

# REPORT OF AN INTERNATIONAL BETA GENETIC RESOURCES WORKSHOP

held at the Centre for Genetic Resources,  
the Netherlands (CGN)  
Wageningen, the Netherlands  
7-10 February 1989

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**INTERNATIONAL  
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Report  
of an  
International Workshop on  
Beta Genetic Resources

held at the  
Centre for Genetic Resources, the Netherlands (CGN),  
Wageningen, the Netherlands

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The International Board for Plant Genetic Resources (IBPGR) is an autonomous international scientific organization under the aegis of the Consultative Group on International Agricultural Research (CGIAR). IBPGR was established by CGIAR in 1974. The basic function of IBPGR is to promote and coordinate an international network of genetic resources centres to further the collecting, conservation, documentation, evaluation and use of plant germplasm and thereby contribute to raising the standard of living and welfare of people throughout the world. Financial support for the core programme is provided by the governments of Australia, Austria, Belgium, Canada, China, Denmark, France, FRG, India, Italy, Japan, the Netherlands, Norway, Spain, Sweden, Switzerland, the UK and the USA, as well as the United Nations Environment Programme and the World Bank

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## INTRODUCTION

An international workshop on Beta genetic resources was convened by IBPGR at the International Agricultural Centre, Wageningen, the Netherlands, 7-10 February 1989, with the objective of setting up an international Beta network. Dr J. Holden, IBPGR Trustee, had kindly agreed to act as Chairman. A list of participants is provided in Appendix I.

Prof. Verhoeff, Director General of Agricultural Research, welcomed the participants and Ir L. van Soest, on behalf of the director of the Centre for Genetic Resources the Netherlands (CGN), Dr J. Hardon, gave a short introduction to the activities of his organization and on its collaboration with the Institut für Pflanzenbau und Pflanzenzüchtung (FAL), Braunschweig, FRG, within the framework of the Dutch-German cooperation on genetic resources, the latter having allowed the implementation of the International Data Base for Beta. The Chairman started the meeting by making some introductory remarks on the Agenda and presenting the IBPGR point of view on the implementation of international networks. He stated that the main objective of the workshop was the implementation of collaborative efforts by participating countries in Beta genetic resources. A general discussion was held on the Beta network concept. The idea was strongly supported by the participants. The Agenda, as approved, is provided in Appendix II.

On Thursday morning, a statement on the Beta network aims and principles was issued by the meeting. This statement directly follows the report of the first International Beta Workshop.

The participants had the opportunity to visit the SVP and CGN on Thursday afternoon.

## REPORT

### International Data Base for Beta (IDBB)

Ir Th. van Hintum (CGN) presented the structure and format of the IDBB and Dr L. Frese provided participants with summary tables of the current content of the database. The introduction paper of L. Frese and Th. van Hintum is provided in Appendix III. The participants congratulated those responsible for the IDBB for the work achieved to date. Those collections that are still missing were identified and all participants agreed to provide the IDBB with their passport data, so that a full inventory may be built up in the near future.

### Safety duplication in base collections

Dr H. Cortesi gave an introduction to this topic which is reproduced in Appendix IV. The meeting noted that the majority of the material kept in IBPGR-designated base collections for Beta (Dutch/German collection, Greek Gene Bank) had originated from IBPGR-supported collecting missions. It was further noted that because of regeneration difficulties with Beta, the target of duplicating systematically all original material in a single international base collection was difficult to achieve. Nevertheless, after a lengthy discussion participants agreed that original samples kept in each active collection should be systematically duplicated in long-term storage conditions. This means that the most original available samples should be kept under  $-18^{\circ}\text{C}$  (if possible) as recommended by IBPGR and that they should be kept for the purpose of further rejuvenation when necessary. Participants committed themselves to systematically duplicate their most original samples in a long-term storage collection of their own choice.

## **Regeneration of accessions**

Dr L. Frese presented a survey drawn from the available data in the IDBB on the current availability of accessions held in different genebanks (Appendix V). Availability for exchange was defined as weight of seeds per accession being above 50 g of seeds. Dr Frese stated that a priority list for regeneration could be provided by the IDBB if all participants sent information on their seed stock data. Information on how to exchange seed stock data is available in Appendix VI.

It was agreed that, in addition to the management data, participants would send a list of accessions they intend to regenerate within the next two years to the IDBB. The IDBB would then produce a list of remaining accessions still in need of urgent regeneration. The meeting agreed that collaborative action within the network was needed for regeneration of these accessions. In this context, Dr D. Doney mentioned the possibility that the US programme would continue to regenerate *Beta vulgaris* 'wild' accessions as an input in kind to the network. He also mentioned that help would be welcome for regeneration of *Corollinae* material. Dr Firat offered to regenerate material originating from Turkey and Dr Schrank thought that GDR could regenerate 10-20 additional *Beta sect. Beta* accessions per year. Prof. Laby mentioned the already good collaboration between the Dutch/German programme and private breeders for regeneration. Members welcomed these offers and recommended that the IDBB prepare this priority list of accessions needing regeneration for wide circulation. It was hoped that further offers would be accumulated.

Dr U. Meyer (KWS) presented an introductory paper on technical problems of seed increase and germination tests (Appendix VII). An exchange of information followed on seed dormancy problems. It was agreed that much research had been done on sugar beets but that further intensive research was required to study the problem of dormancy and hardseededness of wild species, which affect not only the proper testing of germination but also hinder the use of *Corollinae* species. It was mentioned that the University at Stuttgart Hohenheim (FRG) had adequate facilities and expertise to carry out such research. The meeting strongly recommended that all possible funding sources should be approached to solve this problem.

### **Taxonomy of the genus *Beta***

Ir J. Letschert presented an introduction paper on taxonomy of *Beta* sect. *Beta* (Appendix VIII). A lively discussion followed on the different approaches adopted to try to understand better the patterns of diversity within sect. *Beta*. Prof. Vernet mentioned that a French project was under way to analyze genetic relationships and gene flow between populations growing along the coastlines and in continental areas of France. Dr Abe presented a paper on the evolutionary aspects and species relationships (Appendix IX). The meeting urged the wider use of isozyme analysis as a tool for the identification of relationships between different forms within the genus *Beta*.

It was recognized that for the time being it was impossible to recommend a standard taxonomical system to be used by all *Beta* curators and researchers. Therefore, it was agreed that curators should continue to send any data relating to their classification to the IDBB. The IDBB will conserve this original information. Four cultivar groups relating to the use of the crop have been distinguished: leaf beets (spinach beets and chards), garden beets, fodder beets (including mangels) and sugar beets. The facilities of the IDBB allow the current botanical name to be decoded into end-use code. The concept of biological species was favoured for section *Beta* and this means that all wild forms within this section fall into one species.

### **Characterization and evaluation**

A draft IBPGR descriptor list edited by L. Frese was presented to the meeting. It was emphasized that not all the descriptors in this list were for compulsory use but that the intention was to provide a comprehensive list of descriptors to facilitate exchange of information at an international level. A few members already provided some technical comments on precise descriptors and it was agreed that further comments on omissions or illogicalities would be sent to the editor within four months. As soon as it is ready, the *Beta* descriptor list will be published by IBPGR and all participants of the network agreed to use this list for the international exchange of data.

Considering the amount of material that will be regenerated in the following years, the meeting thought that the observation of a minimal set of characters during regeneration would be a positive step towards better knowledge of the material. It was agreed that Male Sterility Expression, Multigermicity and Annuality should be recorded during regeneration.

In addition, the participants agreed to provide information on their evaluation activities to the IDBB as well as previous evaluation data. The IDBB will contact all interested parties to recommend a format for sending these data. Problems of scoring heterogeneous populations were discussed and the system used by the CGN was explained (Appendix X).

The meeting also strongly recommended that a set of standard checks be included during evaluation. This will allow meaningful comparison of data between different locations. It was also recommended that the possibilities of introducing international standards be discussed at the next meeting.

#### **Strategies for selecting subsets within collections**

Ir Th. van Hintum presented a paper on this topic (Appendix XI). There was a general consensus that implementation of subsets for specific purposes should be encouraged but it was felt that at this time no definite recommendations should be issued.

#### **Prospects for beet breeding and use of genetic resources**

Dr N.O. Bosemark presented an introduction paper on this topic (Appendix XII). Members were impressed that wild germplasm could, after a few cycles of recurrent selection, be very quickly incorporated into breeding programmes (feeder populations). It was stressed that genetic resources were not only a source of disease resistance and drought tolerance, but a large untapped reservoir of resources. Interaction between curators and breeders should be promoted. To start with, Prof. Laby would examine possibilities for projects directed towards enhancement of the sugar beet germplasm within the IIRB Study Group on Breeding and Genetics. The problems of exploiting hidden useful characters of annual forms were again discussed.

### **Needs and priorities for further collecting and germplasm acquisition**

Dr D. Doney reported on the dynamics of wild populations collected within the UK in 1987 and described the patterns of distribution of variability along the coastline. These results could be used for determining sampling strategies for future collections (Appendix XIII). Dr B. Ford-Lloyd gave a status report on priorities which had previously been set for collecting, as well as on action taken until now (Appendix XIV). It was recommended that the preliminary mapping of Turkish collections prepared by the IDBB be continued, along with mapping in other countries and areas. This will allow further selective germplasm acquisition to be recommended.

Participants informed the meeting about envisaged collecting missions over the following years. USDA/ARS will continue its collecting programme in northern and western Europe. CGN will collect wild section Beta in Portugal and southern Spain this year and plans, in association with the Plant Genetic Research Institute at Izmir, to collect further in Turkey. In addition, VIR and CGN are planning a joint collecting mission in Caucasus, USSR, in 1990, followed by further collecting in southern USSR in 1991 and 1992. The meeting gave high priority to collecting in Caucasus in particular.

Prof. Sun Yi-Chu gave useful information on the very interesting diversity of the genus existing in China. Dr H.M. Srivastava drew attention to the presence of wild species and landraces of leaf beets and availability of *B. maritima* on the southern coast of India. There are strong possibilities of getting many wild forms of Beta in the northeastern part of India (Manipur, Assam and Nagaland). He also informed the meeting about a report of new wild forms of section Beta from India, the seed of which has been sent to USDA. Members gave a high priority to further exploration in China and India and requested IBPGR to follow up. Dr Nasser Arjmand informed the meeting that several wild forms can be found in Iran near the border with Turkey and USSR, on the Persian Gulf, Khouzistan and along the border near Pakistan. A short collecting mission was started two years ago and it is hoped that further collecting will be undertaken by the Iranian national programme. Dr Nagata, Japan, would like to collect in Morocco and members strongly supported this idea. Dr El-Gharbawy informed participants of the continuous occurrence of wild and cultivated forms distributed along the Nile and in the Delta, Egypt, and collecting should be recommended. Similarly, possibilities for collecting in southwest Asia and Yugoslavia were mentioned. Finally, Dr I. Dalke provided interesting information on the occurrence of Corollinae species across Bulgaria, a matter that should, it was said, be followed up by IBPGR.

Dr H.M. Srivastava emphasized that availability of breeding material was of great importance for breeding programmes in developing countries. It was pointed out that information on more than 1000 accessions of sugar beet germplasm were available in the IDBB. However, it was stressed again that the primary task of curators was to deal with wild forms, landraces and open pollinated varieties. It was agreed that maintenance of hybrids was not the responsibility of genebanks.

### **Acknowledgements**

There was a general consensus that no Beta network could have been achieved without the work performed by the IDBB and the meeting conveyed its appreciation for the expertise and dedication of the CGN staff.

The meeting also thanked the CGN for organizing the meeting and for its kind hospitality.

## **STATEMENT ON THE AIMS AND PRINCIPLES OF THE WORLD BETA NETWORK**

### **1. General principles**

This meeting was held as a consequence of the activities begun by the ECP/GR on the initiative of IBPGR with the purpose of establishing a partly self-sustaining world Beta network. Its function would be to bring together curators, researchers and users of Beta germplasm to work in close collaboration for their mutual benefit. The world Beta network will be the first in a number of world crop networks which IBPGR wishes to implement. Previous experience in promoting the operation of crop networks in 26 countries has shown the effectiveness of this mode of operation. The costly activities of collecting, documenting, conserving, regenerating and evaluating germplasm can most effectively and economically be performed through collaborative efforts.

### **2. Organization**

Two essential requirements for the continued operation of a viable network are i) a central database to collate, analyze and disseminate information and ii) a network coordinating committee. The International Data Base for Beta (IDBB) is a database located in the CGN and operating under the auspices of the Dutch-German cooperation on genetic resources. The function of the network coordinating committee would be to provide a central link between all members and to work towards achieving the aims of the network. The coordinating committee should be able to assist in overcoming organizational constraints which may emerge in the execution of the agreed plan of action of the network. The committee will also function as the recognized link between the network and IBPGR and other regional/international organizations. For the first two years, the committee will consist of three members, including the IDBB, and the term of membership (excluding IDBB) is of two years. A member can be re-elected for a second term. This committee should meet at least once a year. The constitution of the coordinating committee will have to be discussed again at the next meeting. Four members were proposed for the coordinating committee: Dr H.M. Srivastava, India; Dr N.O. Bosemark, Sweden; Mrs A. Tan, Turkey, and Dr D. Doney, USA. Dr Bosemark and Mrs Tan were elected for the first term of this committee.

The active association of IBPGR with the coordinating committee and subsequently the network is envisaged.

### 3. Activities

It is appropriate that the network should function in all aspects of Beta genetic resources collection, maintenance, documentation and evaluation. At this first meeting of the network the following collaborative activities were agreed upon:

1. Exchange of data through the IDBB
  - a. To complete the inventory of passport data of all collections
  - b. To send seed stock data
  - c. To send plans of national programmes for regeneration of accessions for the next two years
2. Regeneration
  - a. To list remaining accessions needing urgent regeneration and subsequent collaborative action
  - b. To transmit data on essential agreed characters to be observed during regeneration
3. Evaluation
  - a. To transmit plans on ongoing evaluation activities and to send past and subsequent data
  - b. To use standard checks in the evaluation programmes
  - c. To stimulate cooperative activities within the network or within other groups (e.g. IIRB) for evaluation of beet germplasm, including the often necessary making of crosses to enable evaluation

4. **Collecting**

- a. To implement collecting missions as recommended in the report
- b. To analyze the information of the IDBB for selective germplasm acquisition

5. **Safety duplication**

Duplication of original material held in active collections into long-term storage (base collections)

6. **Research**

To promote specific research on problems affecting the development of the activities of the network

- a. research on seed dormancy, hardseededness for wild species
- b. biosystematic research
- c. research on patterns of diversity

7. **Utilization**

The promotion by whatever means seems most appropriate of the utilization of Beta genetic diversity in breeding programmes

4. **Sharing of responsibilities**

The CGN, within the framework of the Dutch/German cooperative programmes, accepts responsibility for maintaining and expanding the IDBB. As the network is above all a voluntary association of workers with a common goal, members will contribute, within the limits of their capabilities and those of their organizations, in the following ways:

1. By communicating data to the IDBB
2. By performing activities for which they feel their expertise and location are most appropriate
3. By contributing to joint activities which are not within the capabilities of one national programme

The IDBB will supply all available information on request.

## 5. Future meetings

To keep up the momentum the coordinating committee should meet as early as possible on the initiative of the IDBB and a world Beta network meeting should be convened by the coordinating committee in 2 years' time.

## 6. Funding

Members are already involved in the expenditure of funds within the framework of their national programmes. The operation of the network should not be regarded necessarily as an additional financial commitment but rather as a means of gaining maximum return from resources which are already committed. It may be, however, that with the development of the network programme resources greater than those presently available may become necessary. It is expected that these resources should be sought firstly by the coordinating committee from national funding bodies and, if necessary, from industry or regional/international organizations. In this connection, it should be pointed out that IBPGR has largely funded this first meeting but regards this as a pump-priming exercise. It does not have the resources to continue to provide significant financial support in future, since it expects to stimulate the formation of similar networks for all major crops. However, for the sake of the future of the world Beta network, IBPGR is committed to finding funds for the first meeting of the coordinating committee as well as for the second world Beta network meeting. IBPGR is anxious to provide technical support and encouragement to the world Beta network and this could take the form of helping to mobilize funds from other sources as may be necessary.

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**AGENDA**

Tuesday, 7 February 1989

1. Opening Addresses
2. Implementation of international networks of crop collections: the IBPGR point of view (presentation by the Chairman: Dr J.H.W. Holden)
3. Adoption of Agenda
4. The International Beta Data Base (IDBB)
  - 4.1 Presentation of the IDBB (Drs L. Frese and T. van Hintum)
  - 4.2 Discussion on current strategies for inventory of passport data and recommendations
5. Safety duplication in base collections
  - 5.1 Current extent of safety duplications - introduction paper (Dr L. Frese and Ms H. Cortessi)
  - 5.2 Enhancement of safety duplications
6. Regeneration of accessions
  - 6.1 Current state of collections - introduction paper (Dr L. Frese)
  - 6.2 Technical problems of seed increase and germination tests - introduction paper (U. Meyer)
  - 6.3 Determination of priorities and sharing of the tasks

Wednesday, 8 February 1989

7. Taxonomy of the genus Beta
  - 7.1 Evolutionary aspects and species relationships - introduction paper (J. Abe)
  - 7.2 Taxonomy of Beta section Beta: a biosystematic approach - introduction paper (Drs J. Letschert and L. Frese)
  - 7.3 Use of a common system for an international network
    - 7.3.1 Cultivated beets
    - 7.3.2 Wild species

8. Characterization/evaluation
  - 8.1 Standardization of descriptors: finalization of the IBPGR Descriptor List for Beta
  - 8.2 Selection of characters for minimal description during regeneration
9. Strategies for selecting subsets within collections - introduction paper (Ir Th. van Hintum)
10. Prospects for beet breeding and use of genetic resources - introduction paper (Dr Bosemark)
11. Cooperative evaluation projects
12. Needs and priorities for further collecting - introduction paper

Thursday, 9 February 1989

13. Commitments and funding needs for implementation of the global Beta network
14. Other matters
15. Visit of CGN/SVP/IVT

Friday, 10 February 1989 (morning)

16. Consideration of report and approval by the meeting

## THE INTERNATIONAL DATA BASE FOR BETA

L. Frese and Th.J.L. van Hintum,  
Centre for Genetic Resources, the Netherlands (CGN)

### 1. Introduction

IBPGR has, in recent years, supported the establishment of a number of crop-specific databases within ECP/GR programmes. The main objective of these databases is to enhance and streamline genetic resources activities. The International Data Base for Beta (IDBB) is implemented by the CGN within the framework of the German-Dutch cooperation on Beta genetic resources. The German-Dutch Beta project was established as a joint programme of the CGN, the Institute of Crop Science and Plant Breeding of the FAI and the Foundation of Agricultural Plant Breeding (SVP). The German partners have, since 1979, shared the responsibility for the IBPGR Beta base collection with the Greek Gene Bank. The establishment of the IDBB can be seen as a logical extension of already existing international activities in the field of Beta genetic resources.

The objective of the IDBB is to help in the rationalization of Beta genetic resources activities. The purposes are (i) to inventory the international Beta germplasm holding, (ii) to trace duplicate accessions and (iii) to coordinate activities like collecting missions and seed rejuvenation/seed increase programmes.

