PN-AAN-634

INTERNATIONAL CROP NETWORK SERIES. 9

IBPGR

Barley Genetic Resources

Report of an international barley genetic resources workshop held at Helsingborg Kongresscenter Helsingborg, Sweden 20-21 July 1991

INTERNATIONAL BOARD FOR PLANT GENETIC RESOURCES

INTERNATIONAL CROP NETWORK SERIES. 9

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IBPGR
ROME 1992

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 the CGIAR in 1974. The basic function of IBPGR is to promote and coordinate an international network of genetic resources centres to foster 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, Germany, India, Italy, Japan, the Netherlands, Norway, Spain, Sweden, Switzerland, the UK and the USA, the United Nations Environment Programme and the World Bank

Citation
IBPGR, 1992. Barley Genetic Resources. Papers of an International Barley Genetic Resources Workshop held at Helsingborg Kongresscenter, Helsingborg, Sweden, 20-21 July 1991. International Crop Network Series No. 9. International Board for Plant Genetic Resources, Rome

ISBN 92-9043-219-5

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INTRODUCTION

The International Workshop on Barley Genetic Resources was convened in the Kongresscenter of Helsinborg, Sweden, 20-21 July, just before the Sixth International Barley Genetics Symposium held in the same place, on the kind initiative of Prof. R. von Bothmer, Chairman of the Organizing Committee of the Symposium.

The objective of the Workshop was to call for the implementation of a world-wide barley genetic resources network and to define its mode of operation. This initiative followed the recommendations of an International Barley Working Session held at the Institut für Genetik und Kulturflanzenforschung, Gatersleben, Germany, 21 April 1989, which had also been convened by IBPGR. An Interim Committee had been created during this meeting to pursue the creation of a barley genetic resources network. The members of this Interim Committee were in 1991 Drs Fraleigh (Canada), Franckowiak (USA), Konishi (Japan), Valkoun (ICARDA) and von Bothmer (Sweden), and formed, with IBPGR logistic support, the Organizing Committee of the International Workshop.

Prof. von Bothmer, as host, and thereafter Dr S. Blixt, as Director of the Nordic Genebank, welcomed the participants in their opening addresses. Mr Perret explained the IBPGR point of view on the implementation of international crop genetic resources networks (refer Appendix III, p.10). The meeting adopted the Agenda as provided in Appendix I and elected for each session two discussion leaders (see Agenda, Appendix I). 46 participants from 28 countries attended the Workshop. This reflects the interest of barley genetic resources workers to organize themselves into a network. The list of participants is provided in Appendix II.

IBPGR wishes to express its gratitude to Prof. R. von Bothmer for his key role in the organization of this Workshop, as well as to the Nordic Genebank, and especially to its Director, Dr S. Blixt, for his continued support and co-sponsoring of the meeting.

Recommendations of the International Barley Genetic Resources Network

A revised IBPGR descriptor list

The meeting agreed on the need to revise the IBPGR descriptor list and asked Drs. J. Franckowiak and T. Konishi to circulate the draft prepared by Dr. Franckowiak. Suggestions for any modifications will be welcome particularly for the descriptors recording genetic markers. It was also recognized that a system to adequately record heterogeneity within accessions should be adopted. That used by the Center for Genetic Resources the Netherlands, and described by Th. van Hintum, was considered as a useful starting point.

An international barley genetic resources database (IBGRD)

The establishment of the IBGRD is a crucial component of the network. The first step should consist of an inventory of existing accessions (passport data) by regional databases as previously recommended by the International Barley Working Session. Participants recommended Gatersleben, Germany (European Barley Data Base, EBDB), USA/Canada, ICARDA, Japan and a barley programme from S. America (tentatively EMBRAPA, Brazil) as regional databases. Those institutes should obtain data from collections within their designated regions. Documentation officers of those regional databases will constitute a task force, which will:

i) denote whether or not to include data from programmes which are not part of the network,

ii) be responsible for acquiring data from programmes participating in the network which are not covered by any of the above-mentioned regional databases,

iii) propose an Institute which will put together the regional databases files and thereby establish the IBGRD,

iv) establish mechanisms for continuous updating of the IBGRD.

Base and active collections

An approach consisting of a three-tier collection structure was agreed as follows:

a) Active collections:

Perform all primary genebank activities associated with serving germplasm users. Provide duplicate samples of all unique accessions to designated regional base collections.

b) Regional base collections (between 4-6).

Serve as a base collection for active collections in their region (for definition of base collections, refer to IBPGR Advisory Committee on Seed Storage, Report of the Third Meeting).

c) Global base/safety duplicate collection:

Storage function only.

Members unanimously agreed that the participation in the barley genetic resources network requires free availability of genetic resources accessions.

The global structure of the network should be developed and implemented concurrently with the IBGRD.

Members asked the Coordinating Committee (refer mission statement below) to contact genebanks building upon existing designations to identify and register the commitments of genebanks as base and/or active collections within the network. The Coordinating Committee should also develop, where necessary, appropriate technical standards in co-operation with IBPGR/FAO for each type of collection.

Wild species

Recognizing that genetic diversity of wild species is not only present *in situ* but also sampled in genebanks, members emphasized that accessions of wild species are needed in genebanks more to provide documented material for breeding and research than for purposes of conservation. The Workshop recommends more studies on the genetic diversity of wild material in genebanks to better determine how many accessions really need to be kept.

Participants outlined that the maintenance of wild species is difficult in a genebank setting. To minimize problems it was recommended:

- that the IBGRD be used to identify duplicate samples held in different genebanks.
- that genebanks preserving wild species keep up-to-date information on the viability of accessions, and
- that genebanks reverify taxonomic determinations at each regeneration to prevent contamination.

The Workshop recommends the following for collecting wild species:

- *H. spontaneum*: to collect for useful traits and in under-represented areas;

- secondary and tertiary genepools: representative diversity based on ecological-geographical distribution. A pilot strategy should be developed after one model species is selected;

- need for urgent collection in situations of significant genetic erosion.

The Workshop recommends more research to study the genetic control of traits in wild species.

Participants expressed their concern about the constant reduction of pre-breeding activities and called for more support to these activities. It was stressed that non-traditional sources of funding should be sought.

The barley core collection

The Workshop endorsed the development of a barley core collection as initiated by the ECP/GR Barley Working Group. It recommends its world-wide continuation and expansion with continued IBPGR support. The first international barley core collection should be identified within three years. Participants called for financial support in order to secure the multiplication of the selected accessions (ca. 2000) and subsequent distribution to participating genebanks. Identified specific subsets of the barley core collection should be widely promoted and publicized. Some of the participants were concerned that procedures in selecting and multiplying accessions of the core do not fully respect genetic diversity and asked that due attention be paid to this.

Genetic stocks

The Workshop agrees that genebanks should accept the responsibility for preserving genetic stocks when their descriptions have been published.

Appropriate structures within the International Barley Genetic Symposium should be responsible for supplying material and information to the genebanks; those should serve as repositories of both material and information on the genetic stocks.

Participants recommend that the coordinating role of the IBGS be maintained and strengthened.

An International Database for Barley Genetic Stocks

The proposal of an international database for genes and genetic stocks of barley compiled by a group of scientists and described by S. Bjarnason (refer Appendix III) was fully endorsed by the Workshop which emphasized that such database should be developed in close association with IBGRD and that the stocks must be identified to the allele level.

Participants fully agree that the database should be compiled, utilizing, among others, already existing databases, e.g. that on barley gene loci al Carlsberg, that on barley powdery mildew

resistance genes (alleles) at Cambridge and Risö, and those on mutant genes and translocation lines at the Nordic Gene Bank and Svalöf.

It was recognized that many practical and technical problems have to be solved including the commitments of the coordinators for barley genes/genetic stocks and other barley scientists, as well as technical and financial issues arising during the implementation of the database.

The Workshop calls upon the Nordic barley geneticists and the Nordic Gene Bank to proceed in developing this proposal.

