crops Research, UK
ICAR	Indian Council of Agricultural Research, India
IDBB	International Database for <i>Beta</i>
IHAR	Plant Breeding and Acclimatization Institute, Poland
IIRB	Institut International de Recherches Betteravières, Belgium
IISR	Indian Institute of Sugarcane Research, India
INRA	Institut National de la Recherche Agronomique, France
IPK	Institut für Pflanzengenetik und Kulturpflanzenforschung, Germany
ISCI	Istituto Sperimentale per le Colture Industriali, Italy
ITB	Institut Technique Français de la Betterave Industrielle, France
KWS	Kleinwanzlebener Saatzucht AG, Germany
LIA	Lithuanian Institute of Agriculture
LIH	Lithuanian Institute of Horticulture
NPGS	National Plant Germplasm System, USA
NSSL	National Seed Storage Laboratory, USA
RAPD	Random Amplified Polymorphic DNA
RFLP	Restricted Fragment Length Polymorphism
RICP	Research Institute of Crop Production, Prague, Czech Republic
RIPP	Research Institute of Plant Production, Piešťany, Slovak Republic
SBCC	Synthetic <i>Beta</i> Core Collection
SBSI	Sugar Beet Seed Institute, Iran I.R.
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, Russia

WBN

World *Beta* Network