This paper provides information on the current status of the database. First a brief description of the hardware and software of the IDBB will be given, followed by an account of how the data were acquired, and how they were loaded into the database. Then information will be given about the contents of the IDBB, followed by some closing remarks considering the future.

## 2. **The system**

The IDBB was created on an Olivetti M28 computer. This is a PC with 1 Mb RAM and a I80286 chip. The system was programmed using the database management system ORACLE (version 4). ORACLE is a sophisticated relational DBMS allowing for all possible needs of database management. CGN's experience with this DBMS for its main information system GENIS (van Hintum, 1988) has been positive.

The logical structure of the IDBB consists of two parts: the passport data and the seed data. The structure of the passport data was essentially based on the recommendations of the meeting in Radzikow (IBPGR, 1984). However, some modifications were necessary to adapt the structure to the requirements of a relational model. This resulted in a 'passport table' with data on the origin, sample type, names, collection site, etc. of the samples and a 'parallel table' with different identification numbers of the accessions in the IDBB. For a complete description of these tables see the 'Documentation IDBB' (annex of Appendix III, p. 36). For the seed data a structure was chosen that allowed storage of data on the quantity and quality of the seeds per accession. The total database now consists of nine tables composed of 46 distinct elements.

## 3. **Gathering information from the sources**

About 26 Beta collections exist worldwide. Since February 1987 genebanks and plant breeding institutes in Europe and the USA have been asked for their Beta passport and seed administration data. Data were requested on magnetic media or on an IDBB input sheet. Genebanks provided the data set on floppy disc, tape or on a printout whereas data of some working collections were sent on the input form. The registration of most of the data (4119 records) was finished in October 1987. During the ECP/GR Beta Workshop (IBPGR, 1987) the first achievements of the database were presented and discussed by the participants. It was recommended that passport data from remaining collections be added and data on seed availability as well as characterization and evaluation data be included. Accordingly, curators of Beta collections were requested to send more information, a request which received a generally positive response. Today, contributions from Japan, Yugoslavia and the USSR are still awaited. Genebanks in Bulgaria, China, India and Italy have not yet been contacted.

TABLE 1. The contributing institutes

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Genebank	Address
AISBRC	The Agricultural Institute, Sugar Beet Research Centre, Thurles, Co. Tipperary, Ireland.
AARI	Aegean Agricultural Research Institute, Plant Genetic Resources Research Institute, PO Box 9 Menemen, 35661 Izmir, Turkey.
BARCPI	Beltsville Agricultural Research Center, Plant Genetics and Germplasm Institute, Beltsville, Maryland 20705, USA
BIRDPB	University of Birmingham, School of Biological Sciences, PO Box 363, Birmingham B15 2TT, UK.
BLOBAI	Plant Breeding and Acclimatization Institute, Radzikow near Warszawy. 05-870 Blonie, Poland.
DYOSAP	Station d'Amélioration des Plantes, INRA, B.P. 1540, 21034 Dijon Cedex, France.
GGB	North Greek Agricultural Research Centre, Greek Gene Bank, Postbox 105 14, 541 10 Thessaloniki, Greece.
INRALR	Station d'Amélioration des Plantes, INRA, Domaine de la Motte-au-Vicomte, B.P. 29, 35650 Le Rheu, France.
MERRVP	Rijksproefstation voor Plantenveredeling, Burg. van Gansberghelaan 169, 9220 Merelbeke, Belgium.
NEDBEG	Dutch German Cooperation on Beet Genetic Resources, CGN/SVP/BGRC, PO Box 224, 6700 AE Wageningen, the Netherlands.
NGB	Nordic Gene Bank, Postbox 41, 23053 Alnarp, Sweden.
NVRS	National Vegetable Research Station, Wellesbourne, Warwick CV35 9EF, UK.
NYONRA	Station Fédérale de Recherches Agronomiques de Changins, Route de Duillier, 1260 Nyon, Switzerland.
OLORBI	Research and Breeding Institute of Vegetable Crops, Holice, 770 00 Olomouc, Czechoslovakia.
PRAGGR	Research Institute of Plant Production, Div. of Genetics and Pl. Breeding Methods, Genebank, Dept. of Genetic Resources and Taxonomy, Ruzyně 507, 161 06 Praha 6, Czechoslovakia.
TAPRCA	Research Centre for Agrobotany I.P.P.Q., Section for Plant Introduction and Gene Bank, 2766 Tapioszele, Hungary.
ZARAEI	Estación Experimental 'Aula Dei', Apartado 202, Zaragoza, Spain.
ZIGUK	Zentralinstitut für Genetik und Kulturpflanzenforschung der A.D.W., Correnstrasse 3, 4325 Gatersleben, GDR.

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Currently, the IDBB stores passport information on 6875 accessions from 18 different holdings (Tables 1 and 5) and seed stock data on 2694 samples provided by 14 institutions (Table 4). Evaluation data were only transmitted by the US Beta collection, the Nordic Gene Bank and the Plant Breeding and Acclimatization Institute in Poland.

#### 4. Entering the information in the IDBB

Once the CGN received the information, there were many problems to be solved before the data could be integrated in the IDBB. First there was the problem of reading the data and transferring them from the medium they were sent on into our computers. At times this step proved to be extremely time consuming, since it was sometimes necessary to find a computer that could read the data from the medium they were sent on, and write them on to a medium we could read. Fortunately MS-DOS is the most common operating system, so most data were directly readable.

To be able to load the data in the database, fixed format files were needed with record sizes not exceeding 200. The data came in a variety of formats which sometimes had to be transformed. We once received data in a DBase file that had to be loaded into the right version of DBase and exported as a fixed format file. We also received files with extremely long records. These had to be split into smaller parts, using small FORTRAN or BASIC programs, before they could be loaded into the database.

The data were loaded into temporary tables with the same format as the files to be loaded. Once in the database, the data had to be altered to fit the format rules of the corresponding elements of the IDBB tables concerning field length, capitals etc. Thanks to the features of ORACLE this was quite easy. More difficult was the adaptation of the logical content of the fields.

Firstly, the type of information had to comply with the IDBB fields. For example, in the IDBB, the location of the collection site can be described using a 25-position-long field, 'DISTRICT', and a 40-position-long field, 'LOCATION'. When the description of the collection site was received as a

100-position-long field having information on the location and the collection district as well, it was very difficult to decide what to put where without additional information from maps. Some genebanks store their information on collection sites and ecogeographic data in an unformatted manner. It was almost impossible to enter this type of information automatically. Instead, the content of the field had to be split up into several IDBB fields and entered manually using input screens.

Secondly, the coding of different elements had to correspond to the IDBB coding. When information on the codes in the datafiles was available, the codes were updated or new codes were added to the IDBB decode tables.

Thirdly, taxonomic names had to be translated into the classification system used by the IDBB. For the time being the database uses an informal classification system for the genus *Beta* as shown in Table 2. This system is based on recommendations given by Ford-Lloyd and Williams (1975) for section *Beta* and Buttler (1977) for sections *Nanae*, *Corollinae* and *Procumbentes*. The taxonomic system adopted for section *Beta* should be regarded as a compromise between two extremes, i.e. the sophisticated nomenclature recommended by Mansfield (1986) and the very simple classification system proposed by the ECP/GR *Beta* Workshop (IBPGR, 1987).

For practical reasons botanic names used by the IDBB will remain unaltered as long as the taxonomy of *Beta* section *Beta* is inconsistent and needs more research. In addition, at least some information is attached to the names of wild taxa of section *Beta*. Once deleted from the database by joining all wild taxa into the new group *B. vulgaris* 'wild', this information will be difficult to recover. Instead, it is proposed to change botanic names later when the germplasm collection will be sufficiently characterized and research will have thrown new light on the taxonomy and biosystematics of *Beta* section *Beta*. Such research is in progress at the Department of Plant Taxonomy of the Agricultural University in Wageningen, in cooperation with the CGN. Meanwhile, the database management system can be applied to decode the botanic names, following the recommendations of the workshop, and to compile lists for official purposes.

TABLE 2. Informal IDBB classification system of the genus *Beta*

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Section <i>Beta</i>	Section <i>Corollinae</i>
<i>B. vulgaris</i>	<i>B. corolliflora</i>
<i>B. vulgaris</i> ssp. <i>maritima</i>	<i>B. macrorhiza</i>
<i>B. vulgaris</i> ssp. <i>maritima</i> var. <i>maritima</i>	<i>B. lomalogona</i>
<i>B. vulgaris</i> ssp. <i>maritima</i> var. <i>macrocarpa</i>	<i>B. intermedia</i>
<i>B. vulgaris</i> ssp. <i>maritima</i> var. <i>atriplicifolia</i>	<i>B. trigyna</i>
<i>B. vulgaris</i> ssp. <i>maritima</i> var. <i>trojana</i>	
<i>B. vulgaris</i> ssp. <i>adanensis</i>	Section <i>Nanae</i>
<i>B. vulgaris</i> ssp. <i>orientalis</i>	
<i>B. vulgaris</i> ssp. <i>patula</i>	<i>B. nana</i>
<i>B. vulgaris</i> ssp. <i>cicla</i>	
<i>B. vulgaris</i> ssp. <i>cicla</i> var. <i>cicla</i>	Section <i>Procumbentes</i>
<i>B. vulgaris</i> ssp. <i>cicla</i> var. <i>flavescens</i>	
<i>B. vulgaris</i> ssp. <i>vulgaris</i>	<i>B. procumbens</i>
<i>B. vulgaris</i> ssp. <i>vulgaris</i> var. <i>conditiva</i>	<i>B. patellaris</i>
<i>B. vulgaris</i> ssp. <i>vulgaris</i> var. <i>crassa</i>	<i>B. webbiana</i>
<i>B. vulgaris</i> ssp. <i>vulgaris</i> var. <i>altissima</i>	

After the fields in the temporary tables had been made compatible with those in the IDBB, the data could be transferred into the IDBB tables. Information not fitting into the general structure of the passport table such as the original botanic name, number of plants sampled and in some cases important characterization data (ploidy level) were entered into the 'REMARK' field.

The last step was updating the information. According to the proposals of the workshop two columns were later added to the passport table, the first one defining the sample category of an accession and the second one holding the IDBB number of the corresponding most original accession. The objective was to identify different kinds of duplicates and to identify the genebank holding the original accession. The IDBB distinguishes between six sample categories (see 'Documentation IDBB'). The sample category was identified by matching similar sounding variety names (with the ORACLE 'soundex' procedure) or similar or identical collection numbers.

During previous collecting missions samples were labelled by collection numbers. In general the usual IBPGR format of the collection number was followed (the number should consist of the country code, year of collection and a number). In these cases the most original sample (MOS) and the corresponding safety duplicates (SDS or SDA) were easily identified though the format sometimes slightly deviated. Much more attention had to be given to pure numbers (for an example see Table 3). Then additional information such as district, location and collection year were used to ensure the proper classification of the sample. In the case of the Sicilian Beta collection, e.g., the field 'DISTRICT' was used to distinguish between samples collected during the same year in Sicily and Sardinia. As yet, samples unambiguously identified as duplicated material were only labelled as security samples if they had been sent to the IBPGR Beta base collection at Braunschweig. The category SDA (security duplicate sample in active collection) was assigned to accessions using information on seed availability from the seeds table. A safety duplicate is considered to be in the active collection (SDA) if it is available for distribution.

TABLE 3. Identification of sample category (examples)

1. Security duplicate samples (SDS and SDA)

Duplicates found via collection numbers

Most orig. sample (orig.:SIT0HE)			Duplicate				
Genebank	IDBB no.	Coll. no.	Genebank	IDBB no.	MOS no.	Sam	Coll. no.
GGB	502	1	NEDBEG	2248	502	SDA	SI/81 001
GGB	502	1	NEDBEG	2283	502	NOC	SI/81 001
.	.	.	.	.	.	.	.
GGB	521	23	BIRDPB	1697	521	PRD	23
GGB	521	23	NEDBEG	2755	521	NOC	SI/81 023
GGB	521	23	NEDBEG	2723	521	SDS	SI/81 023

2. Different subgroups of probable duplicates (PRD)

Subgroup I

Most original sample (orig.:UIE) Duplicate

Genebank	IDBB no.	Coll. no.	Genebank	IDBB no.	MOS no.	Sam	Coll. no.
BARCPI	5759	WB611	DYOSAP	6740	5759	PRD	WB611

Subgroup II

MOS no.	Sam	IDBB no.	Acc. no.	Genebank	Origin	OC	Name
3363	MOS	3363	868880	NEDBEG	KLEINW	BRD	EW Erta
3363	PRD	4855	NSL4733	BARCPI	KLEINW	BRD	Kleinwanzleben E
3363	PRD	6255	Beta 81	ZIGUK	PERAGI		Kleinwanzlebener E

TABLE 3 (continued). Identification of sample category (examples)

Subgroup III

MOS no.	Sam	IDBB no.	Acc. no.	Genebank	Origin	OC	Name
1291	MOS	1291	B0237	BIRDPB		FRA	Rouge-Noir Plate D'Egypte
1291	PRD	1823	B1001	BIRDPB	SVALCF		Egyptian Flat Round
1291	PRD	1813	B0799	BIRDPB		ITA	Bietola Da Orto Piatta D'Egitto
1291	PRD	5426	P1269308	BARCPI		SWE	Egyptisk Plattrund
1291	PRD	3925	00021	OLORBI	VIR	SUN	Egiptskaja
1291	PRD	5376	P1205987	BARCPI		SWE	Egyptist Plattrund W:S/51
1291	PRD	4915	NSL28015	BARCPI			Crosbys Egyptian
.	.	.	.	.	.	.	.
1291	PRD	3926	00022	OLORBI	VIR	SUN	Egiptskaja Ploskaja
1291	PRD	3924	00020	OLORBI	OLORBI	CSE	Egyptska Plocha
1291	PRD	3928	00024	OLORBI	LJUBBU	YUG	Egiptovska
1291	PRD	6218	BETA 34	ZIGUK	003CSK	DDR	Aegyptische Plattrunde
1291	PRD	6841	6775	NVRS	BYHAR	POL	Egipslii
1291	PRD	6864	7214	NVRS	NVRS	ESP	Plato De Egipto
1291	PRD	6867	7303	NVRS	BIRDPB	ITA	Barbabetola Da Orto Piatta

NOTE: Sam - sample category; OC - origin country; Coll. no. - collection number

3. Accessions identified as not within genebank responsibility (NOG)

IDBB no.	Sam	Acc. no.	Variety name	Ploidy
2142	NOG	RCA3700052	Maribo Monova	2x/4x
2143	NOG	RCA3700053	Hilleshog Monika	2x/4x
5441	NOG	P1274395	Tetra-Tri-Polish Poli-0	
5463	NOG	P1296541	Tetra-Tri-Polanowice	
6598	NOG	06B019025	KWS-8455	3x

Probable duplicates (PRD) form a rather heterogeneous bulk of accessions consisting of three major subgroups (see Table 3). In general, host country and collector share seed samples at the end of a collecting mission. Such germplasm could be classified as security duplicate samples if both partners holding the two subsamples are aware of their responsibilities and agree to this classification (Table 3, subgroup I). Many probable duplicates were traced by means of the soundex procedure searching for names with a similar sound. It yields two different groups of probable duplicates when applied to cultivar names, namely more or less modern open-pollinated cultivars widely used in breeding (subgroup II) and accessions which could be considered as more distant related landraces (subgroup III). The latter subgroup may actually represent rather different populations of a certain morphotype used for centuries by plant breeders worldwide. In this context it must be emphasized that the soundex procedure is only a useful tool in decision making. It does not replace careful checking of the sample category.

Many of the samples that are considered not to be within genebank responsibility (NOC) could be recognized by their cultivar name having a string like 'poly' or 'tri'. Others were identified using a European list of fodder and sugar beet varieties (OECD, 1988). Samples no longer in the collection (NOC) have mainly been marked for the German-Dutch Beta collection as a result of the recent inventory (Table 5).

The sample category should be considered provisional as it may imply the availability of the germplasm. Genebanks holding the most original sample should officially accept this classification as the curator should indeed be able to provide seeds

In 1988 most of the passport data sets were sent back to the contributors, whose comments are now being used to update the IDBB.

## **5. The current content of the IDBB**

Table 4 shows the number of records/field loaded into the passport and seeds table. This summary illustrates in a very comprehensive form the achievements made since mid-1987. The international holding of Beta germplasm (Table 5)

TABLE 4. Number of records/field in the tables PASSPORT and SEEDS

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PASSPORT		SEEDS	
Field	Number	Field	Number
IDBBNR	6875	IDBBNR	2694
R_DATE	6875	U_DATE	2694
D_ADDR	6875	AVAILAB	2694
D_COUNTRY	6875	S_WEIGHT	1704
D_PNR	6789	S_NUMBER	405
S_NAME	6830	E_YEAR	1726
SS_NAME	4381	LM_YEAR	693
V_NAME	3003	GERM_YEAR	262
ANCEST	246	GERM METH	7
O_ADDR	4793	GERM PERC	262
O_TYPE	4417		
COLLNR	2968		
O_DATE	3412		
O_COUNTRY	5451		
DISTRICT	3116		
LOCATION	2978		
LONGI	1671		
LAT	1671		
ALT	2273		
SAM_STAT	4378		
SAM_CAT	6875		
MON_IDBBNR	1427		
REMARK	3871		

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In the REMARK field the following numbers of codes appeared:

Code	Number
DNO	2463
NPL	637
ORN	222
ONR	218
PLO	301
RSN	78
RVN	51
SDO	2015

TABLE 5. Sample category of accessions held by genebanks

Genebank address/country	MOS	SDS	SDA	PRD	NOG	NOC	Total
AISBRC (Ireland)	15						15
AARI (Turkey)	114						114
BARCPI (United States)	1680			111	11	2	1804
BIRDPB (United Kingdom)	846			174	4	1	1025
BLOBAI (Poland)	49				47		96
DYOSAP (France)	8			37			45
GGB (Greece)	669			61		1	731
INRALR (France)	14						14
MERRVP (Belgium)	86			25	5		116
NEDBEG (Netherlands)	1007	333	167	72	4	322	1905
NCB (Sweden)	28			1			29
NVRS (United Kingdom)	51				28		79
NYONRA (Switzerland)	56			10			66
OLORBI (Czechoslovakia)	122			65	1		188
PRAGGR (Czechoslovakia)	96			16	65		177
TAPRCA (Hungary)	76			23	11		110
ZARAEF (Spain)				1	110		111
ZIGUK (GDR)	195			55			250
TOTAL	5112	333	167	679	258	326	6875

contains about 74% most original samples (MOS). The IBPGR Beta base collection held by the Institute for Crop Science and Plant Breeding at Braunschweig (FRG) has received a total of 500 security duplicate samples in passive (SDS) or active (SDA) collections indicating fairly good achievements in safety duplication for Mediterranean Beta germplasm. A more careful analysis of the data set will probably lead to a larger total number of accessions in columns PRD (probable duplicates), NOG (not within genebank responsibility) and NOC (no longer in collection).