Mission statement

A motion to accept the recommendations was moved and seconded by Profs. Fischbeck and von Bothmer and carried unanimously.

Participants decided to establish a Coordinating Committee with the following mission:

i) implement the recommendations of the Workshop

ii) seek funding for activities of the International Barley Genetic Resources Network beyond the commitments made by the participating institutes;

iii) nominate additional members to the Coordinating Committee (in between plenary network meetings);

iv) convene the next plenary meeting planned in five years.

The members of the Coordinating Committee were nominated on the basis of geographical representation: two members from North America, two members from Europe, two members from West Asia and North Africa, two from Asia and the Pacific and one from South America.

The following people were nominated:

Chairman:	
A.A. Jaradat	College of Agriculture, JUST, Jordan
B. Fraleigh	Plant Gene Resources of Canada, Canada
J.D. Franckowiak	Department of Crop & Weed Sciences, USA
K. Hammer	Institut für Pflanzenggenetik und Kulturpflanzenforschung, Germany
J.H. Jorgensen	Riso National Laboratory, Denmark
T. Konishi	Institute of Genetic Resources, Japan

M.C. MacKay	Australian Winter Cereals Collection, Australia
J. Valkoun	ICARDA, Syria

The representative from South America has still to be identified.

These recommendations will take effect subject to ratification according to national circumstances. IBPGR agreed to assume the secretariat of the Coordinating Committee. The term of office will be until the next Network meeting. The Workshop agreed that the Coordinating Committee should eventually become self-sustaining. However, IBPGR agreed to support the first meeting(s) as far as possible.

Presentation of the barley genetic resources network to the 6th International Barley Genetics Symposium

A Workshop on Barley Genetic Resources, organized by IBPGR, met during the period 20-21 July 1991 and made the following recommendations:

1. Revise the IBPGR Barley Descriptor list.
2. Develop an "International Barley Genetic Resources Database".
3. Develop regional base collections and a global base collection for safety duplication.
4. Study genetic diversity of wild material in genebanks and use the IBGRD to determine how many accessions are maintained, and identify needs for further collecting.
5. Develop a "Barley Core Collection" as indicated by the ECP/GR BCC Working Group.
6. Request that Genebanks accept responsibility for the preservation of genetic stocks.
7. Form an "International Barley Genetic Resources Network. Nine members of a Coordinating Committee were nominated on the basis of geographical representation and IBPGR agreed to act as the secretariat of the Coordinating Committee.

The Coordinating Committee of the International Barley Genetic Resources Network (IBGRN) expresses its willingness to collaborate and interact with all the structures of the IBGS and its participants. It emphasizes that its activities will be to the benefit of barley breeders and other scientists. Therefore, the Coordinating Committee, on behalf of its participating members, calls upon the IBGS to formally endorse and support the objectives of the International Barley Genetic Resources Network.

The following resolution was fully endorsed by the participants of the IBGS:

The 6th IBGS recognizes the formation of an International Barley Genetic Resources Network with the overall objectives of:

A. Maintaining more efficiently barley germplasm held in collections.

B. Making this germplasm and its related data more easily available to all interested users.

C. Enhancing the use of the diversity existing in collections.

D. Opening new avenues for collaborative research.

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APPENDIX II **AGENDA**

Saturday, 20 July

1. Opening addresses (Prof. R. von Bothmer and Dr. S. Blixt)

2. Implementation of international crop genetic resources networks: the IBPGR's point of view (Mr. P.M. Perret)

3. Previous achievements (Dr. J. Helms Jörgensen)

   a. presentation of the ECP/GR Barley Working Group

   b. recommendations of the International Barley Working Session and overview on progress

4. Adoption of Agenda

5. A revised IBPGR descriptor list (Prof. J. Franckowiak)
   Discussion leaders: A.H.D. Brown and T. Konishi

6. An international barley documentation system (Drs. H. Knüpffer and M. Perry)
   Discussion leaders: S. Blixt and G. Arias

7. Base and active collections (Dr. B. Fraleigh)
   Discussion leaders: M.C. MacKay and J. Valkoun

8. Wild species (Prof. R. von Bothmer)
   Discussion leaders: B. Fraleigh and A.A. Jaradat

9. Barley core collection (Dr. Th. van Hintum)
   Discussion leader: J. Franckowiak

Sunday, 21 July

10. Genetic stocks (Prof. J. Franckowiak)
    Discussion leaders: J. Helms Jörgensen and R.T. Ramage

11. Other objectives of an International Barley network
    Discussion leaders: B. Harvey and R. von Bothmer

    a. an international database for genes (Drs. U. Lundqvist and S. Bjarnason)

    b. enhancement of use of barley germplasm (J. Valkoun)

    c. research projects: (J. Valkoun)

i) RFLP
ii) genetic diversity

12. Other matters

13. The global barley genetic resources network
Discussion leaders: J. Helms Jörgensen and P.M. Perret

a. review of recommendations (items 5 to 12 of the Agenda)

b. commitments and funding needs for the implementation of the network

APPENDIX III INTRODUCTION PAPERS

IMPLEMENTATION OF INTERNATIONAL CROP GENETIC RESOURCES NETWORKS: THE IBPGR POINT OF VIEW

P.M. Perret

As a tool for improving the global status of crop genetic resources, IBPGR is proposing the implementation of genetic resources networks based on the concept of the crop genepool. Indeed the crop and its genepool is the building block which allows to bring together specialists from different fields and to agree on a collaborative action plan.

The network is conceived as a partnership in learning and problem solving. Its activities are not only based on exchange of information about methodologies and results and on the scientific consultation in planning, but it also includes the sharing of material and data and defined commitments for all partners of the network and also the acceptance of special duties/responsibilities by the partners which are in the best position to provide services, bringing benefits to all participants of the network.

Crop genetic resources networks are the most adequate approach for better exchange of information between participants. A crop network allows first to establish the necessary inventory of all existing accessions of the specific crop around the world with the help of one or more institutes acting as international databases, then to collate or at least make more easily available, all type of data which are required by different groups, such as the managers of barley collections or the breeders or any other group of researchers.

A better status of the documentation of genetic resources of a crop may not be sufficient to encourage the use of genetic diversity present in crop collections. Potentially useful characters have to be transferred into a favourable genotype. Crop networks create an ideal basis and structure to stimulate collaborative activites for the enhancement of the germplasm from wide-crosses to pre-breeding. The core collection is certainly one of the most attractive concept to be pursued by crop networks, firstly the establishment of core collections on a regional or international basis is more meaningful than on a collection's basis, secondly it implies better focusing and sharing of evaluation efforts and thirdly it stimulates the collaborative research for a better understanding of the genetic diversity. Another important advantage of core collections is that it improves the usefulness and applicability of basic research (e.g. RFLP or other studies) by providing different researchers all over the world with the same material for their studies.

Finally crop networks favour the building of a crop strategy for a global and integrated conservation approach. A global conservation approach means that we should aim at considering all widespread collections of a crop all over the world as one crop world collection in which the different collections managers share commitments and responsibilities for the maintenance, in order to avoid unnecessary and costly duplication of effort and also to ensure the safety duplication of all original material. An integrated conservation approach means that, for each genepool, an optimal combination

of different conservation methods, i.e. *ex situ* in cold storages, in field genebanks and in vitro and in situ conservation is looked for, as well as the most appropriate management techniques for each of these methods.

To conclude, crop networks lead to the strengthening of collaboration between national genetic resources programmes, to more systematic and coordinated efforts for the collections of the disappearing germplasm, to an increase of the safety duplication of the existing material and its more efficient maintenance and to better availability of existing data related to the material. We are also concerned that such collaboration at the crop genepool level can open new avenues for collaborative research to solve bottlenecks and to enhance the use of the diversity existing in genebanks.

This is why, since the end of 1988, IBPGR has started a programme to catalyse the creation of crop genetic resources networks. Until now, three such networks catalysed by IBPGR are fully operational. *Beta* under the actual coordination of the Institute of Crop Science and Plant Breeding, Braunschweig, Germany, *Musa* under the coordination of the INIBAP, rice for the Asian region under the coordination of IRRI. Two more networks are becoming operational: okra and sweet potato for Asia and the Pacific regions. Activities and work are going on to create more of them, like cassava, coconut, maize and groundnut.

The structure and plan of operations of each crop genetic resources will, obviously, depend on the status and specificities of each crop genepool. It will be the task of the participants of this Workshop to decide on the activities and priorities as well as on the structure of a barley genetic resources network, assuming, of course, that they first agree on the usefulness to create such a network for barley genetic resources. IBPGR is not seeking a coordinating role in the barley network, but rather believes that such coordination should be endorsed by a Steering Committee elected by all the participants. Of course IBPGR is ready to provide logistical support and, in very special occasions, even financial support to the activities of this network as far as this will be possible. IBPGR is ready to be actively involved or associated with the development of the strategies of this network; as an international organization which has for mandate to foster genetic resources activities around the world, it can provide with some expertise and good advice.

PREVIOUS ACHIEVEMENTS

J. Helms Jorgensen, Riso National Laboratory, Roskilde. Denmark

The ECP/GR Barley programme 1980-1991

1. Introduction

The situation in Europe as to genebanks of agricultural crop plants can be described essentially by the single workd "heterogeneous". In 1982 it was reported that 61 institutes in 26 countries possessed a total of about 80,000 barley accessions (cf IBPGR 1983). Some collections were at private or public plant breeding institutions, some at universities and botanical gardens, others at "real" genebanks, and some were "working" collections serving specific research purposes. The documentation of these collection varied tremendously: a portion was computerized and extensive, but the rest was for the most part limited and manual. Only a few of the collections were described in the literature and the germplasm was thus not generally accessible to research and plant breeding, except locally. In the 1960s and 1970s it was realized that this situation was ineffective, and initiatives were taken to remedy it.

2. European Cooperative Programme

The European Cooperative Programme for the Conservation and Exchange of Crop Genetic Resources, abbreviated ECP/GR, was defined by a UNDP/FAO mission in the late 1970s and became operational in 1980. The programme, which since Phase II is coordinated by IBPGR, is financed by UNDP and by the participating countries, which gradually covered an increasingly larger share of the budget. The work was centred around working groups that were formed for six selected crops: *Allium*, barley, forages, oat, *Prunus* and sunflower. The working groups comprised genebank curators and crop specialists from some of the participating countries. Each group was to consider the status of existing collections in Europe, to produce plans of action, and to review the progress throughout the phases of the programme (Phase I: 1980-1981, Phase II: 1983-1986; Phase III: 1986-1989; Phase IV: 1990-1992).

3. ECP/GR Working Group on barley

The WG on barley met for the first time in 1983. The main objectives of the barley programme were 1) to obtain complete, computerized documentation of European collections, 2) to detect replicates and gaps in the collections. 3) to rationalize present collections and future collecting, 4) to promote and effective exchange of germplasm and data. To reach this goal the group focused on the following:

re 1 All collections should complete their documentation on passport, characterization and management data using IBPGR descriptors and a common European Barley Data Base (EBDB) in Gatersleben, Germany, should be established.

re 2 By systematic screening of the EBDB to identify replicates and define the most original one of

the replicates; and to identify geographical areas that were under-represented (gaps) in the collections.

re 3 Each collection could rationalize its collection by maintaining and further evaluating the "original" accessions only, and the "original" should be on deposit in the safety duplication collection.

re 4 An effective, computerized "information flow" system is to be established between collections so that the entire European holdings of seeds and data become easilty accessible to all breeders and scientists.

4. Status per 1991

The goals originally defined are, by and large, reached. The European Barley Data Base (EBDB) has become operative (Knüpffer, 1988. 1989) and progress is made in identifying replicates and gaps. This has been brought about by vast efforts at Gatersleben, supported by efforts at the participating collections in Europe, and by coordination by IBPGR and the WG on barley. The extent of the EBDB may be illustrated by registration of data on 55,369 accessions from 35 collections in 26 countries; the database comprises 52,584 cultivated (*H. vulgare*) and 2,785 wild barley accessions. Among the cultivated barleys 23,418 are cultivars or otherwise named accessions, and 29,166 are collected and unnamed accessions. The EBDB is available on diskettes from Gatersleben (Knüpffer, 1989) which also responds to individual requests (Knüpffer et al, 1987).

Among the many issues discussed in the Barley WG (IBPGR, 1983, 1986, 1989a), one was on the number and identity of descriptors to be included in the EBDB. This was resolved by identifying the primary use of the data. The identification of replicates and gaps in genebanks requires a complete set of relatively few "standard" descriptors comprising mainly passport data. However, most of these descriptors are of limited value for barley breeders and scientists. Therefore, an "information flow" system is being set up. It comprises exchange among the participating genebanks of updated files in which details of descriptors and descriptor states have been used in each collection as well as the total number of accessions observed for each descriptor. The ultimate goal is a yearly exchange of all available data between genebanks. This enables each genebank to provide information to individual users on which genebank possesses material with the traits desired by the user.

5. Conclusion

The activities of the ECP/GR barley programme have been successful and extremely useful for genebank activities in Europe. The establishment of the European Barley Data Base has paved the way for efficiently detecting replicates and gaps in existing collections, and for planning future collecting activities. The information flow system will make all collections and their matching data easily accessible to all potential users in Europe. This has been attained while maintaining the integrity of the cooperating genebanks. Further, a common European safety duplication collection for the "most original" accessions is implemented.

The International Barley Working Session

1. Introduction

The IBPGR programme for implementing international crop networks comprises eight crops: banana, barley, *Beta*, groundnut, rice, medics, okra and sweet potato. An international barley network was discussed at an international barley Working Session at Gatersleben, Germany, in 1989. The Working Session comprised representatives from major barley genebanks in Europe, West Asia, North America and Japan, and aimed at exploring strategies for building up an international barley network. The recommendations from the Working Session are summarized below (for details see IBPGR 1989b).

2. Documentation

The establishment of one (or more) formal international database(s) was considered unrealistic and beyond the financial possibilities of any one institute at present. Therefore, it was agreed that the linkage of 1) the USDA barley collection/Plant Gene Resources of Canada, 2) ICARDA, 3) the Barley Germplasm Center of Japan representing genebanks in Japan, and 4) the European Barley Data Base, into an integrated documentation system was the best approach. These institutes possess data on around 150,000 accessions (of the estimated total of about 270,000 worldwide).

The philosophy for exchanging data at the international level could be the one developed during the establishment of the European Barley Data Base (cf above). Firstly, it comprises a common database established by mutual exchange of databases among the four major genebanks, but it includes only a limited number of descriptors (passport data mainly) that enables curators to identify potential named replicates in the databases and to identify gaps in the collections.

Secondly, lists of characterization/evaluation descriptors which have been applied to their material and the number of accessions observed for each descriptor should be exchanged among the participating genebanks. This enables curators at any one entry-point in the network to identify genebanks possessing accessions evaluated for specific traits and to advise users where to acquire material with the desired traits.

3. Safety duplication collections

It was recommended that curators send small seed samples of their "original" accessions (not "replicates" to a safety duplication collection Nordic Gene Bank for Europe, the Ottawa Gene Bank in Canada, or ICARDA, Syria) from where it may be returned to the originator to substitute a lost accession only.

4. Core collections

There was a general consensus that one of the immediate services to be provided by the international barley data network was the support of the establishment of an international barley core collection for offering to all users a limited set of highly relevant material representing the typical genetic variation that occurs.

The ECP/GR Barley Working Session's proposal to establish a core collection across European barley holdings was endorsed by the WS. This was considered as a pilot project which will explore the methodologies and at the same time provide the first subset of an international barley core collection.