Counts for number of accessions per species and genebank (Table 6) were restricted to most original samples (MOS). Smaller collections (AISBRC-Ireland, BLOBAI-Poland, INRAIR-France, NGB-Sweden, NYONRA-Switzerland) have been summarized in column 'Others'. Expressed as a percentage of the total number of 5112 most original samples registered by the IDBB the international holding consists of less than 1% unclassified material, 82% section Beta (cultivated forms 42%, wild forms 20%, unspecified *B. vulgaris* 20%), 13% sections Corollinae and Nanae and about 4% section Procumbentes. There are large national collections covering the whole range of species and some smaller but highly specialized holdings such as those of MERRVP-Belgium (fodder beets), OLOBBI-Czechoslovakia (garden beets) and NYONRA-Switzerland (leaf beets).

A very large number of countries of origin (52) has been recorded, ranging from Sweden, the Mediterranean countries and the Near East to China and Argentina. Table 7 lists some of the major origin countries with remaining countries grouped together in column 'Others'. The analysis was again restricted to most original samples. The total number of 3963 instead of 5112 (Tables 6 and 7) is the result of incomplete recording of geographic data. Much of the content of Table 7 reflects recent collecting missions by IBPGR and the USDA/ARS and their duly recorded passport data. These explorations have led to a fairly comprehensive collection of cultivated as well as wild germplasm of section Beta from Mediterranean countries and northwest Europe. In contrast, the Corollinae species were mainly sampled in Turkey, though this type of germplasm is known to occur in regions adjacent to this country (e.g. the Caucasus). Such surveys can be used to roughly indicate gaps within the global Beta holding (e.g. France and Portugal have obviously not been explored so far), or to develop plans for more careful sampling of previously explored subareas or to recollect germplasm lost from collections.

TABLE 6. Number and botanic names of most original accessions by genebank

Botanic name	AARI	BARCPI	BIRDPB	GGB	MERRVP	NEDBEG	PRAGCR	TAPRCA	NYONRA	ZIGUK	Others	Total
<u>Beta</u> sp. unknown	8	6	10			19	1					44
<u>B. vulgaris</u>	68	513	63	313		40	12			16	3	1028
ssp. <u>maritima</u>	1	301	164	316		93	6			17	15	913
var. <u>maritima</u>						4				9		13
var. <u>macrocarpa</u>		9	8	12		8				4	1	42
var. <u>atriplicifolia</u>		7	3			2					2	14
var. <u>trojana</u>			1			2						3
ssp. <u>adanensis</u>	2		23			2						27
ssp. <u>orientalis</u>		1	2			1				1	2	7
ssp. <u>patula</u>		4	5			3	1				1	14
ssp. <u>cicla</u>	29	26	22			26				17		120
var. <u>cicla</u>			1				23		9	18	2	53
var. <u>fiavescens</u>		13	6			1			46	6		72
ssp. <u>vulgaris</u>		1	93	1		44			1	8	1	149
var. <u>conditiva</u>		6	40			28	83	25		46	50	278
var. <u>crassa</u>			42		86	70	33	24		38	36	329
var. <u>altissima</u>		670	193			154	45	27		6	39	1134
<u>B. corolliflora</u>		8	6			81	1			2	2	100
<u>B. macrorhiza</u>	1	12	7			27	1				2	50
<u>B. lomatogona</u>	4	24	26			96	3			3	3	159
<u>B. intermedia</u>		8	5			206						219
<u>B. trigyna</u>	1	17	26			30	6			1	2	83
<u>B. nana</u>	1	1	27			29						58
<u>B. procumbens</u>		16	45			6	2			1	2	72
<u>B. patellaris</u>		28	36			30	1			2	1	98
<u>B. webbiana</u>		9	18			5					1	33
<b>TOTAL</b>	<b>115</b>	<b>1680</b>	<b>846</b>	<b>669</b>	<b>86</b>	<b>1007</b>	<b>218</b>	<b>76</b>	<b>56</b>	<b>195</b>	<b>165</b>	<b>5112</b>

TABLE 7. Number and botanic names of most original accessions by country of origin

Botanic name	GRC	CYP	TUR	ISR	DZA	ITA	ESP	HUN	SUK	GBR	IRL	NLD	Others	Total
<u>Beta</u> sp. unknown			23				5						2	30
<u>B. vulgaris</u>	216	5	196		25	121	42	6	1	2	1		254	885
ssp. <u>maritima</u>	281	32	15	60	1	102	49			147	47	6	96	853
var. <u>maritima</u>	1					1							2	4
var. <u>macrocarpa</u>	2	2	1	4	2		9						4	31
var. <u>atriplicifolia</u>							5						1	6
var. <u>trojana</u>			3											3
ssp. <u>adanensis</u>	18		9											27
ssp. <u>orientalis</u>													3	3
ssp. <u>patula</u>							1						2	3
ssp. <u>cicla</u>	6		38			12	27		2				22	107
var. <u>cicla</u>			1			11	1		1	1		1	31	47
var. <u>flavescens</u>						11						2	33	46
ssp. <u>vulgaris</u>	29		50		1				13			1	26	120
var. <u>conditiva</u>	3		6			12		28	48	35		20	83	236
var. <u>crassa</u>	1		2			3	2	28	15	6		45	166	268
var. <u>altissima</u>	4		18			2	1	23	44	85	1	21	424	623
<u>B. corolliflora</u>			77						5				2	84
<u>B. macrorhiza</u>			26						10				4	40
<u>B. lomatogona</u>			121						7				2	130
<u>B. intermedia</u>			209											209
<u>B. trigyna</u>			28						10				2	40
<u>B. nana</u>	58													58
<u>B. procumbens</u>							44						1	45
<u>B. patellaris</u>							44						7	51
<u>B. webbiana</u>							17							17
<b>TOTAL</b>	<b>619</b>	<b>39</b>	<b>823</b>	<b>64</b>	<b>29</b>	<b>275</b>	<b>247</b>	<b>85</b>	<b>172</b>	<b>276</b>	<b>49</b>	<b>96</b>	<b>1167</b>	<b>3963</b>

A more detailed analysis has been conducted for sampling undertaken in Turkey, a country where much germplasm has been collected in recent decades. About 60% of these accessions have been sufficiently described to allow an analysis of the number of accessions collected per district. The results are presented in Fig. 1. Obviously much of the material was found in just a few provinces. Such surveys are designed to be helpful in complementing germplasm collections.

## 6. Perspectives

Thanks to the willingness of many collaborators to support the establishment of an International Data Base for Beta, much of the work was completed in less than two years. Today, the IDBB can function as a comprehensive database for users involved in plant breeding and related fields. Currently, the IDBB is able to provide users with passport information and, for parts of the holdings, seed stock data including storage locations, numbered cross references for duplicates and the availability of seeds. For the time being the major task of the database will be to act as a central administrative unit within the envisaged world Beta network programme. The IDBB can assist in developing guidelines for joint activities taking account of the specific interests and facilities of the members of the network. Today, the IDBB can take action in two major fields:

- a) Rejuvenation of accessions. About 75% of accessions currently registered have proved to be unique material. Joint seed increase programmes should focus their efforts on this particular group. With the precondition that more seed stock data will be transmitted to the database in the near future the IDBB will be able to submit a priority list for rejuvenation.
- b) Future collecting missions. Summarized information presented in Table 7 gives an idea of major gaps within the total collection and enables genebanks to define target areas and priorities for further collecting. Surveys or specific listings can be generated by the IDBB for many parts of the distribution areas previously explored and this information can be used to close minor gaps within the global holding.

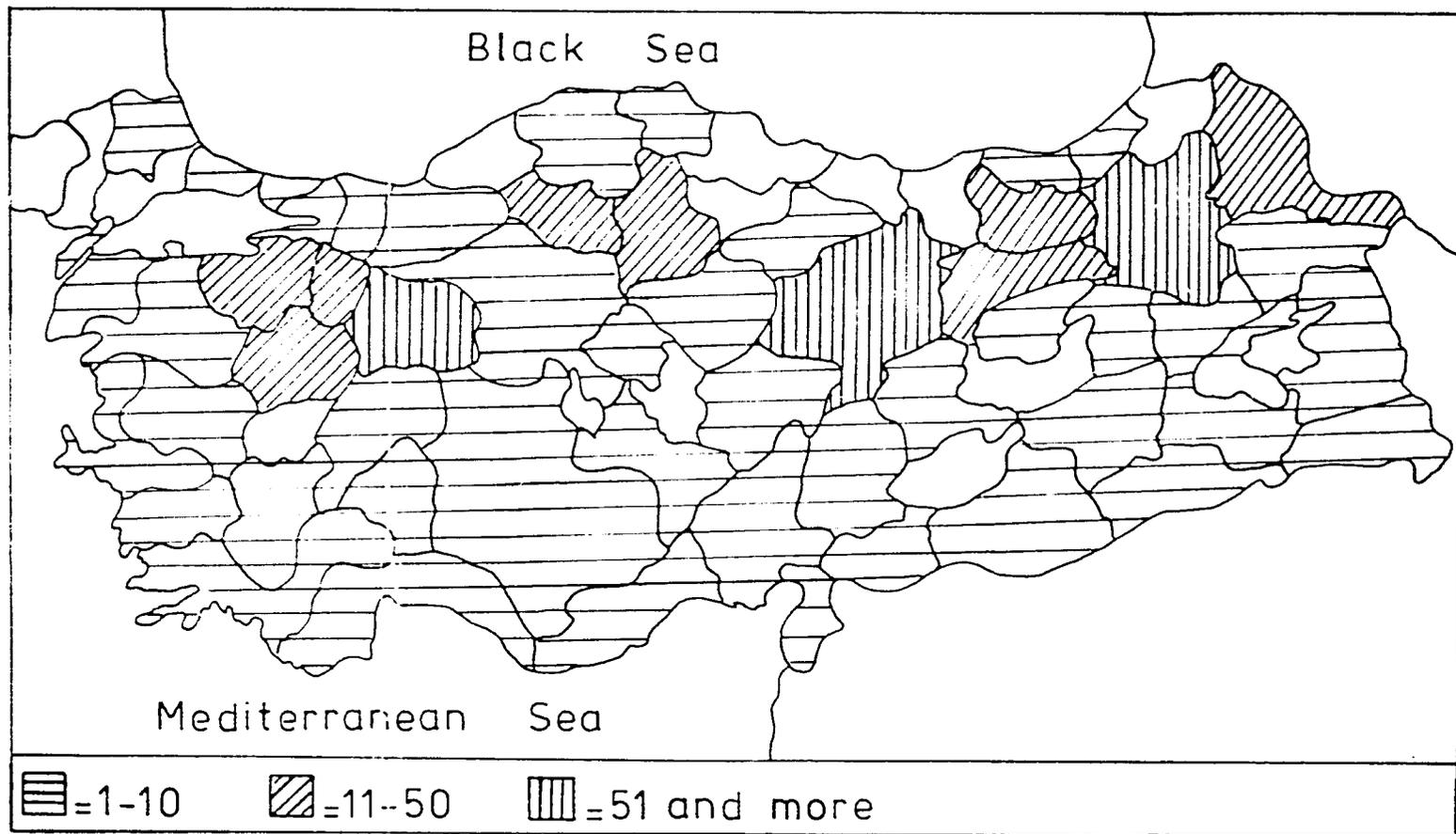


Fig. 1. Number of most original accessions per district collected in Turkey

The potentialities of the database as well as the reliability of information disseminated by the IDBB depends very much on the amount and quality of the data received. What has to be done to improve the current content of the database? Firstly, much emphasis should be given to further recording of seed stock and passport data. Secondly, the IDBB has to be expanded by characterization and evaluation data. One important objective of characterization and evaluation is to get more insight into the structure of genetic diversity, which will eventually enable genebanks to guide better plant breeding by more methodical germplasm selection from collections. Considering the potentialities of a well-structured database for evaluation data it is worth thinking about future ways of recording, registering and distributing data within a Beta network. First of all the set of mandatory characters proposed by the workshop should be reviewed considering the features of specific groups of Beta germplasm. For instance, characters of eminent importance for the cultivar group of sugar beets may be of no relevance to garden beets. Thus, sets of mandatory characters might be defined per distinct group of germplasm. Secondly, specific information, e.g. resistance to the root maggot, a pest of strictly regional importance, should be registered by national genebanks only. The latter type of information could be entered into the IDBB in summarized form indicating the group of accessions, the character evaluated, a summary of the results and the genebank holding the detailed data. Provided with this information the public user can request more specific data from the national collections.

Generally a public user is less concerned with details of the structure of a database and how it functions than with how he can get access to the information. There are three different options for disseminating data: (i) printing a catalogue; (ii) providing the total data set or parts of it on magnetic media; and (iii) the establishment of facilities for on-line communication in the future. The major and most efficient way to get information from the database is to address a specific query to those responsible for the IDBB. The IDBB is prepared to provide users with any of the data loaded into the database as simple listings or as different kinds of more comprehensive surveys. The information will be provided free and without restrictions.

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## DOCUMENTATION IDBB

### **The general structure**

In this section the general structure of the International Data Base for Beta (IDBB) is explained.

The IDBB uses the database management system ORACLE. This DBMS is relational, which means that two-dimensional tables are used, tables with rows and columns. The IDBB has the following tables: ADDRESS, COUNTRY, END USE, GERM METH, O TYPE, OK, PARALLEL, PASSPORT, SAM STAT, SAM CAT and SEEDS. These tables are listed below, first giving the table name, followed by the columns (between brackets), and a short description. The use of the tables PASSPORT, PARALLEL and SEEDS is explained in the following sections

ADDRESS (ADDR, NAME, ADDRESS, PLACE, PCODE, COUNTRY, INT ADDR): The address table decodes the address codes used in the PASSPORT table (in the columns D ADDR and O ADDR) and the PARALLEL table (in the column ADDR), and makes it possible to link with the internationally agreed address codes as far as they are available

COUNTRY (COUNTRY, N COUNTRY): The country table decodes the country codes used in the passport table (in the column COUNTRY).

END USE (END USE, N END USE): The end-use table decodes the end-use codes used in the passport table (in the column END USE).

GERM METH (GERM METH, GERM REF): The germination testing method table decodes the code used in the SEEDS table (in the column GERM METH) to indicate the method used for the germination test

O TYPE (O TYPE, N O TYPE): the origin type table decodes the origin type codes used in the PASSPORT table (in the column O TYPE)

OK (OK): A process table, only used to make certain processes possible.

PARALLEL (IDBBNR, ADDR, PNR): The parallel table stores parallel numbers, numbers given by other institutions to the IDBB accessions.

PASSPORT (IDBBNR, R DATE, D ADDR, D COUNTRY, D PNR, S NAME, SS NAME, END USE, V NAME, O ADDR, O TYPE, COLLNR, PLANT NR, O DATE, O COUNTRY, DISTRICT, LOCATION, LONGI, LAT, ALT, SAM STAT, SAM CAT, MON IDBBNR, REMARK): The passport table stores the passport information on the IDBB accessions. Passport information is information on the classification, origin and background of the material.

SAM STAT (SAM STAT, N SAM STAT): The sample status table decodes the sample status code used in the PASSPORT table (in the column SAM STAT).

SAM CAT (SAM CAT, N SAM CAT): The sample category table decodes the sample category code used in the PASSPORT table (in the column SAM CAT).

SEEDS (IDBBNR, U DATE, AVAILAB, S WEIGHT, S NUMBER, E YEAR, LM YEAR, PM YEAR, GERM YEAR, GERM METH, GERM PERC): The seeds table stores information on the availability, quantity and quality of the seeds of IDBB accessions.

## **The parallel table**

The PARALLEL table is used for storing parallel numbers. Parallel numbers are the numbers given by others to the accessions in the IDBB.

The PARALLEL table has the following columns: IDBBNR, ADDR and PNR. These columns are listed below, first giving the common name, followed by the name used in the computer and the format (between brackets), an explanation of the use and finally one or more examples.

IDBB number (IDBBNR, a number): The IDBB number is the unique number given to each description of a sample that is received by the International Data Base for Beta.

e.g. '2113'

Parallel address (ADDR, existing code): The IDBB code for the institution that gave the parallel number.

e.g. 'NEIDBEG'

Parallel number (PNR, up to 12 characters, upper and lower case): The number given to the sample by the institution coded in the column parallel address.

e.g. 'Bm 45/1182'

## The passport table

The PASSPORT table is used for storing passport information. Passport information is information on the classification, origin and background of the genetic material that is to be documented.

The PASSPORT table has the following columns: IDBBNR, R DATE, D ADDR, D COUNTRY, D PNR, S NAME, SS NAME, END USE, V NAME, O ADDR, O TYPE, COLLNR, PLANT NR, O DATE, O COUNTRY, DISTRICT, LOCATION, LONGI, LAT, ALT, SAM STAT, SAM CAT, MON IDBBNR and REMARK.

These columns are listed below, first giving the common name, followed by the name used in the computer and the format (between brackets), an explanation of the use and finally one or more examples.

IDBB number (IDBBNR, a number): The IDBB number is the unique number given to each description of a sample that is received by the International Data Base for Beta.

e.g. '2113'

Name (V NAME, up to 25 characters, upper and lower case): The original name given to a sample. This can be a variety name, but also a local name or the name used as an identification code of research material.

e.g. 'Monohill'

Entry date (R DATE, 9 characters: DD-MMM-YY): The date, generated by the system, the data were added to the IDBB.

e.g. '19-OCT-87'

Accession number (D PNR, up to 12 characters, upper and lower case): The identification number given to the sample by the institute donating the data.

e.g. 'BV332-3a'

Genebank address (D\_ADDR, existing code): The IDBB code for the institute that donated the data.

e.g. 'GGB'

Genebank country (D\_COUNTRY, existing code): The IDBB code for the country where the institute donating the data is located.

e.g. 'GRC'

Species (S\_NAME, up to 25 letters, upper and lower case): The species of the accession.

e.g. 'vulgaris'

Subspecific name (SS\_NAME, up to 30 letters, upper and lower case): A subspecific taxonomical name of the accession.

e.g. 'maritima'

End use (END\_USE, existing code): The IDBB code for the end use of the material. Only the following codes can be used:

- 1 Leaf vegetable
- 2 Root vegetable
- 3 Leaf and root vegetable
- 4 Fodder
- 5 Sugar extraction
- 6 Biomass
- 7 No apparent use
- 8 Other (specify in REMARK)

e.g. '2'

Sample status (SAM\_STAT, existing code): The IDBB code for the status of the sample. There are the following codes :

- 1 Wild
- 2 Weedy
- 3 Breeders' line
- 4 Landrace
- 5 Advanced cultivar
- 6 Other

e.g. '5'

Origin address (O\_ADDR, existing code): The IDBB code for the most original institute or expedition working with the sample, if possible the one breeding or collecting it.

e.g. 'BLOBAI'

Origin type (O\_TYPE, existing code): The IDBB code for the type of the origin of the sample. There are the following codes :

- 1 Wild habitat
- 2 Ruderal
- 3 Farm field
- 4 Farm store, threshing place
- 5 Backyard
- 6 Local market
- 7 Commercial market, seed trade
- 8 Institute, university, genebank, breeding company
- 9 Other

e.g. '8'

Origin country (O\_COUNTRY, existing code): The IDBB code for the country where the sample originated.

e.g. 'GRC'

District (DISTRICT, up to 25 characters, upper case): The district, province, island (etc.) of the collection site.

e.g. 'CHIOS'

Location (LOCATION, up to 40 characters, upper case): The exact location of the collection site.

e.g. 'KARFOS'

Origin date (O\_DATE, 4 digits: MMY): The month and year the sample was collected (wild material and landraces) or introduced (breeding material). If only the year is known, '00' must be inserted for the month number.

e.g. '0784'

'0078'

Collection number (COLLNR, up to 20 characters, upper and lower case): The number given to the sample during the collection.

e.g. 'EC 13/45'

Number of sampled plants (PLANT NR, five characters): The number of plants that were sampled during the collection.

e.g. '5'  
'>100'

Longitude (LONGI, six characters: DDDMMII): The longitude of the collection site. The first three positions for the degrees, the next two for the minutes and the last ('E' or 'W') for the hemisphere. For unknown parts blanks can be inserted.

e.g. '02610E'  
'034 W'

Latitude (LAT, six characters: DDDMMII): The latitude of the collection site. The first three positions for the degrees, the next two for the minutes and the last ('N' or 'S') for the hemisphere. For unknown parts blanks can be inserted.

e.g. '03819N'  
'003 S'

Altitude (ALT, number): The altitude of the collection site in metres.

e.g. '50'

Sample category (SAM CAT, existing code): The IDBB code for the category of the sample. The following codes can be used:

MOS Most original sample, in the active collection.  
SDS Security duplication sample, not in the active collection.  
SDA Security duplication sample, in the active collection.  
PRD Probable duplicate, in the active collection.  
NOC No longer in the collection.  
NOG Not within genebank responsibility.  
e.g. 'SDA'

Most original number (MON\_IDBBNR, a number): The IDBB number of the accession that is considered to be the most original if the sample is a (probable) duplicate, a safety duplicate or if it is no longer in the collection.

e.g. '2133'

Remark (REMARK, up to 120 characters, upper and lower case): Additional information on the sample, always preceded by a three letter code and ':'. Starting codes that have been used till now are :

ANC Ancestral information.