5. An international database for barley genes

The descriptors used to characterize and evaluate barley germplasm relate to the phenotype of the accessions. Data describing the presence or absence of individual genes (alleles) give a much precise description. Therefore, it was recommended that an international database for barley genes (genetic stocks) be established and associated with the international barley documentation system. This also implies that barley research workers deposit stocks possessing newly identified genes in a genebank and include the genebank accession number in their publication(s), and that genebanks accept genetic stocks alongside other germplasm.

6. Conclusion

The linkage of major databases is only a first step on the way to create a truly international documentation system for barley. The ultimate goal is two-fold. One is by utilizing passport data in an international database to: i) rationalize existing collections by identifying replicates, ii) concentrate evaluation, etc. on "original" accessions only, and iii) coordinate future collecting activities to fill gaps in the present collections internationally.

The other goal, which is the ultimate one, is to give users all over the world easy access to the wealth of data present in the genebank databases around the world (supplemented by the data in the scientific literature, and to identify and gain access to seed samples in the genebanks that possess genes for traits desired by the user.

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An International Barley Documentation System Concepts and Strategies

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I. Introduction

The necessity and usefulness of a comprehensive database containing germplasm sample data as a central information source for network activities has been discussed (Perret 1991). These databases are usually assembled through the cooperation of network participants and begin, for the most part, with passport descriptors. In some instances they have been expanded to include data for characterization descriptors. Although a lengthy and somewhat complicated process, the completed data can help to perform many functions including: (1) the determination of the scope of the holdings of participating collections; (2) the identification of duplication of genetic resources and information between collections; (3) the determination of the scope of geographical coverage of the accessions held in the collections, at least on a country level; (4) setting a basis for the safety duplication of material between collections; and (5) setting priorities for future germplasm collecting and collaborative characterization trials.

The development of a global database for barley genetic resources data has been determined to be a priority by the barley genetic resources network (IBPGR 1989). There has been substantial effort put into the development of a cooperative European barley database. The existence of this database and the experience that has been gained through its compilation will undoubtedly assist in the facilitation of a database with global coverage. The purposes of this paper are to present an overview of the relevant experiences that have been gained through the compilation of the European Barley Database (EBDB) as they relate to the development of a global barley database and to outline the planning and progress that has been made towards its compilation as well as to offer suggestions that will make its development realized with fewer difficulties.

II. European barley database - past lessons

The details of the EBDB have been given previously (Knüpffer 1987, 1988, 1989, 1991). The objectives of the project were: (1) to assemble all the IBPGR descriptor list passport and characterization data and to incorporate these data into a computer database; (2) to identify duplicate records and gaps in the geographical representation of germplasm; (3) to rationalize the participating barley collections with the aim of reduction in the waste of resources that may be occurring during storage, multiplication, characterization and evaluation of redundant accessions; (4) to provide additional information to help to plan further collecting; and (5) to facilitate the free and effective exchange of data between genebanks and collaborators.

The establishment of and the resulting database can be summarized as follows. All common passport descriptors known were used as a basis for data compilation. Characterization and evaluation

data were not included. Hardware and software platforms were modified several times during the life of the project (1984-1990) as technology became available. The structure of the database during development was flexible in that additional data fields were added or space provided as data were received. The number of accessions and the ECP institutions that participated in the EBDB have been given (Knüpffer 1989). Relative to the total number of accessions reported by the participating collections (Bettencourt and Konopka 1990), the EBDB contains information for only one-half of the existing European accessions.

The genebank of the former Zentralinstitut für Genetik und Kulturpflanzenforschung (Gatersleben, then East Germany) agreed to host this database. This was due to: the importance of barley in Germany; expected support for the computer technology needed for the task; and the high expected use of the database by barley breeders in Germany.

Constraints encountered during the development of the EBDB have been discussed elsewhere (IBPGR 1986, 1989a, 1989b) and will not be elaborated here. The particular concepts behind the identified constraints and the experiences gained in overcoming them, however, are a valuable source of information for the compilation of the global barley database. Computer hardware and software were, until the completion of the project very suboptimal. The access to appropriate and current computer technology is a prerequisite to the rapid development of a large database. There was a wide variety of storage media in use among collaborators during the development of the EBDB. This created bottlenecks and time delays. These were solved by locating other institutes that had the capability of transferring the data onto compatible media. The number and coding of descriptors varied considerably between institutes. This resulted in the need for transformation into EBDB standard format and a standardization of the descriptor states allowed for some descriptors. Also, in many instances, the definitions of the descriptors received were not clear. Inconsistent and unclear use of *Hordeum* botanical nomenclature was encountered. The lack of infraspecific classification, mainly by institutes that did not have available expertise, was found and some of these problems were managed on a case by case basis.

Very little feedback came from those to whom the EBDB was distributed. There have been requests for: the entire database; specific information, such as where a specific barley cultivar is being held; and for the European Barley List.

Little effort has been put into the maintenance of this database since 1987. Even though several collaborators have sent updates of their data, and another institute joined the network, these data have not been incorporated. The database was moved onto a dBase IV platform and broken down into several smaller files that were then related by common data fields. It was then distributed to about 20 institutions worldwide on request. It was thought, depending on the size of the collection, that updated and/or new records should be sent to the EBDB about every two years.

III. Global cooperation between barley databases

Crop network activities are dependent on a reliable source of information on which to base their activities. Generally, this will take the form of a database, composed of least accession specific passport data records held by all collaborating institutes. The 1989 International Barley Working Session recommended that an "integrated documentation system" be formed between the databases

of the United States Department of Agriculture, Plant Gene Resources of Canada, ICARDA, the Barley Germplasm Center of Japan and the EBDB (IBPGR 1989b). This documentation system was thought to be the best approach towards the formation of one or more international barley databases. Furthermore, the meeting considered it unrealistic for any single institute to host a single, comprehensive global barley database.

The facilitation and operation of the documentation system was thought to be dependent on several aspects of cooperation between these institutes. First, each of the institutes would be responsible for trying to locate and enter passport data that is considered absent (gap-filling). Second, people from the USA and Canadian collections would cooperatively assess the duplication within and between their databases and eventually compile a joint database that would be made available to the other collaborators. Third each of the other institutes would attempt to identify duplicate records and accessions within their collections. Forth, each institute would attempt to determine the major duplication that they may have with any of the other collaborators. Fifth, that a consultation be held among the institutes to develop a format for data exchange. Sixth, each major database would supply to all the others a copy of the data in two files. One of these will contain the complete database and the other a list of only the accessions considered original. Characterization and evaluation data were not a priority, but during the present workshop, the descriptors that may be appropriate for this should be discussed. Additional institutes that hold collections could then be asked to participate in a similar manner.

1. Overview of participating collections

The initial intention of developing a documentation system was to determine the feasibility of creating a "loose" database of the majority of barley accession passport records. About 148,000 accession records are maintained by the USA (26,782), Canada (35,500), ICARDA (18,000), Japan (12,000), and the EBDB contains records for over 55,000 accessions represented in European germplasm collections. The total world holdings for *Hordeum* is estimated to be about 270,000. Since the 1989 Workshop, additional collections have asked to become involved with the initial phase of this project. Australia (8,000 accessions) and the wheat genebank at CIMMYT (6,500 accessions) have both asked to take part in this initial phase of the project. It is well known that several other important barley germplasm collections exist. In Brazil (EMBRAPA) and in Ethiopia (PGRC/E) collections of 20,000 and 13,000 accessions are maintained respectively, about 5,500 accessions of the latter have been incorporated in the EBDB. VIR, St Petersburg (Russia), at the third meeting of the ECP/GR Barley Working Group, indicated that it was interested in participating in an international barley network. Some or all of the data on the approximately 25,000 accessions from this collection has been sent to the EBDB host institute.