DNO Secondary donor number, the number under which the IDBB donor institute received the sample.

NPL Number of collected plants.

OBN Original botanical name.

ONR Other number, source not yet identified.

PLO Ploidy level.

RSN Additional taxonomical information.

RVN Rest variety name.

SDO Secondary donor, the institute giving the material to the IDBB donor institute.

Remark is also used by the IDBB to store information that can't be interpreted yet (like ONR). If there is more than one 'remark' to be made, they should be separated by ':'.

e.g. 'NPL: 45; PLO: 2x'

## The seeds table

The SEEDS table stores information on the availability, quantity and quality of the seeds of IDBB accessions.

The SEEDS table has the following columns: IDBBNR, U DATE, AVAILAB, S WEIGHT, S NUMBER, E YEAR, LM YEAR, PM YEAR, GERM YEAR, GERM METH and GERM PERC. These columns are listed below, first giving the common name, followed by the name used in the computer and the format (between brackets), an explanation of the use and finally one or more examples.

IDBB number (IDBBNR, a number): The IDBB number is the unique number given to each description of a sample that is received by the International Data Base for Beta.

e.g. '2113'

Update date (U DATE, nine characters: DD-MMM-YY): The date, generated by the system, the information was last updated in the IDBB.

e.g. '19-OCT-87'

Availability (AVAILAB, existing code): An indication of the availability of the seeds of the sample for users. AVAILAB can be '+' indicating that the material is available or '-' indicating that it is not available.

e.g. '+'

Seed weight (S WEIGHT, a number): The total weight (in grams) of the seeds of the sample.

e.g. '50'

Seed number (S NUMBER, a number): The total number of available seeds.

e.g. '1200'

Estimation year (E.YEAR, two characters: YY): The year the amount of seed was estimated.

e.g. '85'

Last multiplication year (LM.YEAR, two characters: YY): The last year the sample was multiplied.

e.g. '84'

Planned multiplication year (PM.YEAR, two characters: YY): The year the curator plans to multiply the sample. Data of the next two years are requested.

e.g. '90'

Year of germination test (GERM.YEAR, two characters: YY): The year the last germination test was performed.

e.g. '86'

Germination test method (GERM.METH, existing code): The IDBB code for the method used in the last germination test.

e.g. '2'

Germinability (GERM.PERC, a percentage): The result of the last germination test.

e.g. '89'

## **SAFETY DUPLICATION IN BASE COLLECTIONS**

### **H. Cortessi, Greek Gene Bank, Thessaloniki, Greece**

Most Beta holdings stored at the Greek Gene Bank (GGB) have originated from IBPGR-supported collecting missions. Gene Bank Braunschweig (FAL) is designated as a keeper for safety duplicates.

From our cooperation with Greek genebanks we have noticed that various meanings are given to the term 'duplicate'.

#### **Safety duplication**

A duplicate is a quantity of the same germplasm or seed material. By this term scientists could possibly mean:

1. Two quantities of seed that come from the same seed lot (considered real duplicates, as was decided at our meeting in November 1987).
2. The originally collected seed lot and the regenerated seed of that accession are kept separately. These two lots are duplicates.
3. Plants produced from two seed lots displaying, when tested, the same morphological characteristics and properties (the lots are occasionally named duplicates).
4. Two seed lots that were collected under the same environmental conditions.

The writer hesitates to call accessions of the last two groups duplicates.

#### **Note on experience in Greece**

In our collection we have 740 accessions (see table). As mentioned, it was decided to store safety duplicates at FAL. We aimed to safeguard beet germplasm and at the same time give interested scientists the opportunity to do research. As a result, in some cases five or more samples from the same accession ended up at Braunschweig.

TABLE 1. Greek Gene Bank Thessaloniki (GGB)  
Beta holdings January 1989

Species name	No. of accessions
<i>B. vulgaris</i>	403
<i>B. vulgaris</i> ssp. <i>maritima</i>	226
<i>B. nana</i>	28
<i>B. vulgaris</i> ssp. <i>macrocarpa</i> (var. <i>maritima</i> )	6
<i>B. vulgaris</i> ssp. <i>atriplicifolia</i> (var. <i>maritima</i> )	1
<i>B. patellaris</i>	4
<i>B. vulgaris</i> ssp. <i>patula</i>	2
<i>B. webbiana</i>	1
<i>B. procumbens</i>	1
<i>B. maritima</i> x <i>vulgaris</i>	32
<i>B. vulgaris</i> x <i>maritima</i>	32
<i>B. vulgaris</i> x <i>macrocarpa</i>	1
<i>B. macrocarpa</i> x <i>maritima</i>	2
<i>B. maritima</i> x <i>macrocarpa</i>	2
TOTAL	740

Accessions stored at the GGB were collected in Greece (415) or abroad (325) with or without a Greek collector in the team. For these samples, the following possibilities exist.

- There was enough seed in a lot and real duplicates were sent to FAL.
- There were few seeds in an accession and seed samples were sent after regeneration.
- Foreign scientists who collected in Greece got subsamples and sent real duplicates or multiplied seed to FAL.
- When collecting abroad we leave part of each accession in the area of collection. Some of these subsamples were sent to FAL.
- Researchers from other parts of the world who received subsamples of the above-mentioned accessions sent material to FAL.

Another weak point of this system is seed increase.

We consider a sample regenerated when more than 5000 seeds have been produced. Because germinating capacity of wild beets is in general low, we sometimes have to repeat our seed increase activities until we get sufficient seed. In this way, a large part of the original sample is consumed.

Beet is a cross pollinator and we need to multiply at least 50 mother plants to get representative samples of the original germplasm.

For our seed increase activities we sow in a glasshouse and instead of using rye isolation in a field, we use isolation cages to avoid the danger of cross pollination.

From our example, it is clear that seed increase activities are consuming a lot of time and money. The opinion of the writer is that regenerating for safety duplication at a foreign genebank with the communication constraints involved can sometimes bring more problems than benefits.

## REGENERATION: A SURVEY ON CURRENT STATE OF COLLECTIONS

L. Frese, Centre for Genetic Resources the Netherlands (CGN),  
Wageningen, the Netherlands

During the first Beta workshop an acute need for regeneration of germplasm was recognized. However, there was general agreement that the problem of a temporary shortage of seed increase capacity could be solved within a cooperative network of genebanks with additional support from commercial sugar beet breeders (members of the IIRB Breeding and Genetics Study Group). The IDBB had been asked to prepare a priority list for seed multiplication of unique germplasm as a base document for joint activities. The following procedure was proposed:

- (i) Identification of duplicates,
- (ii) Registration of seed stock data;
- (iii) Combining both types of information, presentation of a priority list;
- (iv) Circulation of the list among genebanks, final approval and taking action.

Meanwhile fairly good progress has been made in identification of duplicates. Seed storage administration data, however, are not yet sufficient to develop a complete list of material requiring urgent rejuvenation. The content of the seeds table depends of course on the availability of seed inventory data at different genebanks. The lack of such data (not recorded or not available in computerized format) seems to be a feature especially of genebanks holding large collections.

The seeds table (see Appendix III, Table 4) contains 2694 records, which is about 40% of the 6875 accessions registered in the passport table. The following percentages refer to the total number of records of the seeds table only. About 56% of the germplasm has been described as available (for definition see IBPGR, 1987). Information on germination percentage has been recorded for 10% of accessions. So far most of the estimates for germination have been given as number of seedlings/100 seed-balls ranging from 0 to 192% with an average of 68%. Generally the germination has been assessed for section Beta whereas little information is available for sections Corollinae, Nanae and Procumbentes. However, there are strong indications that the viability of seeds of hardseeded species is often below 20%.

TABLE 1. Availability of accessions

Genebank	Total number of accessions		Number of MQS samples	
	Available	Unavailable	Available	Unavailable
ARARI	49	55	49	55
BARCFI	231	162	195	143
BIRDPB	5	55	4	44
BLOBAI	88	6	43	6
DYOSAP	0	45	0	8
INRALR	11	3	11	3
MERRVP	116	0	86	0
NEDBEG	510	773	314	477
NGB	24	2	23	2
NVRS	39	40	20	31
NYONRA	42	23	36	19
PRAGGR	144	0	75	0
TAPRCA	20	1	16	0
ZIGUK	179	71	126	69

NOTE: Numbers refer to current content of the seeds table of the IDBB

What could easily be done if we had sufficient data is illustrated in Tables 1 and 2. The first table shows a survey on the availability of material in a number of genebanks which transmitted at least some seed stock data. The last two columns of Table 1 were generated by joining the passport and seeds table followed by a selection on most original samples. This procedure allows the number of unique accessions per national holding requiring regeneration (due to small quantities of remnant seeds) to be counted.

Genebanks holding smaller collections have in general duly recorded their seed stock data and have checked at least parts of their seed stock for germination. The most comprehensive data set came from the National Vegetable Research Station (Wellesbourne, UK). This data set was chosen to demonstrate the potentialities of the HDBB. The collection consists of 51 most original samples (MOS) and 28 probable duplicates (PRD). 31 of the MOS samples are not available for exchange according to the definition given by the first Beta workshop (IBPGR, 1987). The printout of the 51 most original samples (Table 2) shows the accession number, the subspecific name, the availability, germination percentage, seed weight, seed number, the year the germination percentage was estimated and the year of last seed increase. Accessions were sorted by germination percentage, putting the lowest percentage at the top of the list. Final decisions on which of the accessions should have priority for regeneration could e.g. be based on the germination percentage irrespective of the amount of available seeds, or on a combination of germination percentage and seed weight, giving an estimate of the number of viable seeds per accession.

Results presented in this short contribution may not reflect exactly the true state of the total holding. However, if they provide a rough estimate of the current state of the global Beta collection then we have the following situation: (i) about 50% of the global Beta stock is available for seed exchange, (ii) the average germination percentage for section Beta germplasm is about 60% and (iii) the viability of samples of sections *Corollinae*, *Nanae* and *Procumbentes* remains unknown.

TABLE 2. Priority list for regeneration - an example  
(data from National Vegetable Research Station)

Acc. no.	Subspecific name	A	GER%	S. Weight	S. Number	GE	LM
3081	vulgaris var. conditiva	-		7			
7621	orientalis	-		10			88
7623		-		10			88
3076	vulgaris var. conditiva	-	3	22		82	
3090	vulgaris var. conditiva	-	3	45		82	
3093	vulgaris var. conditiva	-	5	20		82	
3086	vulgaris var. conditiva	-	7	20		82	
3091	vulgaris var. conditiva	-	7	38		82	
3089	vulgaris var. conditiva	+	12		53	82	
7285	vulgaris var. conditiva	-	14	24	1589	88	
3082	vulgaris var. conditiva	-	16	26		82	
3072	vulgaris var. conditiva	-	18	21		82	
3088	vulgaris var. conditiva	-	18	25		87	
7635	vulgaris var. conditiva	+	28	60		87	
3069	vulgaris var. conditiva	-	29	25		82	
7284	vulgaris var. conditiva	-	29	31	2348	88	
3095	vulgaris var. conditiva	-	30	30		82	
7634	vulgaris var. conditiva	+	32	60		87	
3073	vulgaris var. conditiva	-	40	43		82	
6392	maritima	-	42	25		86	
7211	vulgaris var. conditiva	+	45	234	30390	88	87
3609	vulgaris var. crassa	+	46	125		82	
3083	vulgaris var. conditiva	-	47	24		82	
3087	vulgaris var. conditiva	-	55	11		82	
7119	vulgaris var. conditiva	+	57	250	11211	87	
6773	vulgaris var. conditiva	+	58	107	6729	87	
7209	vulgaris var. conditiva	+	60	298	19605	88	87
3608	vulgaris var. crassa	+	61	94		82	
5969	vulgaris var. conditiva	-	67	25		85	
3068	vulgaris var. conditiva	-	70	30		87	
5893	vulgaris var. conditiva	-	71	16		85	
7213	vulgaris var. conditiva	+	71	458	32714	88	87
6391	vulgaris var. conditiva	-	74	17		86	
3077	vulgaris var. conditiva	-	76	46		87	
6866		+	76	250		87	86
5176	vulgaris var. conditiva	-	78	18		84	
5152	vulgaris var. conditiva	-	79	7		84	
7120	vulgaris var. conditiva	+	79	462	72188	87	
.							
.							
6774	vulgaris var. conditiva	+	95	110	7534	87	
7212	vulgaris var. conditiva	+	95	256	16101	88	87
7210	maritima	+	99	385	22000	88	87
6861	vulgaris var. conditiva	+	100	152		87	86

NOTE: Acc. no. - NVRS accession no.; A - availability ('-' = no, '+' = yes); GER% - germination percentage; S Weight - seed weight (g); GE - year of last germination test; LM - year of last seed multiplication

**Reference:**

IBPGR. 1987. Report of a ~~Beta~~ Workshop. European Cooperative Programme for the Conservation and Exchange of Crop Genetic Resources. International Board for Plant Genetic Resources, Rome.

## FORMAT FOR EXCHANGE OF SEED STOCK DATA

Exchange of data should follow some formal rules. However, the IDBB is quite flexible and can accept information on different kinds of media. The CCN uses a VAX 11/750 with a TU80-unit which can handle any 8 bit ASCII tape written with 1600 bpi. If possible the data should be sent with the eighth bit set low, in a FILES-11 format and with the COPY command. A list with the volume label, all files with their record length and other characteristics and the way it was recorded to tape should be included. Data on floppy disc should be of format 5.25 in., soft sector, MS-DOS 2.11 or 3.1 PC-DOS. Please use the COPY command. The floppy disc can be DS-DD or DS-HD. Data on tape or floppy disc are preferred but typed listings or printouts are also accepted though they will delay data loading.

A full description of the seeds table is given in Appendix III. Some of the descriptors will be automatically put into the seeds table by the DBMS while others have to be transmitted by curators of Beta holdings such as:

1. Donor number
  2. Availability  
IBPGR definition (1987)
  3. Seed weight
  4. Thousand grain weight or
  5. Seed number
  6. Estimation year  
The year the amount of seed was estimated
  7. Last multiplication year
  8. Year of germination test  
The year the last germination test was performed
  9. Germinability  
Result of the last germination test, see 10.
  10. Germination test method  
The IDBB has facilities to store a detailed description on how a test was conducted, e.g. 'Two times 100 seeds/accession tested 6 months after seed harvest. Seeds watered for 2 hours then sown in soil. Counting 21 days later. Germinability expressed as number of seedlings/100 seed-balls'.
- The IDBB will choose a code for each distinct method. When transmitting the information on germination test method to the IDBB it should be evident from the original data set which of the accessions were tested by which method.
11. Planned multiplication year  
The year of the next seed multiplication

**Reference:**

IBPGR. 1987. Report of a Beta Workshop. European Cooperative Programme for the Conservation and Exchange of Crop Genetic Resources. International Board for Plant Genetic Resources, Rome.

**TECHNICAL PROBLEMS IN SEED INCREASE AND GERMINATION TESTS;  
SEED DORMANCY AND HARDSEEDED SPECIES**

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**1. Introduction**

One of the main tasks of genebanks is the conservation of genetic resources. For this purpose, seed samples especially of wild species are collected and partly multiplied and stored. For multiplication as well as long-term storage of seeds, their quality is of special importance, as only seeds with high germination capacity guarantee representative multiplication and high storing quality. Therefore, seed quality and its determination and subsequently the determination of germination capacity and the production of high-quality seed are basic requirements for the successful work of genebanks.

**2. Simple methods for seed-quality testing of seed lots of Beta**

The fruits of wild species of Beta frequently show low germination. In general, these low values are due to two fundamental reasons. First, it is possible that the proportion of well-filled fruits is small. Second, even when the proportion of well-filled fruits is high, it may be that these seeds are not viable and/or are not able to germinate because of different germination-inhibiting mechanisms. The percentage of filled fruits can be determined by physical methods, while the percentages of viable and non-viable and germinating and non-germinating seeds may be determined by physiological methods.

## 2.1 Physical methods

A freshly harvested, precleaned seed sample contains a main fraction of well-filled fruits, but also a certain fraction of very small fruits usually with low germination as well as empty fruits or fruits containing shrivelled seeds which will never germinate at all. The very small fruits can easily be separated by grading. The percentage of empty fruits or fruits with shrivelled seeds can be determined by X-ray examination or by cutting the fruits. These fractions may be separated from the well-filled fruits by air separation, which is most effective if the fruits are homogeneous in size.

Grading and air separation are two simple but very effective techniques in seed processing to improve the quality of the seed sample stored without a greater risk of selection.

## 2.2 Physiological methods

To determine the percentage of viable seeds which are theoretically able to germinate in optimal conditions, provided that there is no germination inhibition, first of all the Topographical Tetrazolium Test (TTC) can be performed. Completely viable seeds are stained red, while completely dead seeds are not stained at all. The partially stained seeds can be classified as viable, dead or as seeds which give abnormal seedlings, depending on the extent and position of the stained tissue.

To determine the percentage of germinating seeds different germination-test methods which are described in the International Rules for Seed Testing (Anon., 1985) of the International Seed Testing Association (ISTA) can be used. The most common method for Beta seeds is to test germination in pleated paper at 20°C with four replications of 100 seeds per box. It may occur though that especially for very large multigerm fruits, the contact area between the fruit surface and the paper may be too small for sufficient imbibition of the fruits. In this case the germination test should be carried out in sand.

When a germination test is done without any pretreatment to overcome germination inhibition, a fraction of normally germinating seeds and a fraction of non-germinating seeds or abnormal seedlings can be differentiated. When a germination test with pretreatment, e.g. hulling or washing, is done, the same two fractions as before are obtained, but the percentage of germinating seeds will be higher if the pretreatment was successful. By comparing these germination percentages both without and with pretreatment with the total percentage of viable seeds, the total degree of germination inhibition as well as the success of the pretreatment may be determined.

The best way of finding out about the seed quality of the sample tested is to carry out all of these three testing methods. But as this is very time-consuming, two methods can be combined as follows: germination test with pretreatment is done to determine the percentage of normally germinating seeds. The non-germinating seeds then undergo the Topographical Tetrazolium Test. Provided that the seeds are not damaged by microorganisms, the amount of viable seeds which were inhibited from germinating can be determined. Hence it is necessary to remove the cap for the Topographical Tetrazolium Test to get additional information about the percentages of empty fruits and fruits with shrivelled seeds.

### **3. Methods of overcoming the inhibition of germination**

The basic conditions for the germination of Beta seeds are sufficient water and oxygen and adequate temperature. Nevertheless some kind of germination inhibition may exist for individual samples which inhibit germination even in optimal conditions. These mechanisms of germination inhibition can be very different.

For the wild species of Beta the pericarp especially may act as a barrier to the uptake of water and oxygen. Furthermore the caps of the fruits may be a physical obstacle for radicle emergence and the pericarp can contain different amounts of chemical germination inhibitors. Therefore, all methods of loosening the seed caps, improving water and oxygen supply and reducing the amounts of inhibitory substances favour germination.

The most effective methods for overcoming germination inhibition are polishing or hulling the seeds to remove parts of the pericarp and washing or soaking the seeds to leach out inhibitory substances. Both methods result first of all in a decrease of inhibitory substances and often also in better water uptake.

Fruits with very hard pericarp tissue can be treated with chemicals. Peto (1964) treated the fruits of sugar beet with different acids and enzymes in various concentrations. The concentration of the chemicals used and also the duration of the treatment depend first of all on the properties of the pericarp, which can be very different, especially among the different species of Beta. Furthermore, the different fruit sizes within a seed sample have to be taken into account. Grading the fruits before acid treatment reduces the risk of selection. However, for acid treatments the concentration and duration of the treatment to overcome germination inhibition without damaging the true seeds have to be determined for every single seed sample separately.

The last, but most laborious method - if the acid treatment is not effective - is decapping the fruits. Removing the seeds from the fruits can sometimes improve germination. But often many seeds are damaged during this procedure. Usually the prepared seeds will germinate, provided that they are viable and undamaged.

#### **4. Determination of the decrease of vigour during long-term storage**

In general the decrease of vigour and of germination during storage is distinctly lower for Beta seeds than for cereals, maize or legumes. Thus for Beta seeds effective test methods have been developed for predicting field emergence rather than for predicting storability. The most frequently investigated vigour-test methods for Beta seeds are germination tests at low temperatures and/or with high amounts of water, determination of speed of germination, emergence tests with various substrates, at various temperatures and with various amounts of water, and also ageing tests.

One of the most simple methods to get information about the vigour of sugar beet seeds is the germination test with high amounts of water. Ageing tests have been useful for predicting storability, especially for soybeans and peas, but for Beta seeds the technique of ageing is very difficult. For accelerated ageing a uniform water uptake is required, and for controlled deterioration a constant seed moisture content is needed. Since for Beta seeds the water uptake and therefore the imbibition of the seeds depends on the structure of the pericarp, which differs greatly, it is difficult to ensure a uniform physiological deterioration of the seeds and subsequently obtain reproducible results.

Therefore, up to now no standardized vigour-test method has been invented that gives reliable and reproducible results for Beta seeds and correlates well with storability.

#### **5. The influence of environmental factors on the degree of germination inhibition**

The most important environmental factors that influence seed quality as a whole and thereby also germination and the degree of germination inhibition are temperature and, to a lesser extent, relative humidity. Seed production in warmer climates gives higher germination percentages than production in regions with lower temperatures. Most of the production areas of Beta seeds are therefore located in southern Europe.

The results of some experiments by Wood et al. (1980), who carried out seed production in climate chambers with controlled conditions, are shown in Table 1. Germination and field emergence decreased markedly with decreasing temperatures. The seeds ripened under low temperature conditions showed a lower percentage of fully developed seeds, a higher amount of pericarp tissue, tighter seed caps and also higher quantities of germination inhibitors. But on the other hand, very warm, dry climates may also give low germination percentages as a result of disturbances during pollination and ripening, which cause large fractions of underdeveloped seeds.

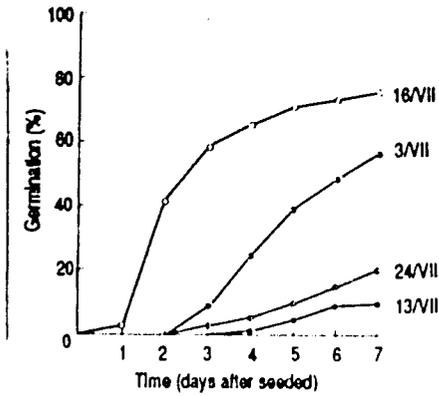
TABLE 1. Effects of temperature during seed ripening on germination and emergence in the field

Temperature (°C)				
Day	20	16	12	
Night	12	8	5	
				SE
Germination (%)	86	89	29	±4.0
Emergence in field: seedlings/m	12.3	10.9	3.2	±0.57

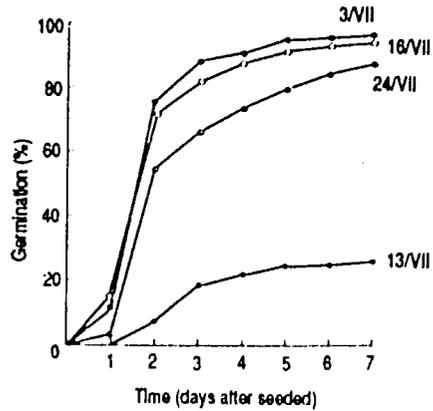
Source: Wood et al. (1980)

Inoue and Yamamoto (1977) investigated the changes in the germination inhibiting content of fruits during maturity (Figs. 1A and 1B). The increased germination of unwashed fruits harvested at intervals from June 13 until July 16 is mainly due to the increasing maturity of the seeds (Fig. 1A). Comparing the germination percentages of unwashed fruits with the germination percentages of washed fruits of the very same lot (Fig. 1B), the effect of leaching out inhibitory substances is immediately evident. Although this effect decreases with increasing maturity, an effect can still be seen at the last harvest date. As many other investigations have clearly demonstrated, the amount of inhibitory substances decreases with increasing maturity.

Hence, for the production of high-quality seed, cold and wet conditions have to be avoided, as well as all factors which delay maturity and thereby increase the amount of inhibitory substances, like for instance high doses of fertilizers. Instead, warmer and drier conditions which allow sufficient pollination and undisturbed maturity should be chosen.



**Fig. 1A.** Percentage germination of unwashed seed-balls harvested at intervals of ten days when seed-balls were mature



**Fig. 1B.** Percentage germination of washed seed-balls harvested at intervals of ten days when seed-balls were mature

### General concluding remarks

Not enough is known at present about the germination inhibiting mechanisms of Beta seed. That also holds for the different environmental factors which influence seed quality as a whole as well as the degree of germination inhibition during seed production. No pertinent information is available in the literature about seed samples of wild species of Beta that clearly demonstrates the urgent need for more research work.

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## TAXONOMY OF BETA SECTION BETA

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The species *Beta vulgaris* L. comprises a variable genepool including both wild and cultivated taxa. How can beet cultigens and closely related wild plants be satisfactorily classified? Clearly, for both groups there is a need for appropriate classification and it would be preferable to combine them in one system in which the relations between them can be understood and the genetic boundaries demarcated.

Generally, cultivated plants often show a greater amount of variation than their wild relatives. In classification special formal categories may be called for, several of which only apply to cultigens (e.g. cultivar, provariety, convariety). Consequently, the infraspecific treatment of wild and cultivated plants may cause separate systems to evolve with different infraspecific categories.

### **Taxonomy of the cultigens**

The taxonomic treatment of the cultigens has proved difficult due to their recent domestication. The evolutionary affinities both towards wild taxa and towards the variable primitive landraces are unknown (Ford-Lloyd and Williams, 1975).

Different authors (Ulbrich, 1934; Zossimovitch, 1940) have produced elaborate classification schemes with a confusing multitude of taxonomic ranks. Helm (1957) produced a clear and simple classification based on morphological characters only. This classification was later adopted (and partly altered) by Mansfeld (Mansfeld, 1986). His classification has been criticized for the number of taxonomic ranks in his hierarchical system. In fact these ranks have little biological significance since Helm did not consider any genetic relationships among the crop beets. An alternative to this hierarchical way of classifying is to assign cultigens directly to informal categories, i.e. the cultivar and the cultivar group (Table 1).

**TABLE 1. Hierarchical and non-hierarchical classification of cultivated beets**

Taxa	Authors (examples)		
	Helm (1957)	Mansfeld (1986)	IBPGR (1987)
	species	species	species
	subspecies	subspecies	
	convariety	convariety	
	provariety		
	variety	variety	cultivar
	forma		

### Taxonomy of wild taxa of section Beta

The situation regarding wild taxa of section Beta has long remained obscure due to lack of adequate description and an exceptional geographic distribution. Some taxa are rather narrowly distributed, others occupy large areas.

To illustrate some of the taxonomic problems Dr Ford-Lloyd's treatment of the wild taxa (Ford-Lloyd, 1986; Ford-Lloyd and Williams, 1975) will be discussed. In his latest revision a number of wild forms at the level of variety and subspecies are lumped together and only two subspecies remain. By doing this the discontinuous morphological variation pattern between subspecies *maritima* and subspecies *macrocarpa* is emphasized. Subspecies *maritima* represents the homogeneous perennials with a northern distribution, whereas subspecies *macrocarpa* comprises a number of highly variable annual plants from the Mediterranean. According to Ford-Lloyd, a high level of variability is maintained through ecotypic development. It is argued, however, that populations have not become sufficiently different as to be reproductively isolated from each other and therefore do not qualify for separate taxonomic treatment.

Close relationships among members of section Beta are exemplified by the frequent naturally occurring hybridizations between crop beets and representatives of subspecies *maritima*. When examining the potential for wide crossing, Dale and Ford-Lloyd (Ford-Lloyd, 1986) found that all wild varieties, including the self-pollinating varieties, crossed successfully with red garden beet. In contrast to these observations we have the reports of Dr Abe (Abe et al., 1987; Abe and Tsuda, 1987). The information obtained from their crossing experiments points to genetic divergence in section Beta. Crossings of *B. macrocarpa* both with crop beets and wild perennials resulted in partial pollen sterility in F<sub>1</sub> hybrids and the segregation of chlorosis, weakness and sterility in the F<sub>2</sub> generation. Electrophoretical analysis of isozymes in different taxa revealed that *B. macrocarpa* possesses many unique alleles. Moreover, the hybrids of the crosses showed the distorted segregation of enzyme coding loci, supporting the theory that reproductive barriers do exist. Obviously there is an inconsistency in the reported crossing experiments. An explanation for this may be found in the fact that only a limited number of genotypes were tested and that the sources from which they had been obtained differed.

In the context of taxonomy and phylogeny, a decision to be taken regarding the classification of section Beta cannot be based solely on estimation of intersterility in an artificial environment. A broad evaluation of each particular case is necessary. It is of equal importance to identify coherent morphological groups and to describe morphological differentiation in relation to ecogeographical conditions.

Concerning the wild taxa of Beta, the record shows that distinct taxonomic characters are difficult to trace, and sometimes seem to occur in many possible combinations within populations, e.g. plant habit (Jassem, 1985; Buttler, 1977), plant pigmentation (Tjebbes, 1933) numbers of flowers per cluster and annuality (Buttler, 1977; Ford-Lloyd, 1986; Aellen, 1938). Buttler has argued that there is a geographical pattern in certain features of the flower; he describes three types in annual Beta. In my opinion further evaluation of accessions of the entire distribution area is necessary in order to determine whether this character is taxonomically meaningful. A more quantitative approach may prove useful. Special attention should be given to variation in flower morphology of perennial beet. Already Jassem has recognized great variation in petals of plants from maritime populations in Brittany, France (Jassem, 1985).

The use of annuality as a taxonomic instrument is still under discussion. It is a variable character and depends to a certain extent on environmental conditions. As the genetics of annuality in wild taxa are not yet understood (Abe et al., 1987), we have to be careful when discussing genetic relationships on the basis of annuality.

### **Biosystematic research in Wageningen**

In the next three or four years we will examine a great number of accessions representing different geographic areas. The Beta genebank collection that has been built up since 1972 can provide us with representative Beta sources, and we may also collect additional material ourselves (e.g. a collecting trip to Portugal and Spain). For 1989 our attention will be focused on geographic subareas in the eastern Mediterranean and along the coasts of Italy, Yugoslavia and eastern Spain. Other geographic subareas will be examined in 1990.

Our aim is to assess coherent regional groups morphometrically. Last year a statistical multivariate study was performed on 35 populations of wild beet from the island of Sicily. We noted that variation between inland and maritime populations was limited and that many weedy types of beet were represented. These weedy beets may have originated from wild beets or from introgression between cultivars of foliage beet (cv. Lucullus, cv. Verde a Costa Bianca) into wild beet.

In addition to sampling morphological data, we are planning allozyme electrophoresis experiments. At this stage we are trying to improve the extraction procedures in order to obtain sharp and clear bands that can be scored with no difficulty. So far we have tested several systems on PAA gels (Table 2).

TABLE 2. Isozyme systems applied in biosystematic research in section Beta

PGM	MDH	LAP	GOT	IDH	SKDH
GDH	GPI	ACP	PX	6-PGDH	esterase

Our reasons for using the electrophoresis technique are: Firstly, unlike morphological markers, enzyme coding loci are codominant and will give us precise and quantitative information about genetic variation. From the point of view of effective sampling of populations these properties are essential. Secondly, in plant breeding research allozymes have been applied as markers of sugar-beet chromosomes (van Geyt and Smed, 1984). Integration of allozyme research with taxonomic research can enable us to link allozyme patterns to morphological characters (Abe et al., 1987) or ecophysiological characters. Thirdly, the assessment of allozyme patterns may allow us to interpret phenotypic plasticity. This factor is suspected of being a significant component of variability and may be responsible for a great deal of the taxonomic difficulties in section Beta.

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## **EVOLUTIONARY ASPECTS AND SPECIES RELATIONSHIPS**

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### **I. Introduction**

The effective utilization of wild germplasm should be based on extensive information on the taxonomy and phylogeny of cultivated crops and their wild relatives. For this reason, morphological and physiological traits characterizing each taxon, variation of isozymes and seed storage proteins, and structure of chromosomes and genes have been extensively analyzed in many plant species.

In the genus *Beta*, species relationships have also been examined through the study of crossing affinity, reproductive barriers, morphological features, secondary compounds, genomes and karyotypes. Although each of these approaches has provided valuable information, there are still several unsolved problems, such as the taxonomy of section *Beta* and the genome constitution of polyploid species.

In this paper, we will present information on isozyme variation in the genus *Beta*. Isozyme analysis may be useful for taxonomic and evolutionary studies, because the genetic relationships among taxa can be elucidated at the level of homologous loci. Isozyme analysis may also provide a means to identify genome donors of polyploid species, because isozymes are nearly always expressed as codominants even when different genomes are combined.

On the basis of isozyme variation, we will discuss the taxonomic relationships in section *Beta*, and the possibility of an amphidiploid origin of a tetraploid cytotype of *B. vulgaris* var. *macrocarpa* and *B. patellaris*. In addition, the data for reproductive barriers found among the taxa of section *Beta* will be presented as circumstantial evidence supporting the taxonomic relationships inferred from the isozyme variation.

## 2. Variation at enzyme-coding loci in section Beta

Table 1 shows nine enzyme systems assayed in this study and the genes responsible for the observed variation. These enzymes were estimated to be coded by at least 15 loci. Of these, ten loci could be analyzed with certainty. Information on the genetic bases can be found in van Geyt and Smed (1984), Abe and Tsuda (1987), and van Geyt et al. (1988). The observed phenotypes and their genotypes are presented in Fig. 1.

Table 2 shows the alleles observed in each of the six taxa examined. The nomenclature of section Beta followed the classification proposed by the ICP/GR Beta Workshop (IBPGR, 1987). *Ssp. vulgaris* had the alleles  $Aco^1$ ,  $Aco^2$ ,  $Aph_1^1$ ,  $Aph_1^3$ ,  $Aph_1^5$ ,  $Gdh_2^2$ ,  $Gdh_2^3$ ,  $Got_2^2$ ,  $Idh^1$ ,  $Idh^3$ ,  $Mdh_1^3$ ,  $Mdh_1^5$ ,  $Pgm_1^2$ ,  $Pgm_1^3$ ,  $Pox_1^1$ , and  $Pox_1^2$ . *Ssp. maritima* including var. *macrocarpa* and var. *atriplicifolia* had all of the alleles found in *ssp. vulgaris* and a total of 11 additional alleles which were not observed in *ssp. vulgaris*;  $Aph_1^2$ ,  $Aph_1^4$ ,  $Gdh_2^1$ ,  $Got_2^1$ ,  $Idh^2$ ,  $Lap^1$ ,  $Mdh_1^1$ ,  $Mdh_1^2$ ,  $Mdh_1^4$ ,  $Pgm_1^1$ , and  $Pox_2^1$ . Of these, the four alleles,  $Got_2^1$ ,  $Gdh_2^1$ ,  $Lap^1$ , and  $Pox_2^1$ , were characteristics of var. *macrocarpa*.

TABLE 1. Assayed enzymes and genes responsible for observed variation in section Beta

Enzyme	No. of loci concerned	Locus tested
Aconitase (ACO)	1	Aco
Acid phosphatase (APH)	2 <	Aph <sub>1</sub>
Glutamate dehydrogenase (GDH)	2	Gdh <sub>2</sub>
Glutamate oxaloacetate transaminase (GOT)	2 <	Got <sub>2</sub>
Isocitric dehydrogenase (IDH)	1	Idh
Leucine aminopeptidase (LAP)	1	Lap
Malate dehydrogenase (MDH)	2	Mdh <sub>1</sub>
Peroxidase (POX)	2 <	Pox <sub>1</sub> , Pox <sub>2</sub>
Phosphoglucosmutase (PGM)	2	Pgm <sub>1</sub>

In particular, the *Pox*<sub>2</sub> locus which is tightly linked to the *Pox*<sub>1</sub>, (Abe and Tsuda, 1987) was expressed only in var. *macrocarpa*. The *Idh*<sup>2</sup> and *Mdh*<sub>1</sub><sup>1</sup> were found only in a few annual accessions of ssp. *maritima* and var. *macrocarpa*. Ssp. *adanensis* shared the *Got*<sub>2</sub><sup>1</sup> and *Gdh*<sub>2</sub><sup>1</sup> with var. *macrocarpa*, and the other alleles with ssp. *maritima*. All of the alleles found in ssp. *patula* were also observed in ssp. *maritima*.