Contact with the five institutes that were initially thought to participate has shown encouraging results. The USA and Canada have agreed to work together on the filling of gaps in their respective data records and to determine duplication within and between their databases. ICARDA has provided information on the holdings of its collection and can identify some duplication with other collections. Collaborators at the collections in Japan are also willing to participate. CIMMYT has also expressed willingness to work with ICARDA on the identification of duplication between the collections and to provide data for use by other interested parties. The Australian Winter Cereals Collection has expressed willingness to compile the data records from the existing Australian collections and will

provide this to other collaborators.

2. Discussion on the intended plan of action

The overall success of the development of a barley documentation system will depend on the cooperation of the major collections, communication between them and the organizational capabilities of the network to keep the activities proceeding. After collections have, in general, accessed the need and performed some gap filling of their records, the development of a standard data exchange format should be adopted. It has been suggested that the format given by Knüpffer (1989) be used as a starting point and that all collections should try to fill the gaps for this information, as a priority. If possible, the standardization of descriptor states should be attempted to the greatest extent possible. Again, it is useful to consider the standardization that was done by the EBDB exercise and to inform participants of these values in the event that coding of their data has not taken place. It will then be possible for the collections themselves to provide translation of the descriptor states that they use to the others to whom the data is sent. Eventually, a common format for the documentation system should be determined. The lengths and type of the fields can be modified if not applicable. It is also reasonable that all data is exchanged on a common medium and if possible, in a common format. All data should be exchanged with a comprehensive data dictionary that explains, in detail, the definitions of each of the descriptors used, if these are not used as given in an agreed upon standard, such as the IBPGR Barley Descriptor List. Statistical summaries of each of the databases should be sent when these are exchanged among the collaborators. These summaries should provide details on the extent of missing data, a listing of the unique states that a descriptor has and a thesaurus of proper names for local names and varietal descriptors.

3. Ideas for the facilitation of the concept and its future

Methodologies for identification of accession duplication that each collection may use should be defined and further elaborated. This exercise has also been performed by many national collections and when compiling other central crop databases. The techniques and tools that have been used (cf Knüpffer 1988) should be further developed and their methodologies and manner of use disseminated to all collections. It is realized that other techniques will be developed that may be applicable to a single database, the algorithm for these should be provided to all collections.

The idea of an initial network of databases for barley is logical. With almost 300,000 accessions maintained worldwide, it is not reasonable to ask one institution to coordinate the compilation of a single database. However, with extensive duplication identified within and among the larger collections, it will become appropriate for a single institute to assume the position of a database host in the future. The host should: (1) preferably be a "centre of excellence" with regard to barley; (2) be willing to provide a long-term continuous effort towards the compilation, distribution and querying of the database in response to questions from all collaborators and other potential users; and (3) be willing to commit computer time and facilities towards its implementation and maintenance. It may be necessary to commit full-time expertise towards this job. Many of the activities of the host should probably be included in the regular budget of this institute (Perret 1991). For costs that the host is not expected to cover, such as travel to relevant meetings and the acquisition of computer hardware and software, external funding may be necessary.

The type of database management system (DBMS) that should be employed for the single database should be determined before the construction of it begins. It is recommended that a completely relational structure be employed to reduce redundancy and the size of the final database. Even though several personal computer based software packages are commonly available and relatively standard as an exchange format most of these are not truly relational. The most common is of the dBASE type (originally marketed by Ashton-Tate). Eventually this standard is expected to shift to a fully relational one, especially for larger databases. Foresight should be used in this respect by assessing the relative size of the database when first constructed and the size it will possibly grow into when additional descriptors are added. Here another constraint of dBase-compatible DBMS should be mentioned, i.e. the fixed-field format which consumes a lot of space if the database contains many character string type fields.

Besides exchange of data between the initial collaborating institutes, it is necessary to consider the appropriate media to use for the distribution and exchange of the completed database. Technically, there are now many possibilities. These include: traditional forms of magnetic media (i.e. tapes and diskettes); optical disks (CD-ROM); printed media; and on-line access. Dissemination via magnetic media will probably continue to be the most widely used. Distribution on diskettes is to be encouraged due to the limited access of some collaborators to tape drives. Optical media are becoming more widely used, especially write-once-read-many types. Since the completed database will be large, this medium is particularly useful in this respect. The acceptance and extent of use of this medium should help to determine if it will be useful for distributing the database. On-line access may be an alternative but it will continue to be expensive and useful only to those that have access to the network that it exists on. Printed media will continue to be used even when providing information to some technically advanced institutes. It is widely applicable for simple queries that do not generate extensive listings as output. The final decision as to which type(s) of media will be used will be based on applicability to the intended users and the overall cost. This aspect should be examined closely at the appropriate time.

Regular updates of the database are dependent on the collaborating institutions. Some collections will not have extensive changes made to their individual databases or their collections for several years. Others will change extensively in a very short time. This aspect of information flow should be determined by the network participants with all of them aware of the need to keep the database current. Participants should not be directed to send data in at regular intervals, especially if significant changes have not been made.

It is recommended, at an early stage, that a directory of all barley collections be produced. This directory could complement that produced by Bettencourt and Konopka (1990) by including additional details about the barley collections' data processing capabilities. This should include: the hardware and software used; formats and media that can be used for data exchange; descriptors and structure of the database.

The information network and eventually the resulting database have a number of potential uses. Time and resources can be saved through the mutual agreement on which institute will be responsible for maintenance and rejuvenation of material and how germplasm should be duplicated. The identification of duplicate records in the resulting single database could assist with additional gap filling and/or error correction. The global identification of duplication will assist with constructing

a realistic picture of the state of the world's barley holdings. Determining the gaps in and variability within the geographical and/or taxonomic parameters of the world collection can be used to plan future collecting and/or *in situ* conservation measures. The database should provide barley breeders and others interested in the crop with fast access to information regarding the holdings of collections and barley samples from specific geographical areas or with certain characteristics.

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PRESENTATION OF THE EXISTING SYSTEM OF BARLEY BASE COLLECTIONS

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The most recent Annual Report of the International Board for Plant Genetic Resources (IBPGR, 1990a) cited five designated barley base collections: global collections at Plant Gene Resources of Canada (Ottawa, Canada) and at ICARDA (Aleppo, Syria), and regional collections for Europe at the Nordic Gene Bank Fund (Lund, Sweden), for Africa at the Plant Genetic Resources Centre / Ethiopia (Addis Ababa, Ethiopia) and for Asia at the National Institute of Agrobiological Resources (Tsukuba, Japan). The author is grateful to IBPGR for allowing him to consult documents specifying the conditions of designation. No active collections were designated on the world level. There is certainly a fair degree of conscious and unconscious duplication among the designated base collections and relative to other national and regional collections.

Plant Gene Resources of Canada (PGRC) collection

The designation of PGRC to maintain a global base collection of barley was based upon an exchange of letters between Agriculture Canada and IBPGR during 1981. The following commitments were made:

(a) that the collection will continue to receive adequate operating funds and personnel and that if, at some future time, this is not possible, FAO/IBPGR will be alerted promptly;

(b) that if the material stored is not available from an active collection, it will be made freely available from the base collection to any professionally qualified institution or individual seriously interested in using it;

(c) that material will be accepted for storage on a global basis;

(d) that appropriate arrangements will be made (if necessary with suitable institutes) for regeneration of the material; and

(e) that arrangements will be made to duplicate the material for safety (preferably in another IBPGR designated genebank).

The PGRC barley collection now contains 36, 192 accessions, as described in the table on the next page. Thirty-eight identified species are represented. The "CN" and "PGR" collections are base and holding collections respectively. "CHC" is the Canadian-Scandinavian *Hordeum* Collection, consisting mostly of accessions of wild species maintained by Agriculture Canada and Danish and Swedish agricultural universities. "IDC" is the international duplicate collection of samples provided by IBPGR seed handling units. Ninety percent of the United States barley collection ("USDA") is

duplicated at PGRC. No other genebank sent duplicate samples to Ottawa.