For the ten loci assayed, var. *macrocarpa* had the six alleles which were not detected or at least were uncommon in the other taxa of section *Beta*. Although in this study only one accession was available for analysis, var. *macrocarpa* is likely to be remote from the other taxa of section *Beta*.

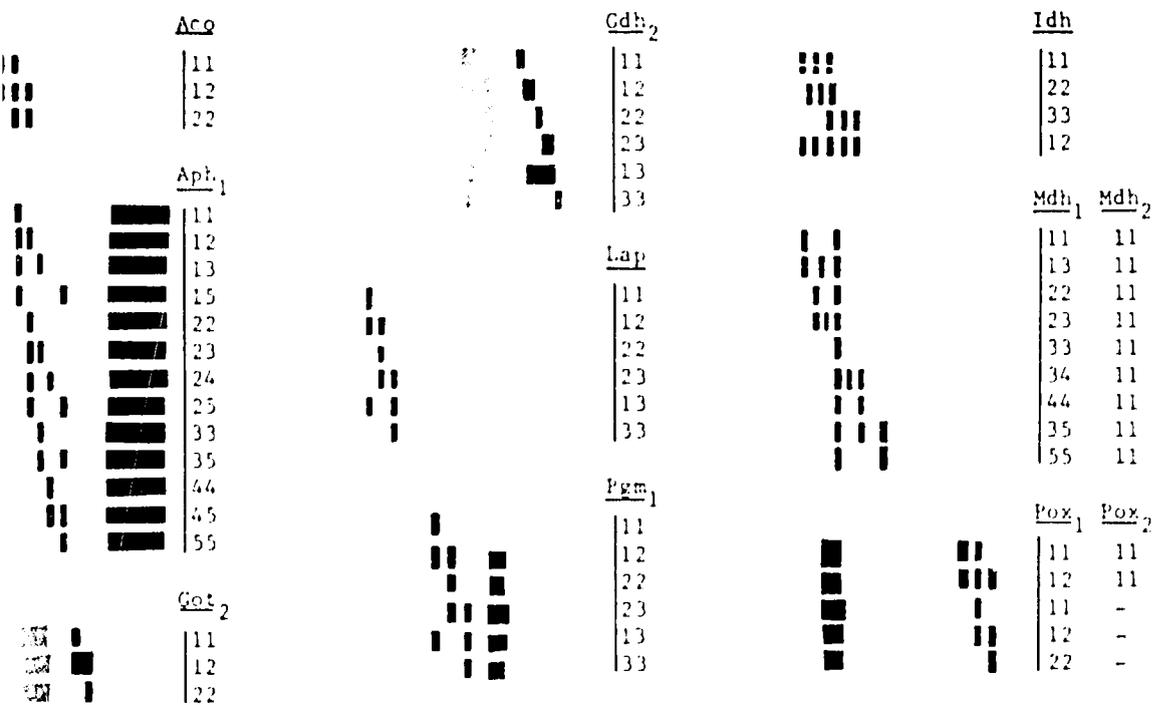


Fig. 1. Isozyme variation for nine enzymes observed in section *Beta* (Mdh<sub>2</sub> is not polymorphic and migrates at an identical position as Mdh<sub>1</sub><sup>33</sup>)

TABLE 2. The alleles observed in six taxa of section *Beta*

Locus	Vul	Mar	Mar-mac	Mar-atr	Ada	Pat
No. of accs. examined	10	12	1	1	1	1
Aco	1,2	1,2	2	2	2	2
Aph <sub>1</sub>	1,3,5	1,2,3,4,5	1	1,3,5	4	1
Gdh <sub>2</sub>	2,3	2,3	1	3	1	3
Got <sub>2</sub>	2	2	1	2	1	2
Idh	1,3	1,2,3	2	1,3	1	1
Lap	2,3	2,3	1	2,3	3	3
Mdh <sub>1</sub>	3,5	1,2,3,4,5	1	3	3	3
Pgm <sub>1</sub>	2,3	1,2,3	3	1,2,3	2	2,3
Pox <sub>1</sub>	1,2	1,2	1	1	2	1
Pox <sub>2</sub>	-	-	1	-	-	-

NOTE: Vul - *ssp. vulgaris*; Mar - *ssp. maritima*; Mar-mac - *ssp. maritima* var. *macrocarpa*; Mar-atr - *ssp. maritima* var. *atriplicifolia*; Ada - *ssp. adanensis*; Pat - *ssp. patula*. Underlines show predominant alleles within each taxon. Pox<sub>2</sub> was not expressed except for var. *macrocarpa*

TABLE 3. Reproductive barriers observed in hybrids of var. *macrocarpa* and *ssp. patula* with the other taxa<sup>1</sup> in section *Beta*

	Var. <i>macrocarpa</i>	<i>Ssp. patula</i>
Fertility of F <sub>1</sub> hybrids		
Pollen abortion	25 - 50%	10 - 20%
Seed abortion	50%	10%
Hybrid breakdown in F <sub>2</sub> (percentage)		
Chlorotic plants	0.3 - 8.0%	Not observed
Dwarf plants	0.3 - 5.3%	0.7 - 7.6%
Complete male sterile plants <sup>2</sup>	4.7 - 7.8%	4.2 - 11.6%
Semi-fertile plants <sup>3</sup>	37.1 - 58.1%	21.6 - 40.0%

<sup>1</sup> *Ssp. vulgaris*, *ssp. maritima* and var. *atriplicifolia*

<sup>2</sup> Plants with no viable pollen grains

<sup>3</sup> Plants with a pollen fertility of 10-70%

A study of comparative morphology in section Beta has suggested morphological similarities between var. *macrocarpa* and annual accessions of *ssp. maritima* (Ford-Lloyd and Williams, 1975). Thus, the isozyme analysis did not necessarily produce parallel results to those obtained from the morphological observations. One of the factors causing the discrepancy between these results may be the complexity of genetic bases of morphology. In general, morphological features are controlled by several genes with alleles at each locus contributing to the phenotype. Thus, equating genotype and phenotype is often difficult for morphological features, especially, when compared with the situation for isozymes. As noted in the introduction, isozymes may be more useful for taxonomic and evolutionary studies.

*Ssp. maritima* is well known to be a highly polymorphic taxon in section Beta. A combination of characters used by some authors to describe new taxa has often been found in *ssp. maritima*. The materials we used for isozyme analysis were limited. To confirm the genetic peculiarity of var. *macrocarpa*, more materials should be examined, especially for var. *macrocarpa* and its sympatric taxa, *ssp. adauensis* and annual accessions of *ssp. maritima*.

### 3. Reproductive barriers among taxa of section Beta

Analyses of reproductive barriers between taxa provide other clues to their genetic relationships. In general, the extent of hybrid breakdown between taxa increases as they differentiate genetically. The viability and fertility were examined in  $F_1$  hybrids and their  $F_2$  progenies among *ssp. vulgaris*, *ssp. maritima*, var. *macrocarpa*, var. *atriplicifolia* and *ssp. patula*.

No consistent barriers were found among *ssp. vulgaris*, *ssp. maritima* and var. *atriplicifolia*, except for the  $F_2$  segregation of chlorotic plants in a cross between *ssp. vulgaris* and an annual accession of *ssp. maritima* (Abe et al., 1987). On the other hand, these three taxa frequently produced partially sterile  $F_1$  hybrids and  $F_2$  segregants with various symptoms of breakdown in the crosses with var. *macrocarpa* and *ssp. patula* (Table 3). Five kinds of reproductive barrier were observed; the abortion of a part of pollen grains or seeds in the  $F_1$  hybrids, and the segregation of chlorotic, dwarf and pollen-sterile plants in the  $F_2$ . The chlorotic plants died at the cotyledon stage without any leaf expansion.

All the barriers were found in the crosses of var. *macrocarpa* with *ssp. vulgaris*, *ssp. maritima* and var. *atriplicifolia*. Approximately one-quarter of the pollen and half the seed of the F<sub>1</sub> hybrids were aborted. In the F<sub>2</sub>, the chlorotic and the dwarf plants segregated. Pollen fertility of F<sub>2</sub> segregants varied continuously from completely sterile plants with no viable pollen grains to plants with a fertility of more than 90%. The frequency of pollen-fertile plants was less than one-third. *Ssp. patula* also produced the dwarf and the pollen-sterile segregants in the crosses with *ssp. vulgaris* and *ssp. maritima*. The F<sub>1</sub> hybrids of these crosses, however, showed almost normal pollen and seed fertilities.

These results mostly agreed with the genetic relationships among the taxa inferred from the isozyme analysis. Both results strongly suggest genetic differentiation in section Beta, in particular, the genetic peculiarity of var. *macrocarpa*. To obtain a final conclusion on the reproductive barriers distributed in section Beta, however, it should be determined whether hybrid breakdown may occur between var. *macrocarpa* and its sympatric taxa, *ssp. adanensis* and annual accessions of *ssp. maritima*, and also between these annual taxa and perennial taxa.

#### 4. An amphidiploid origin of a tetraploid accession of var. *macrocarpa*

A tetraploid cytotype of var. *macrocarpa* native to the Canary Islands is only a spontaneous polyploid in section Beta (Buttler, 1977). In general, polyploid species additively express enzymes observed in their diploid parents because of the co-dominant expression. The enzyme phenotypes of the tetraploid *macrocarpa* were examined to determine whether or not it was autotetraploid.

Of the ten loci assayed, the tetraploid accession examined had the same phenotypes as those observed in the diploid *macrocarpa* for *Aco*, *Pox*<sub>1</sub> and *Pox*<sub>2</sub>, and *ssp. maritima* for *Got*<sub>2</sub> and *Idh*. On the other hand, this accession showed the heterozygous phenotypes found in the diploid hybrids between var. *macrocarpa* and *ssp. vulgaris* for the remaining loci (Abe and Tsuda, 1987). It had both of the alleles which were predominant in each of the diploid *macrocarpa* and *ssp. vulgaris*: *Lap*(1/3), *Gdh*<sub>2</sub>(1/3), *Aph*<sub>1</sub>(1/5) and *Mdh*<sub>1</sub>(1/3).

Thus, the results obtained suggest that the tetraploid *macrocarpa* may be amphidiploid rather than autotetraploid, although the data were not sufficient to identify its genome donors. An analysis of chloroplast DNA by restriction endonucleases indicated a difference of cytoplasms between the diploid and tetraploid cytotypes of var. *macrocarpa* (Kishima, 1988). It suggests the possibility of an amphidiploid origin for the tetraploid *macrocarpa*.

5. **Isozyme variation in section Procumbentes**

Fig. 2 shows the observed phenotypes for three enzymes: malate dehydrogenase, phosphoglucoseisomerase and acid phosphatase. These enzymes may be coded by three genes, tentatively designated *Mdh*, *Pgi* and *Aph*, respectively.

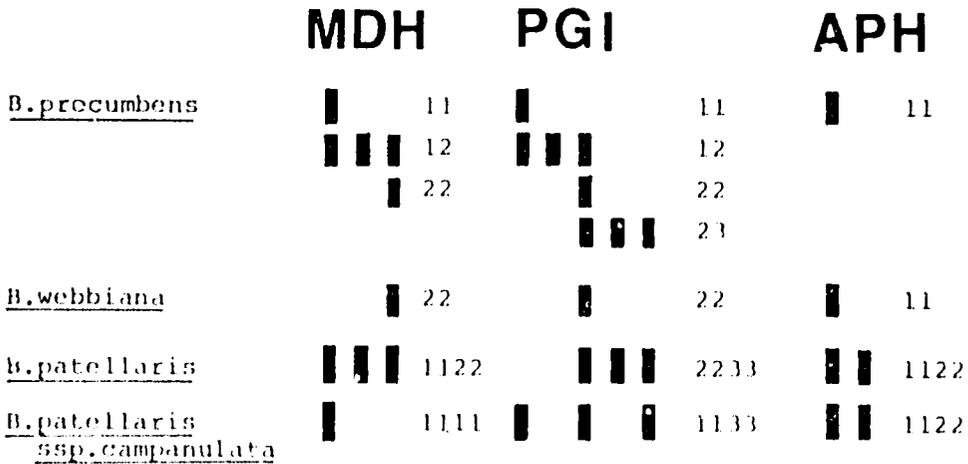


Fig. 2. Variation of malate dehydrogenase, phosphoglucoseisomerase and acid phosphatase isozymes in section Procumbentes

*B. procumbens* had the alleles  $Mdh^1$ ,  $Mdh^2$ ,  $Pgi^1$ ,  $Pgi^2$ ,  $Pgi^3$  and  $Aph^1$ . *B. webbiana* had the alleles  $Mdh^2$ ,  $Pgi^2$  and  $Aph^1$ . On the other hand, *B. patellaris* showed the heterozygous phenotypes found in these diploid species. For the *Mdh* and *Pgi* loci, two different phenotypes,  $Mdh(1/2)$  and  $Pgi(2/3)$ , and  $Mdh(1/1)$  and  $Pgi(1/3)$  were observed. This suggests genetic differentiation within this self-fertile species. Of these phenotypes,  $Mdh(1/1)$  and  $Pgi(1/3)$  were characteristic of *ssp. campanulata*. For the *Aph*, *B. patellaris* had the  $Aph^1$  and an additional allele,  $Aph^2$ , which was not detected in *B. procumbens* and *B. webbiana*.

As in the case of the tetraploid *macrocarpa*, the results obtained suggest that *B. patellaris* may be an amphidiploid species. In addition, it may have closely related but different genomes, one of which may be characterized by the  $Aph^2$  allele. This is also compatible with a regular bivalent formation at meiosis in *B. patellaris* (Walia, 1971). Further, it is suggested from an analysis of chloroplastic DNA that *B. patellaris* has a different cytoplasm from *B. procumbens* and *B. webbiana*, whereas the latter diploid species has the same cytoplasm (Kishima, 1988). This may also provide circumstantial evidence for the amphidiploid origin of *B. patellaris*.

## 6. Concluding remarks

As our studies indicate, the analysis of isozyme variation may be useful for taxonomic and evolutionary studies of the genus *Beta*. This approach may also provide a helpful means of evaluating genetic resources. In this case, it should be determined whether isozymes can be used as taxonomic key characters, in addition to conventional morphological characters. For this purpose, we need to survey a lot of materials, and to elucidate the pattern of isozyme variation within and among the taxa in detail.

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## SCORING HETEROGENEOUS POPULATIONS

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The CGN has, for the past two years, used a standardized method for scoring the heterogeneity of heterogeneous populations. This method can always be used for qualitative traits if the separate scores consist of one digit, and if the symbols 'x' and '≠' are not yet defined.

### Formal rules

This method follows the following rules:

- Put the scores of the separate fractions in decreasing order of size.
- If there is only one fraction, put an '≠' sign after the score.
- If the ratio between two adjacent fractions is between 1.5 and 5.0 put one 'x' sign between the two fractions; if the ratio is higher than 5.0, put two 'xx' signs between them.

This means that scores of homogeneous populations are followed by the '≠' sign, and that the scores of other populations' fractions are put in decreasing order of size, where an 'x' is put between fractions with a large size difference and 'xx' between fractions with a very large size difference.

### Examples:

On the following scale: 1 - white, 2 - purple, 3 - red, a population with only white flowers (100% '1') gets the score '1≠'. A population with just a few more purple than white flowers (55% '2' and 45% '1') gets the score '21'. The populations with mainly purple, but also some white and very few red flowers (85% '2', 14% '1' and 1% '3') gets the score '2x1xx3'.

**Advantages:**

- This method allows the user to indicate variation within the population he or she is scoring, allowing even the smallest fractions in the population to be recognized when analyzing the data.
- The accuracy of the score appears to be nearly as good as an observation without an exact count.
- The method is, after a brief explanation with some examples, easy to learn and use.

Some types of automatic analysis of these variation scores, like the estimation of the percentages, have already been developed. I hope to publish something on this method soon. Please contact me in the mean time for more information.

## **STRATEGIES FOR SELECTING SUBSETS WITHIN COLLECTIONS**

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Wageningen, the Netherlands**

### **Introduction**

The value of a germplasm collection is determined by the use that is made of it, or the use that can be made of it in future. The cost of a germplasm collection is, among other factors, determined by its size.

Via proper use of the documentation it is possible to optimize both the genetic variation in a collection of a given size, and the user's chances of finding the material he is looking for. This would reduce the costs and increase the value of a germplasm collection (Peeters and Williams, 1984). Here I will focus on sampling material from a collection. The classification techniques mentioned in the last part of this paper can also be used to maximize genetic variation within a collection, by adding or replacing carefully selected material, or to select a core collection as defined by Brown (1989).

First the information that can be used for this sampling will be studied, followed by a description of the selection strategy, where clustering techniques will be given extra attention since they are seldom used for this purpose.

### **Information on germplasm collections**

Information on a collection should serve the objectives of that collection. The following definitions and objectives of the two types of collection at opposite extremes will be used, recognizing that most collections are somewhere in between:

A base collection consists of genetic material covering as much genetic variation as possible of a chosen crop, with the aim of safeguarding this variation for future use.

A working collection consists of genetic material best suited for serving a specific group of users in the short and medium term.

Generally there is some information available on germplasm collections. Besides the information that is necessary for proper seed stock management, which I will not discuss here, some passport and evaluation data are usually available (Knüpffer, 1983).

Information on the type (breeding level, taxonomic data) and origin of germplasm is necessary for a curator to compile or extend a base collection. This kind of information is generally called passport information.

Characterization data, highly heritable and/or easily observable traits like flower colour, plant height, anthocyanin presence etc., are generally used for identification of the accessions. This identification is important in monitoring the treatments of the seeds and in tracing duplicates. Characterization data are usually collected during the seed multiplication of a collection.

Evaluation data, besides the characterization data mentioned above, are generally collected to determine the value of the material in a working collection for the users. Sometimes screening programmes are organized to find specific traits.

Most base collections are documented with some passport and some characterization data. The documentation of working collections usually includes some very basic passport data and more or less extensive evaluation data. This information can sometimes be upgraded by processing. The quality can be increased by e.g. checking the plausibility and integrity of the data. If the collection site of the material is well documented, the quantity of the passport data can be increased with climatological data. (In exploring the possible applications of these data, the CGN is compiling, with financial support from IBPGR, a climatological database for the sites of most common origin.)

The utilization of the information can be stimulated by increasing the accessibility and the utility of the data.

## Selecting subsets

The user of germplasm collections usually has specific requirements. To meet these requirements information on the available material and facilities allowing retrieval and interpretation of that information are needed.

The most important facility is the user interface that determines the accessibility of the available information. In the case of not yet computerized data, the archive storing the data should be well structured and well documented. If the information is computerized this user interface can be optimized by the use of database management systems that are specially designed for this purpose.

The user interface should allow material that directly meets the selection criteria of the user to be found. If a user of a working collection searches for a specific cultivar and variety names are documented, he must be able to find it. Or, if he is looking for short Ethiopian material and there is information on plant length as well as origin country, he must be able to find out which material meets his requirements. This is simple mass selection; one could also think of allowing for more complicated selection criteria.

A more difficult problem arises when the criteria cannot be met directly. Consider the user of a base collection who wants to compile a working collection of 100 accessions with as much genetic variation as possible; or the user of a working collection who wants 50 accessions with maximum likelihood of finding a certain disease resistance.

The first step then is to filter from the user criteria the criteria that can be met directly. If the resulting set is too large the second step is to select material as heterogeneous as possible from the selected set, so maximizing the probability of the user finding what he is looking for. A technique that can be used for this purpose is clustering.

Consider, for example, a user who is looking for a new disease resistance in a certain species. He can screen 50 accessions. The total collection is 5000 items, of which 1500 are of the wanted species. The user expects that the resistance is most likely to be found in the Mediterranean countries, leaving 500 accessions. From these we can select material as heterogeneous as possible on the basis of the available information using clustering techniques.

## Clustering

If, on the basis of the primary criteria, a set of material has been selected, it is often necessary to select a subset of appropriate size. A classification technique can be used to form a number of clusters equal to the required number of accessions. These clusters contain as little polymorphism as possible, but between the clusters the polymorphism is as large as possible. From each of these clusters one sample must be selected. This choice can be a random one, but can also be based on other criteria, such as the variability within the accessions in the cluster, or the quality or quantity of the available seed.

There are many classification techniques. A basic distinction can be made between divisive and agglomerative techniques. The divisive classification techniques start with the entire group as a whole, dividing it in two parts, then dividing one part into two new parts etc. until the required number of groups is achieved. Agglomerative techniques work the other way around, starting with as many groups as there are items, followed by the consecutive clustering of homogeneous groups. Historically the divisive techniques have required much more computing capacity than the agglomerative. This has caused agglomerative techniques to be more commonly used and more developed.

Another distinction that can be made in classification techniques is between hierarchical and non-hierarchical ones. The hierarchical techniques cluster stepwise, each step reduces (agglomerative techniques) or increases (divisive techniques) the number of clusters by one. This sequence makes it possible to give a graphical representation of the process, a dendrogram. The non-hierarchical techniques do not impose such a hierarchical structure on the data.

The techniques we will consider are hierarchical agglomerative techniques. These work with a similarity matrix, a symmetrical matrix with a measure for the similarity, or dissimilarity, of any combination of two items.

The calculation of these similarities is the first problem in using these techniques. The other problem is how to measure the similarity of two groups of items (For a full discussion of these techniques see Gordon, 1981 and Sneath and Sokal, 1973.)

Commonly used measures of similarity are Euclidean distance and city block distance, where we have to decide whether all attributes should have equal weight or not. We also have to decide how to handle missing values. When investigating similarity between groups, single linkage or nearest neighbour clustering, complete linkage or furthest neighbour clustering, and the centroid and minimum variance or Wards method can be used.

These techniques can be applied in a way that automatically allows for the selection of a subset with maximum polymorphism. Problems that arise are the choice of technique and the choice of data. Both can be solved beforehand so that the user can use the facilities without being bothered with these decisions.

Choosing the technique is no simple matter. The agglomerative hierarchical, average linkage or minimum variance techniques, using Euclidean distance, are all worth considering. But much more experience is needed to be able to say which solution is the best in what circumstances.

The polymorphism that is being maximized in any set of data should reflect genetic variation. The data that are used for classification should also reflect this genetic variation. In principle all genetically based data can be used, the environmental component working as a randomly distributed error. The genotype-environment interaction may be a problem since it can conceal differences for some traits in specific groups of material. Both effects can be minimized by using as many traits as possible with a heritability as high as possible. But also non-heritable, origin data can be used, e.g. for selecting material from climatological environments as different as possible, or selecting material with origin sites that are spread equally over a certain region.

## **Conclusions**

Given the fact that germplasm collections are important, but also very expensive, especially for cross-pollinating crops like beet, the curator should try to manage them as efficiently as possible. The first step is to define the objectives of the collection. In pursuing these objectives a need for information arises. This information can be gathered from many sources, using many strategies. But information is ineffective if it cannot be used.

The most important facility allowing use of information is the information system that makes it accessible and allows for selection on well-defined criteria. Another facility can be a classification programme that makes it possible for the user to select from a set those items that have maximum polymorphism. Many techniques are available. The agglomerative hierarchical, average linkage or minimum variance techniques, using Euclidean distance, seem useful for this purpose. The choice of data can depend on the purpose, but should always represent the expected genetic variation.

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## PROSPECTS FOR BEET BREEDING AND USE OF GENETIC RESOURCES

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### Introduction

To maintain the competitiveness of the beet sugar industry in the years ahead, sugar beet varieties will have to be increasingly designed for optimum growing and processing economy and be adapted to the requirements of a sustainable agricultural system. Such varieties must combine good yield with highest possible seed quality, have high levels of resistance or tolerance to major pests and diseases, high technological quality, uniformity with respect to size and shape of roots and crowns as well as ability to withstand environmental stress and make maximum use of available water and nutrients.

It is against this background that I want to discuss the prospects for beet breeding and the use of genetic resources. However, I shall not talk specifically about the use of sources of resistance to cercospora leaf-spot, the sugar beet ellworm, rhizomania or other diseases about which the reader is probably well informed and where there are likely to be few conflicting opinions on matters of principle. Instead, I will discuss the constraints and limitations of current triploid hybrid breeding, and how an alternative diploid system may take better advantage of recent developments in both genetic engineering and molecular biology and make it possible to utilize and benefit from the huge and largely untapped gene pool of the wild Beta beets.

### Current hybrid breeding in sugar beet

The first thing to observe is that in Europe hybrid sugar beet varieties have never been based solely on inbred lines, as has almost always been the case with maize. The most common system has been to use an  $F_1$  hybrid between a more or less inbred cytoplasmic male sterile line and an unrelated maintainer line as a female, and a tetraploid population as the pollinator parent. The resultant triploid top-cross hybrids are not only highly heterozygous but usually also highly heterogeneous. Some quite successful diploid top-cross hybrids have also been marketed, which has been taken as

an indication that diploid hybrids are on the way to replacing the triploids. However, recently the proportion of triploid hybrids has again increased. Thus, out of 95 monogerm varieties marketed in France in 1987, 85 were triploid hybrids, five were diploid and five were anisoploid hybrids.

The combination of a high degree of heterozygosity and genotypic diversity in the triploid hybrids has no doubt contributed to the retention in these hybrids of the wide adaptability of traditional multigerm sugar beet varieties, which were the result of intermating of several unrelated, more or less broad-based lines or populations. Fear of losing this adaptability is probably the main reason why most European sugar beet breeders are sceptical about more narrow-based hybrid varieties, in particular single-cross hybrids involving only two inbred lines. For the same reason, the few diploid hybrids marketed have been rather heterogeneous top-cross hybrids. That even today such diploid hybrids have difficulty competing with corresponding triploid hybrids is probably due to the fact that with both kinds of hybrids exploiting virtually only general combining ability, the more efficient use of heterozygosity at the triploid level becomes decisive.

However, the heterogeneity of current sugar beet hybrids, which is particularly pronounced in the triploids, has many drawbacks both from an agricultural, technical and breeding point of view. Thus, in triploid hybrids both the genetic diversity and aneuploidy contribute to variation in root size and shape, size and shape of the crown and the extent to which the roots grow out of the ground, all characteristics that affect the quality of the harvesting work and thereby both harvesting and storage losses and performance in the factory. With this comes a corresponding variation in sugar content and content of potassium, sodium and amino nitrogen.

Further, hybrid varieties involving non-inbred parents resemble composites and synthetic varieties in that improvement of a character in the variety requires improvement of the average performance of one or more heterogeneous component populations rather than the development of an improved genotype in the form of an inbred line. This influences both the rate of progress and the degree of expression of the character that can be obtained in the hybrid. Finally, in many countries the authorities responsible for variety testing and registration have long complained about the lack of distinctness and uniformity of sugar beet varieties. So far it has been possible to refute these complaints by arguing that the distinctness and uniformity asked for can be obtained only at the expense of a reduction in yield and stability of performance.

However, in recent years, some breeders and researchers have claimed that diploid single-cross hybrids, based on highly inbred lines, are a viable alternative to the type of varieties available at present. It is suggested that such hybrids may be as high yielding and adaptable as the present triploid varieties, and on top of that have considerably better quality and disease resistance (Le Cochee, 1982).

There are good genetic and breeding reasons for these claims. As mentioned earlier, the advantage of triploid top-crosses over corresponding diploid top-crosses probably depends on better use of heterozygosity, which in its turn depends on the larger number of quantitatively different genes brought in by the tetraploid parent. However, over the last 30 years a very large volume of tetraploid sugar beet materials has been developed through chromosome doubling and intermating of the best diploid lines or populations. There is thus reason to believe that the immediately available greater potential for heterotic effects in these tetraploids, as well as in their triploid hybrids, has now been largely exploited, and that further progress will depend on how efficiently we can select our tetraploid pollinator populations. Although micropropagation may be used to facilitate identification and intermating of individual superior tetraploid genotypes, we may still soon reach the stage when the major disadvantages of autotetraploids -- their inflexibility and slow response to selection -- outweighs their long-term genetic advantage (Bosemark, 1971a).

These differences in selection efficiency between diploids and tetraploids will be still further accentuated when we can use RFLPs as an aid in selection for quantitative traits. It should also be observed that due to the complexity of the triploid top-cross hybrids, the introduction of a novel trait into such a variety is a much more time-consuming and costly operation than would be the case with a diploid single-cross hybrid. This applies even to characters governed by a single dominant gene and irrespective of how the gene is introduced, by normal sexual means or by genetic engineering techniques.

### **Diploid single-cross hybrids: advantages and disadvantages**

It has already been mentioned that the wide adaptability of traditional multiline sugar beet varieties, as well as that of triploid top-cross hybrids, is due to a combination of heterozygosity and genetic diversity. Since diploid single-cross hybrids based on highly inbred lines would be practically genetically uniform, they would not be able

to capitalize on the effects of genetic diversity. Whether this will necessarily result in less adaptable sugar beet varieties or not, cannot as yet be said with certainty. However, judging from the development in maize breeding in the USA and Canada, it appears that a high level of individual adaptability can be built into single-cross corn hybrids. Thus extensive yield and stability trials of single and double-cross hybrids conducted in these countries have shown that single-cross hybrids, which have been selected for both yield and stability over a wide range of environments, yield appreciably more than the genetically diverse double-cross hybrids, while at the same time there is no difference in stability between the different types of varieties (Eberhart, 1969; Lynch, et al., 1973). There is reason to believe that these results are applicable also to diploid single-cross sugar beet hybrids, provided sufficient attention is given to individual stability in the hybrid breeding programmes (Gyllenspetz, 1988). Taking everything together there is thus a lot to recommend a strict  $F_1$  hybrid breeding system.

However, for single-cross hybrids to be a viable commercial proposition, the parental inbred lines must not only have outstanding combining ability and produce stable hybrids with superior yield, quality characteristics and disease resistance, but the lines themselves must be vigorous, easy to handle and capable of producing high yields of good-quality seed.

Although, in principle, lines meeting these criteria may be isolated from any adapted open-pollinated breeding population, it may soon become difficult to produce from such sources new inbreds notably better than the present ones. There is then the risk that  $F_2$  populations, developed by crossing two existing lines with desirable and complementary characteristics, become a more and more favoured source of new inbred lines, so-called second cycle lines. Although recycling of elite inbreds may result in considerable progress and thus should not be rejected, too strong emphasis on single-cross sources will result in a gradually accumulating relationship in the source material and a narrowing of the genetic base of the breeding programme.

Today, there is general agreement that the rate of progress in hybrid breeding programmes depends on the efficiency with which new superior parental lines can be generated, and thus is largely a function of the proportion of desirable genotypes in the source populations from which these lines are developed. As emphasized by Eberhart (1970), a sound hybrid-breeding programme should be based on a continuous improvement of source populations through some kind of recurrent selection. Though

originally developed to increase the frequency of desirable genes and gene constellations in corn populations to be used as sources of inbred lines, various types of recurrent selection are now widely used in population improvement in many crops and are highly relevant also in sugar beet breeding (Bosenmark, 1971b, Doney and Theurer, 1978; Hecker, 1985). The most effective system for development of inbred sugar beet lines for subsequent  $F_1$  hybrid production should be a system of reciprocal recurrent selection based on a monogerm maintainer population and a multigerm pollinator population. The maintainer population will become the source of inbred type '0' lines from which will be developed equivalent cytoplasmic male sterile inbreds to be used in crosses with inbreds developed from the pollinator population

Since recurrent selection permits small, successive changes in gene frequency, recurrent selection procedures also offer the best possibility of adapting and incorporating exotic germplasm into breeding populations, thereby increasing the genetic variability and enhancing heterosis. However, this does not mean that wild beet germplasm can be directly introduced into the previously mentioned maintainer and pollinator populations. To be able to yield useful inbreds for hybrid production, the average performance of these populations must be kept very close to commercial hybrids. This applies to all characteristics.

Thus, until adapted and upgraded through several cycles of selection and recombination, the 'wild' gene pool will have to be kept separate. However, once performance approaches that of commercial sugar beet, germplasm from this population can be fed into the elite germplasm populations as illustrated in Fig. 1. If the recessive gene  $a_1$  for Mendelian male sterility and the  $S^F$  gene for self-fertility have been introduced into the elite as well as wild germplasm populations, crosses with the elite and the wild population can be evaluated as half-sib families and/or  $S_1$  families. This makes it possible to assess the value of the exotic germplasm before it is incorporated into the elite population.

#### **Time and cost of upgrading germplasm from wild Beta beets**

Of crucial importance in judging the feasibility and value of the proposed system for gene introduction is the cost and time required to produce, from crosses between cultivated beets and wild Beta beets, material with characteristics approaching those of current sugar beet varieties.

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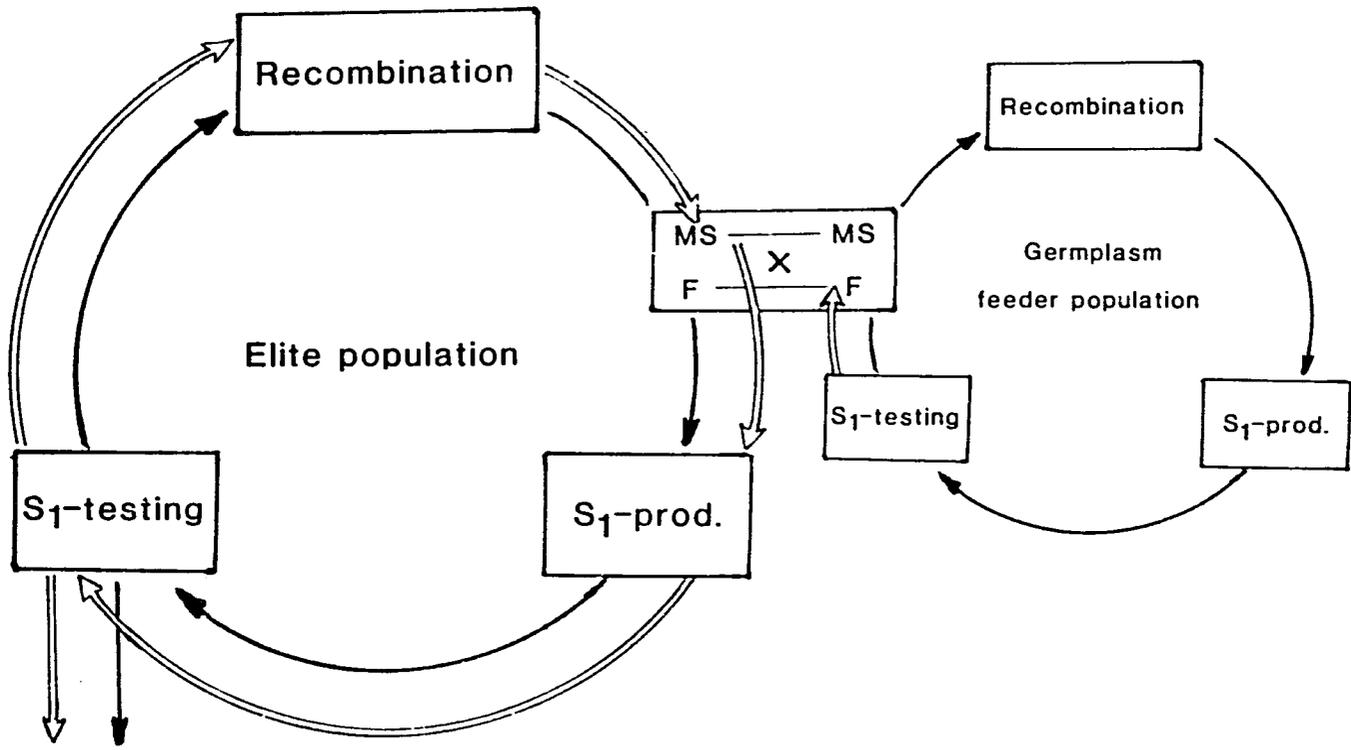


Fig. 1. Method of introducing new germplasm into elite breeding population

To illustrate this, I will give two examples from my own studies several years ago. The first example concerns a cross between the white-skinned fodder beet *Särimer* and a *Beta maritima* population collected near Kalundborg in Denmark (Table 1). The second example comes from a cross between a self-sterile, monogerm maintainer population segregating for Mendelian male-sterility and a primitive leaf-beet (*B. cicla*?) collected in Yugoslavia in 1956 (Table 2).

The *Särimer* x *B. maritima* cross was subjected to two mass selections in the  $F_2$  and  $F_3$  generations (mainly for bolting resistance and root shape), followed by three cycles of recurrent half-sib family selection. No back-crossing to sugar beet was made. The results presented are the average values of families from the third RS cycle.

The sugar beet x *B. cicla* cross was subjected to two cycles of recurrent half-sib selection only. In both groups of materials the half-sib families were produced from roots individually selected for morphological and chemical characteristics.

In view of the limited number of cycles of selection and recombination the results obtained are remarkably good, and suggest that the genepool of the wild Beta beets is not as inaccessible as might be thought. It is my belief that an additional couple of cycles of recurrent selection would have created populations sufficiently upgraded and adapted to be used as germplasm feeder populations in the way outlined in Fig. 1.

Even so, I fear that the steadily increasing pressure on commercial breeders to quickly develop new lines and varieties with improved agronomic characteristics will prevent most of them from engaging in this kind of work. Thus, for genebanks not to develop into museums or libraries where valuable and badly needed germplasm is just sitting on the shelves in the storage rooms, researchers and breeders in government plant breeding institutes may have to step in and take responsibility for some of the development work discussed. With the new tools and techniques combined with traditional selection methods, such work is likely to produce results of great practical value relatively quickly and, besides, be scientifically rewarding.