In mid-term storage at PGRC, seed is kept in paper envelopes at +4°C and 20% R.H. Under these conditions the seed dries out to 6-8% moisture content. Dry seed is then sealed in laminated paper/foil/poly-ethylene envelopes. These are stored at -20°C in long-term conditions.

An inventory providing passport and agronomic information on 7, 000 mostly cultivated barley accessions was published by R. Loiselle (1985). The CHC collection was described by Baum et al. (1984). PGRC's germplasm database is presently being upgraded using fourth-generation language relational database management software; until the new system is implemented, information about the barley collection will be available upon written request in hard copy or computerized formats.

Because no active barley collections were designated, PGRC has distributed small seed samples on request and arranged for regeneration to the extent possible. Genebank staff regenerated seed of 3, 948 accessions. Other Canadian breeders and scientists helped to regenerate seed, for example in 1983-84 the University of Saskatchewan grew out 2, 286 accessions. Part of each of these was sent to the Nordic Gene Bank in 1984-85 for safety duplication.

ICARDA collection

ICARDA accepted designation as a global base collection in 1988 making much the same commitments as Canada, and in addition long-term seed storage was specified. As of October 1990, ICARDA's barley germplasm collection totalled 18, 671 accessions, of which 6, 113 were identified as originating from the West Asia - North Africa ICARDA core region (ICARDA, 1991).

In long-term storage, seeds are dried to 6% moisture content and stored at -21°C in laminated aluminum foil packets. The new medium-term storage units are maintained at 0°C and 25% R.H.; seed is kept in cotton bags (ICARDA, 1991). Unrestricted access has been provided to germplasm samples. Barley gemplasm catalogues gave passport and evaluation data on 12, 129 entries (Somaroo et al., 1986; Somaroo et al., 1988).

Regional designated collections

The IBPGR Directory of Cereals Germplasm Collections (IBPGR, 1990 b) is a good source of information on most barley collections. According to this publication, the Plant Genetic Resources Centre in Ethiopia (PGRC/E) preserves 12, 648 barley accessions. In 1981, PGRC/E "accepted in principle" designation as a regional base collection for Ethiopia and East Africa, and contributed information on 5, 335 barley samples to the European Barley Data Base (Knüpffer, 1987). Seed with 5-7% moisture content is stored in aluminum laminated foil packets for the long-term at -10°C. For medium-term storage, seeds are kept in aluminum packets at +4°C and 35% R.H.

The National Institute of Agrobiological Resources (NIAR) in Tsukuba, Japan accepted designation for an Asian regional base collection in 1985. It preserves 6, 242 *Hordeum* accessions, mostly *H. vulgare* (IBPGR, 1990b). Moseman and Smith (1985) reported that seeds with 6-7% moisture content

were stored in vacuum sealed cans at -10°C for long-term storage and at -1°C and 35% R.H. in screwlid cans for medium-term storage. T. Konishi (IBPGR, 1989b) noted that the Okayama University barley collection consisting of 6, 202 samples is duplicated at the NIAR under long-term storage conditions. A catalogue describing 4, 023 samples of the Okayama collection was published by Takahashi (1983).

The Nordic Gene Bank was proposed for designation as a regional base collection of barley genetic resources, but no document was signed. IBPGR (1990b) reported 14, 100 total accessions preserved at Alnarp, Sweden in long-term storage at -20°C and duplicated in permafrost at Svalbard, Norway. A catalogue was published in 1989 (Nordic Gene Bank, 1989).

European Cooperative Programme for the Conservation and Exchange of Crop Genetic Resources and other national collections

The second edition of the European Barley List (Knüpffer, 1987) lists 55, 369 accessions from 34 genebanks in 25 countries participating in the ECP/GR and from the Ethiopian genebank. Whereas the above designations were base collections, the ECP/GR has essentially established a network of active collections.

Barley accessions preserved in the United States were described by Franckowiak (IBPGR, 1989a). The National Small Grains Collection presently consists of 26, 174 accessions representing 23 *Hordeum* species (Bockelman, 1990). Seed is also stored in the backup collection at the National Seed Storage Laboratory at Fort Collins, Colorado. Samples are freely available to all *bona fide* scientists around the world.

Barley collections preserved in other countries were described in the IBPGR Directory (1990b): Afghanistan, Algeria, Argentina, Australia, Bolivia, Brazil, Colombia, India, Iran, Iraq, Mexico, Nigeria, Pakistan, South Africa, Syria, Tunisia, U.S.S.R. and Yemen. Moseman and Smith (1985) reported that "working collections" of barley germplasm were maintained in the U.S.S.R. and in Brazil. The People's Republic of China also preserves an important collection of barley germplasm.

The time may have come for the barley genetic resources community to build upon the network of previously designated base collections, connecting them to an expanded worldwide network of active collections designated following the European model.

Plant Gene Resources of Canada
Barley database

Number of accessions by species and by collection

--------- Species					Collection ----------		
Hordeum	CN	PGR	CHC	IDC	USDA		Total
1. *agriocrithon*	0	2	1	0	1	=	4
2. *arizonicum*	0	1	5	0	0	=	6
3. *bogdanii*	0	1	9	0	9	=	19
4. *brachyantherum*	0	0	79	0	3	=	82
5. *brevisubulatum*	0	1	20	0	3	=	24
6. *bulbosum*	4	10	389	0	95	=	498
7. *caespitosum*	0	0	8	0	0	=	8
8. *californicum*	0	1	25	0	0	=	26
9. *capense*	0	0	1	0	0	=	1
10. *chilense*	0	1	25	0	6	=	32
11. *comosum*	0	3	43	0	0	=	46
12. *cordobense*	0	0	1	0	0	=	1
13. *depressum*	0	2	29	0	0	=	31
14. *distichon*	599	309	0	27	0	=	935
15. *euclaston*	0	0	12	0	0	=	12
16. *flexuosum*	0	0	12	0	0	=	12
17. *geniculatum*	0	0	59	0	0	=	59
18. *glaucum*	0	0	24	0	0	=	24
19. *intercedens*	0	0	17	0	0	=	17
20. *jubatum*	0	3	76	0	22	=	101
21. *lechleri*	0	0	59	0	0	=	59
22. *leporinum*	2	0	453	0	0	=	455
23. *magellanicum*	0	0	13	0	0	=	13
24. *marinum*	0	4	6	0	17	=	27
25. *murinum*	2	3	7	0	54	=	66
26. *mustersii*	0	0	1	0	0	=	1
27. *muticum*	0	2	4	0	2	=	8
28. *parodii*	0	0	69	0	0	=	69
29. *patagonicum*	0	0	55	0	0	=	55
30. *procerum*	0	3	6	0	2	=	11
31. *pubiflorum*	0	0	73	0	0	=	73
32. *pusillum*	0	10	15	0	9	=	34
33. *pyramidatum*	1	0	0	0	0	=	1
34. *roshevitzii*	0	0	0	0	1	=	1
35. *secalinum*	0	0	0	0	2	=	2
36. *sp.*	1	186	0	0	9,826	=	10,013
37. *spontaneum*	3	8	112	40	1,342	=	1,505
38. *stenostachys*	0	6	35	0	9	=	50
39. *violaceum*	0	2	0	0	0	=	2
40. *vulgare*	7,545	1,296	714	93	12,147	=	21,795
41. *x*	0	1	0	0	13	=	14
Total:	8,157	1,855	2,457	160	23,563	=	36,192

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THE GENE POOL OF BARLEY AND PRESERVATION OF WILD SPECIES OF HORDEUM

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The genus *Hordeum*, distribution and the gene pools of barley

The very diverse genus *Hordeum* is distributed in most temperate areas of the world (Fig. 1). It comprises ca. 32 species which are di- and polyploid and represent a vast amplitude of variation, for example, with different life forms, and different modes of reproduction. Many of the wild species also contain interesting and valuable genes for breeding.

The **primary gene pool** (Fig. 2) of barley comprises: a) breeding lines and varieties; b) landraces, which are still available in some areas; c) the wild progenitor of cultivated barley, ssp. *spontaneum* (C. Koch) Thell. All these forms can easily cross and are hence belonging to the same species, *Hordeum vulgare* L. There are thus no biological hindrance for gene transfer between these forms. The difficulties may be, for example, non-adapted landrace material or, in the case of ssp. *spontaneum*, with "wild" genes, such as britlle rachis and shrunken seeds.

The **secondary genepool** (Fig. 2) of barley comprises the single species, *Hordeum bulbosum* L. which is widely used in barley breeding due to its ability for chromosome elimination. Work with gene transfer is also in progress.

All other species of *Hordeum* belong to the **tertiary genepool** of barley (Fig. 2) and their utilization in breeding is more in the future. However, with increasing efforts on technique development it should also be possible to use these species as gene sources.

The Scandinavian *Hordeum* collection

The Scandinavian *Hordeum* and *Triticeae* collection represents one of the biggest holdings of secondary and tertiary genepools of the cereasl, especially of barley. During the creation of the collection, we have built up a considerable knowledge on the practical aspects of collecting and maintenance of wild and primitive material. Some of the problems concerned with collecting and preservation of wild species will be elucidated here and the examples chosen reflect our own experiences.

The Scandinavian collection of *Triticeae* started 15 years ago. In the beginning it was mostly concentrated on wild species of *Hordeum* but in later years it also included landraces and primitive material of the cereal crops as well as wild species of other genera. We have had the privilege to collect in most areas where wild *Triticeae* species occur. The collection now comprises ca. 6000 accessions and around half of that number constituted of *Hordeum*.

The material in our list fills several purposes:

- it is the basis of our own scientific work in different fields;
- it is the basis for screening, testing and work with agronomic potentials;
- it is the basis for an *ex situ* gene bank collection with multiplication and distribution of material.

Problems in handling of wild species

Collecting

When considering the total number of accessions collected of barley secondary and tertiary gene pools many species seem to be well-collected. However, the available collections are usually from certain areas and do not cover the whole area of distribution or all ecogeographical conditions of a particular species. When comparing the total distribution area of a species, as revealed for example through studies of herbarium material and floras, and compare this with the distribution of the actual collected accessions one gets a first impression of the necessity to collect in certain areas. An example is *Hordeum bogdanii* Wil. with a total distribution in Central Asia. It is well-collected in Western China and Northern Pakistan, but no collections have been made in other areas (Fig. 3).

What is urgently needed for the gene pools of all major crops are studies of genetic diversity as reflected in an ecogeographical pattern. For most species of *Hordeum*, no or very few information is available if the collected material really represents the amplitude of variation found in a species. It may be so that too many accessions from certain areas or of a particular species have been multiplied and preserved in the collection.

Multiplication and handling of accessions

For many reasons the practical seed handling is a matter of great difficulty. It is a labour intensive and thus costly, which all gene bank curators know. The experiences obtained in handling of the Scandinavian *Hordeum* collection can be summarized as follows:

- due to the reproductive and dispersal mechanisms of wild species contaminations and inpurities are difficult to avoid;

- annuals, such as *H. marinum* Huds. and *H. murinum* L., are easy to multiply, due to long-lived seeds which germinate easily and give abundant number of seeds;

- the self-incompatible, perennial species, viz. *H. bulbosum* and *H. brevisubulatum* (Trin.) Link, are difficult to multiply due to short-lived seeds and special precautions in multiplication;

- some South American perennials, such as *H. chilense* Roem. et Schult., *H. comosum* Presl, and *H. parodii* Covas are difficult to multiply due to low germinability and comparatively short-lived seeds;

- material possible to handle with machinery, such as landraces, is easy to multiply (*H. vulgare*).

Wild *Hordeums* in other gene banks

In a questionnaire sent to most of the world genebanks keeping barley and *Hordeum* species information about the holdings was requested. Regarding the actual number of accessions in the genebanks the available material is summarized in Fig. 2.

Of the primary genepool, i.e. material which can be classifiied as spp. *spontaneum* or wild forms of *H. vulgare*, is represented by ca 16,100 accessions. The majority of these collections (ca. 13,900 in Plant Breeding International, Cambridge, UK) represent single seed descents from individual plants from a very low number of populations from Israel. Most other collections of spp. *spontaneum* were made in specific areas and the gene bank collections do not represent the entire distribution area.

Of the secondary genepool, i.e. *H. bulbosum*, ca 1000 accessions are present in the world holdings, and

of the tertiary genepool, ca 3,200 accessions. Of the latter category, more than 95 % is kept by the Scandinavian Collection or Agriculture Canada. One big difficulty for the evaluation of the number of accessions present in gene banks is the high number of duplications.

Some of the obvious difficulties in using gene bank material for research or breeding can be summarized as follows:

There is often restricted information on duplicates among gene banks. It is often very difficult to judge whether an accession is original or not since passport data is often incomplete. Research material for certain purposes, often obtained from other holdings, has been deposited in the local gene bank. There is at present a mess as to the background of most material in many gene banks. Some restrictions and tougher criteria for material to be deposited in gene bank collections should be adopted.

The degree of wrong determinations, contaminations through pollen and seed and unknown accessions, usually without any adequate passport data in the world holdings, is surprisingly high.

In the questionnaire sent to the gene banks the curators were also requested to give their own v c the particular difficulties in handling wild species. The answers were surprisingly uniform and can be summarized as follows:

there are very high resources requirements for regeneration, multiplication and distribution of material;

the maintenance of the genetic integrity of a given accession is very difficult due to contamination;

current taxonomic name changes and generic redefinitions make the practical work very complicated.

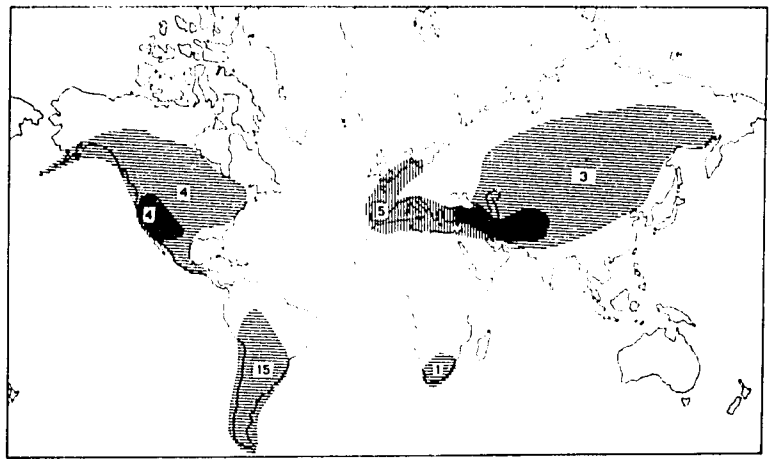

Fig. 1. Distribution of the genus *Hordeum*. The number of native species is given for each area. Only the areas where the species occur naturally are included.

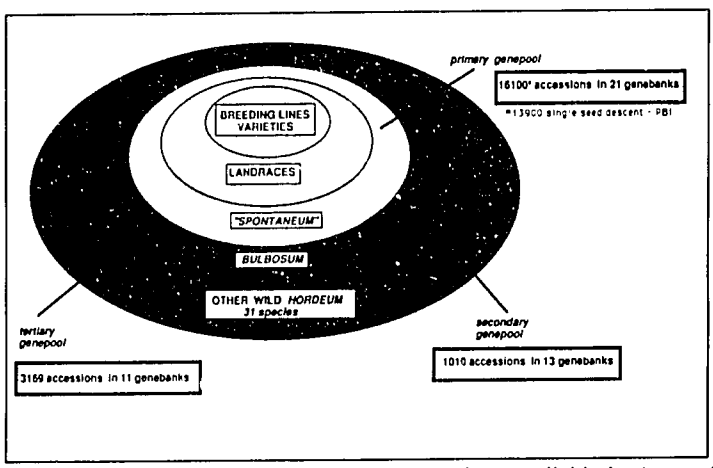

Fig. 2. The genepools of barley and approx. number of accessions available in the world gene banks.