TABLE 1. Results of half-sib families from the third cycle of recurrent selection in Särimer x B, maritima population tested in 1980

	Sugar (tons/ha)	Roots (tons/ha)	Sugar (%)	No. of pl./ha (in 000)	K + Na (meq/100 s)	Amino-N (mg/100 s)
Average (223 families)	6.01	36.6	16.4	63	36	134
Some of the highest yielding families	8.35	49.6	16.8	64	33	157
	8.08	47.5	17.0	69	30	161
	7.54	43.9	17.2	68	34	116
	7.26	43.6	16.7	65	36	99
	7.06	41.4	17.2	68	37	125

TABLE 2. Data for individual roots selected in 1980 among half-sib families from the second cycle of recurrent selection in the sugar beet x B. cicla populations

	Sugar (g)	Roots weight (g)	Sugar (%)	K (meq/100 g)	Na (meq/100 g)	Amino-N (mg/100 g)
A <sup>1</sup>	149	995	15.1	6.17	1.19	49
B <sup>2</sup>	159	989	16.2	5.57	0.93	40

<sup>1</sup> A = 1029 roots selected on morphological characteristics from 159 half-sib families (average values).

<sup>2</sup> B = 272 roots representing 131 families and selected from A on the basis of the chemical analyses (average values).

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**POPULATION DYNAMICS OF *BETA VULGARIS* SSP. *MARITIMA* L. (SEA BEET)  
IN THE BRITISH ISLES**

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The collection, preservation and evaluation of wild germplasm has received increased attention in recent years due to the gradual elimination of natural habitats and the need for stress-resistant germplasm. Native populations may shift in location and genetic makeup due to natural and man-imposed environmental changes. Recent discoveries of pest-resistant germplasm in *Beta vulgaris* ssp. *maritima* L. (sea beet) have focused interest on the status of native populations and the need to collect and preserve this subspecies (Doney and Whitney, in press; Lewellen et al., 1987; Whitney, 1986). The USDA-ARS and IBPGR have conducted numerous *B. vulgaris* ssp. *maritima* collection expeditions over the past eight years.

One such expedition was conducted in 1987 along the coasts of England, Wales and Ireland. The distribution of *B. vulgaris* ssp. *maritima* was similar to earlier sitings. However, many small populations of earlier sitings were in danger of extinction or had already disappeared (Doney et al., 1989). Factors threatening or causing extinction included livestock grazing (particularly sheep), slippage of mud cliffs, industrialization, sea ports and recreational activities. Agents acting to disperse *B. vulgaris* ssp. *maritima* germplasm are high tide, wind, animals and man (Doney et al., 1989).

The collection strategy was to collect every 15-20 km or whenever isolation due to a geographic barrier existed. Site collections were bulk seed from all plants in small populations and a random sample of at least 50 plants in large populations. In addition, 10-20 individual variant plants were sampled in each population.

These collections provide an opportunity to study the genetic variability and dynamics of this wild germplasm. This study was designed to evaluate genetic movement and ecotype development of *B. vulgaris* ssp. *maritima* in the British Isles.

## **METHODS**

### **Field evaluation of collected germplasm**

The collection was evaluated in field plantings at Fargo, North Dakota (latitude 46.5°N). Each population with sufficient seed was planted in a single 6 m row. A commercial hybrid (Hilleshög 5135) was also included as a reference check. Supplemental irrigation resulted in good stands for most of the accessions even though germination was slow. This slow germination was expected since *B. vulgaris* ssp. *maritima* is noted for seed dormancy.

Leaf measurements were taken in mid-August after maximum leaf expansion and prior to stalk initiation. The most mature non-senescent leaves of each plant were measured for leaf thickness, length and width; petiole length and width; and leaf dry weight and dry matter percentages.

### **Greenhouse evaluations of collection germplasm**

A more detailed study was conducted in the greenhouse on a sample of the collection accessions. This study consisted of samples of populations from seven different sites (Pegwell Bay, Deal, Dover, Hythe, Greatstone, Chamber and Rye Harbour), each 15-20 km apart. Ten plants from each of ten plant populations at each location were grown in a uniform potting medium. All plants received equal amounts of fertilizer to ensure uniform nutrition. Measurements were made for leaf thickness, length and width and petiole length when the plants were one month old. A leaf width/length ratio was calculated to obtain a relative measure of leaf roundness. A large ratio (close to 1.0) is indicative of a round leaf.

## **RESULTS**

### **Field evaluation**

There were significant differences among accessions for each of the measured characters. Most of the accessions had smaller leaves (both length and width) and smaller petioles (both length and width) than the sugar beet check, even though significant differences existed among the accessions. Seventy percent of the

accessions had shorter petioles than the sugar beet check, whereas none were longer. *B. vulgaris* ssp. *maritima* of the British Isles has a very narrow petiole. All accessions had significantly narrower petioles than the sugar beet. Ninety percent of the accessions had narrower and shorter leaves than the sugar beet. When relative roundness was compared, the accessions were generally longer (25% of the accessions), whereas only 3% were significantly rounder. The wild 'sea beet' was also lower in percentage dry matter (90% of the accessions) and dry weight per leaf (60% of the accessions) than sugar beet. On the other hand, sea beet from the British Isles has a thicker leaf than sugar beet. All accessions had significantly thicker leaves than sugar beet, with some more than twice as thick. A negative correlation ( $r = -0.52$ ) was observed between leaf thickness and leaf percent dry matter.

### Greenhouse evaluations

Pegwell Bay, Deal and Dover are on the southeastern coast of England, with the Deal location between Pegwell Bay and Dover. Significant differences in all leaf characteristics were found between the populations at the Pegwell Bay and Dover locations. The Deal population, however, contained characteristics of both the Pegwell Bay and Dover populations (Fig. 1). Each leaf measurement at the Deal location was between the locations on either side (Pegwell Bay and Dover). These data suggest that at 15 km, changes in gene frequency were evident but were insufficient to form a new ecotype. However, at distances of greater than 30 km, isolation was sufficient to shift gene frequencies and promote formation of distinct ecotypes.

Older populations, i.e. undisturbed populations, exhibited more variation than newer populations. One such older population was located at Dover. Significant differences among plants in this population were observed for most of the leaf measurements. Individual plant measurements for leaf thickness (Fig. 2) revealed three significant groupings. In addition, six of the ten plants were segregating for leaf thickness (Fig. 2). These observations suggest that significant crossing and segregation was taking place between and within plants of this population.

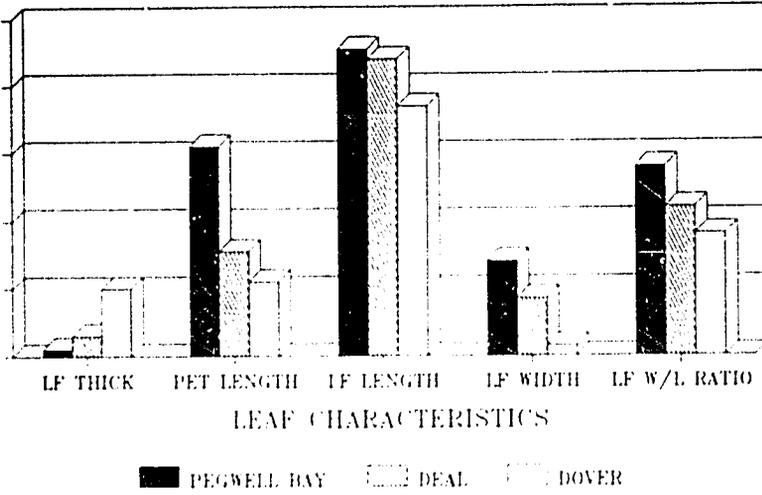


Fig. 1. Leaf characteristics, Pegwell Bay to Dover

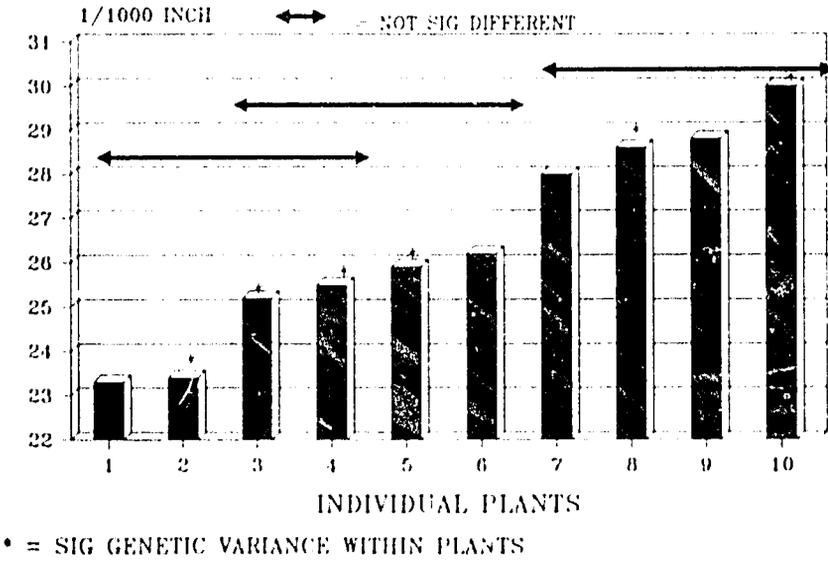


Fig. 2. Leaf thickness, Dover population

Data for the five leaf measurements at the seven locations are shown in Figs. 3, 4 and 5. Non-significant (NS) differences between nearest neighbour population pairs were more prevalent for petiole length than for the other leaf characteristics. However, significant differences in petiole length were observed between the Pegwell Bay and Deal and between the Chamber and Rye populations (Fig. 3). Differences in leaf length were significant between all except the Pegwell Bay-Deal and Greatstone-Chamber nearest neighbour pairs (Fig. 4), whereas leaf width was significantly different between all nearest neighbour pairs (Fig. 4). All except the Dover-Hythe-Greatstone nearest neighbour pairs were significantly different in leaf thickness (Fig. 5). Four of the six nearest neighbour pairs were significantly different for the leaf length/width ratio (Fig. 5). Comparing all measurements, each nearest neighbour pair was significantly different in at least two of the leaf measurements (Figs. 3, 4 and 5).

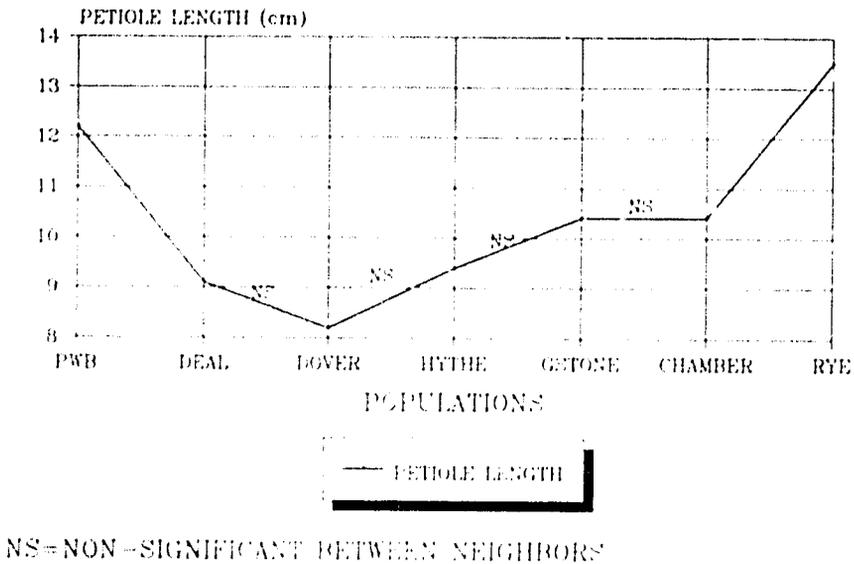
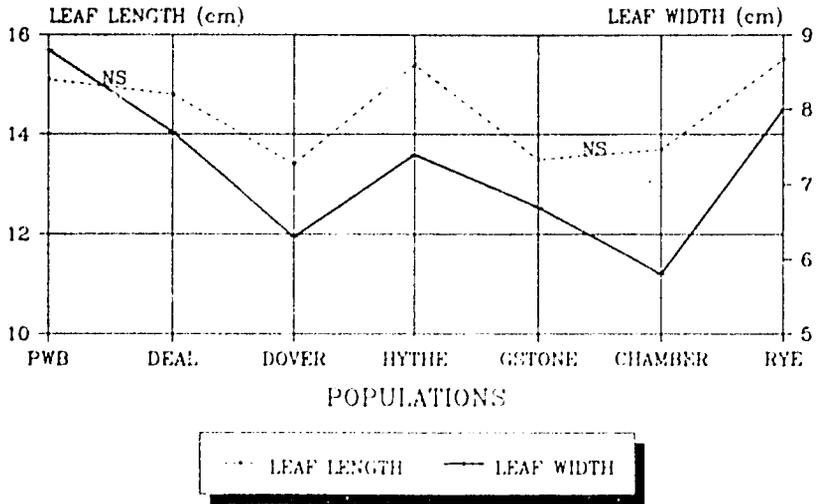
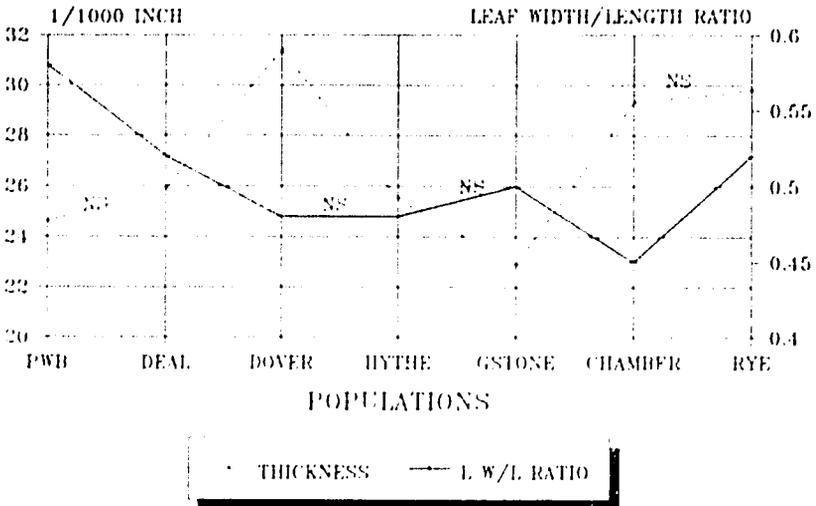


Fig. 3. Petiole length, populations from Pegwell Bay to Rye



NS=NON-SIGNIFICANT BETWEEN NEIGHBORS

Fig. 4. Leaf length and leaf width, populations from Pegwell Bay to Rye



NS=NON-SIGNIFICANT BETWEEN NEIGHBORS

Fig. 5. Leaf thickness and leaf length/width ratio, populations from Pegwell Bay to Rye

## **Conclusions**

Compared with sugar beet, the British Isles sea beet (*Beta vulgaris* ssp. *maritima*) generally has smaller (length and width), longer, thicker leaves with lower percent dry matter. The petioles are also smaller (length and width) than sugar beet.

Significant variation in leaf characteristics exists between sites (locations) and among plants within sites. Older populations are dynamic, exhibiting crossing among and segregation within groups of plants.

A distance of 25-50 km provides sufficient isolation to induce a shift in gene frequencies and favours the formation of distinct ecotypes.

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## **BETA GERMPLASM COLLECTION: CURRENT STATUS**

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Beet germplasm collecting activities have been reported to IBPGR since 1972, and cover a fairly wide geographic area. At least 1180 accessions have been collected during this time (Table 1).

The first discussion on priorities for beet collection was held at a joint workshop of IBPGR and IIRB in 1979 (IBPGR/IIRB Consultation on Beet Genetic Resources, Cambridge, UK). At that meeting, an assessment was made of the known collections of germplasm and their range with respect to wild species and primitive landraces. Priorities were set for the acquisition of germplasm (Table 2) and also for geographical areas to be visited for collecting purposes (Table 3). Some of the recommendations were subsequently acted upon with a number of IBPGR-sponsored collecting missions taking place.

In 1985, the United States Department of Agriculture Sugar Beet Advisory Committee considered its priorities and needs for beet germplasm collecting (Table 4) and has now begun its collecting programme.

Finally, a Beta Workshop, held under the auspices of the European Cooperative Programme for the Conservation and Exchange of Crop Genetic Resources, took place in 1987. It took note of the recommendations which had been made previously in 1979 and 1985, as well as the collecting which had taken place during the intervening period, and set priorities for collecting after 1987 (Table 5).

These data have been presented to this International Beta Genetic Resources Workshop so that a positive agreement can be reached concerning the priorities and needs of future world germplasm collecting of Beta.

TABLE 1. Collections reported to IBPGR

Country/region	Year	Samples	Collector
Algeria	1982	24	Ford-Lloyd/IBPGR
Canaries	1981	93	Ford-Lloyd/IBPGR
Corsica	1985	23	Doney
Greece	1980	86	Crombies/IBPGR
(incl. islands	1980	24	Dale/IBPGR
and mountains)	1981	76	Cortessi/IBPGR
	1982	46	Cortessi/IBPGR
	1983	62	Cortessi/IBPGR
	1984	?	Cortessi/IBPGR
	1985	32	Cortessi/IBPGR
Ireland	1987	44	Doney
Israel	1986	62	Israel GB/IBPGR
Italy	1981	106	Italy/IBPGR
(incl. Sicily)	1984	28	Woodfin/IBPGR
	1985	118	Doney
Libya	1983	?	Libya/Italy/GDR
Morocco	1984	7	?
Spain	1984	22	?
	1987	?	Spain/INIA
Sardinia	1981	8	Toll/IBPGR
Syria	1987	?	Syria
Tunisia	1984	22	IBPGR/INRAT
Turkey	1972	205	Ford-Lloyd/Turkey
UK	1987	99	Doney/Kew
Yugoslavia	1987	?	IFVC

TABLE 2. IBPGR/IIRB Consultation on Beet Genetic Resources, 1979

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Priority for acquisition

Multigerm sugar beet and fodder beet varieties

Railway gardens in France

Bavarian landraces

Belgian landraces

Portuguese landraces

Yugoslavian landraces

Swiss chards, spinach beets and red beets

Europe

Asiatic USSR

South America

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TABLE 3. IBPGR/IIRB Consultation on Beet Genetic Resources, 1979

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Priority collecting areas

Priority 1: Central and eastern Mediterranean

Cyprus, Greece and Sicily

(wild and weedy forms)

Priority 2: Western Mediterranean

Algeria (wild and weedy)

Yugoslavia (hybrid fodder beet)

Bulgaria and Romania (old cvs.)

Priority 3: Atlantic Islands (Patellares)

In addition: Nanae - situation to be clarified

Corollinae - potential to be examined

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TABLE 4. USDA Sugar Beet Crop Advisory Committee, 1985:  
Collection needs and priorities

Country/region	Priority	Section	Time
Cyprus/Israel	High	Beta	1986
N. Europe	High	Beta	1987
Caucasus	High	Corollinae	
Turkey	Medium	Corollinae	
India	Medium	Beta	
Saudi Arabia Egypt	Low	Beta	

TABLE 5. Recommendations of Beta Workshop, Wageningen, 1987

Priorities:

1	Caucasus - South Russia	wild forms and landraces
1	South Atlantic coast of Europe	wild forms
		ssp. patula
		ssp. maritima
		ssp. atriplicifolia
1	North mainland Europe	ssp. maritima
2	Southwest Asia	
2	Yugoslavia (depending on further information)	
3	India and China (depending on further information)	