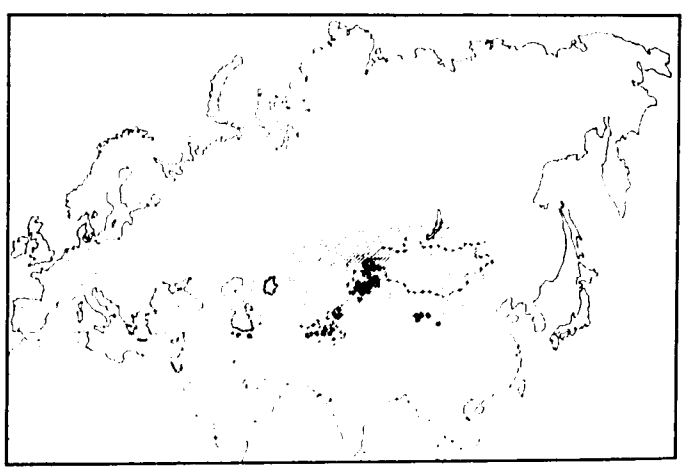

Fig. 3. Total distribution of *Hordeum bogdanii* (hatched area). The dots indicate collected accessions. In total 90 accessions are present in the Scandinavian collection, of these 29 have been multiplied, 1 has completely lost germinability and 11 accessions are duplicates obtained form other holdings and not to be multiplied.

ORGANIZATIONAL ASPECTS OF THE BARLEY CORE COLLECTION

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Much of the information in this paper originates from the last report of the BCC Working Group (Bothmer et al. 1990).

Introduction

During the third meeting of the Working Group on Barley of the European Cooperative Programme for the Conservation and Exchange of Crop Genetic Resources (ECP/GR) in April 1989 a subgroup was set up to study the possibilities of applying the core collection concept to the European barley holding (IBPGR 1989a). This initiative, that was strongly endorsed by the International Barley Working Session as a pilot for an international Barley Core Collection (IBPGR 1989b), resulted after three working sessions in a report prepared as a basis for discussion at the Sixth International Barley Genetics Symposium (Bothmer *et al* 1990).

During the first generation of genetic resources conservation, which was characterized by extensive collecting, exchanging and storing of germplasm, many collections, and especially those of small selfing grains, have become very large, and many of them are still expanding. Often they are too large to be optimally accessible. To improve the accessibility the concept of core collections has been developed (Frankel & Brown 1984): a core collection 'represents with a minimum of repetitiveness, the genetic diversity of a crop and its relatives.' (Fig.1) Core collections will not replace existing collections, but make them more accessible; an accession in a core collection represents accessions in reserve collections (Brown 1989). Such a core collection has two major advantages:

- Thanks to its limited size, it can be more comprehensively documented than an ordinary germplasm collection, thus allowing for a more effective choice of material for utilization.

- Thanks to its well defined structure, a core collection allows for optimization of the genetic diversity within material selected for utilization.

Genetic diversity can be considered as having a hierarchical structure, allowing for the distinction of non-overlapping groups, or strata. Within a genus genetic diversity can be divided in taxa on the basis of biosystematical research. Within taxa further stratification can be accomplished, like in the case of the Barley Core Collection where the first criterium for differentiation within *Hordeum vulgare* was the level of domestication: cultivars vs. landraces. The cultivars were further divided in phylogenetic groups, in turn divided on the basis of relatedness, year of release, etc. Within the category of landraces eco/geographical data were considered more important for differentiation. (Fig.2)

Complementary to this 'top to bottom' approach, stratification can also be accomplished on the basis of morphological, biochemical, molecular genetical or other data with a genetic basis. In this 'bottom up' approach multivariate classification techniques have to be used (Cross 1990; Peeters & Martinelli 1989).

Following the scientific exercise of stratification the number of accessions to be sampled from each group e.g. a group dark seeded landraces from the Syrian Steppe (Weltzien 1989), has to be determined. One way of doing that is by attributing a relative importance to each group. This reflect the objectives of the core collection. With this information the number of accessions to be sampled from existing collections or *in situ* can be determined for each group, resulting in a core collection.

Concepts of the Barley Core Collection

To avoid confusion with respect to the terms used the Barley Core Collection (BCC) was defined by the Working Group as:

a selected and limited set of accessions, optimally representing the genetic diversity of cultivated barley (*H. vulgare* s.lat.) and wild species of *Hordeum*, and providing well known genetic standards.

The inclusion of genetic standards was an addition to the original concept of Frankel & Brown (1984).

The objectives are:

- to increase the efficiency of evaluation and thus of utilization of existing collections,
- to provide for a manageable and representative selection of the available barley germplasm for use in research and breeding,
- to provide adequate material for the needs of standardization in scientific work with barley.

The BCC is not a part of, or a replacement for existing collections, it only tries to provide a standard set of accessions improving the accessibility of existing collections; each BCC-accession will be considered to represent a group of lines, varieties, landraces, etc. E.g. if a user is looking for a certain trait or combination of traits, the well documented and well studied BCC will lead either to a selection of BCC accessions with the optimal diversity for a preliminary screening, or, if this preliminary screening has already been done somewhere before, it will help in choosing the material from the existing germplasm collection for an in depth screening, optimizing the chance of finding the traits in the most suitable genetic background.

It is proposed that where ever possible the accessions in the BCC should be homozygous lines, permitting identical multiplication of the material over generations and locations and avoiding genetic change due to natural selection or random drift.

Organization of the Barley Core Collection

In the establishment of the BCC three phases were distinguished: a first phase for the development and presentation of the concepts, a second phase for the establishment of the collection and the organizational structure, and a third phase where the BCC should be operational.

The first phase is nearly finished. After the first drafts for the concepts were made, selected experts were consulted. Their comments were worked into the report to be presented at the Sixth International Barley Genetics Symposium for amendment and agreement (Bothmer *et al* 1990). After this meeting the individual accessions will be selected in consultation with the appropriate experts.

The second phase for the establishment of the collection and the organizational structure will take at least another three years. Each BCC accession has to be located and requested from an existing collection and where applicable multiplied starting from one kernel. Available passport data will have to be compiled in a central database. An organizational structure will have to be set up, the institutions prepared and able to perform tasks in the third phase have to be identified and an infrastructure for exchange seeds and information has to be set up.

Once the BCC is operational in the third phase, three types of collections will be distinguished :

- Base collection, for long-term safety storage and reference. The seed in the base collection is only used

if all samples in the active collections are lost or if there are problems concerning the authenticity of the material in the active collections.

Security duplication collections, in long-term safety storage, become only active in case of loss of the base collection.

Active collections with seeds for distribution to the users and for multiplication.

The active BCC collections will be located in places with established expertise in barley, such as Institut ur Genetik und Kulturpflanzenforschung Gatersleben or ICARDA. In the longer term, the objective will e to achieve worldwide coverage through the active collection centers. Defined subsets of the BCC may lso be kept and distributed by other institutions.

Following these physical collections the following basic tasks can be distinguished :

Multiplication and rejuvenation.

Due to the workload, multiplication of the BCC will have to be a collaborative activity, probably coordinated by the active collection centers. The workload caused by the cultivars and landraces is due to the relatively large number of accessions in these categories, where as the workload caused by wild species and genetic stock is due to the many complications during multiplication. This relatively small group needs to be handled by specialists.

Seed handling.

Seed handling includes cleaning, checking, packing, and distributing the BCC samples to the active collections.

Seed distribution.

Clearly a task of the institutions handling the active collections. Distribution of the seed should be accompanied by good book keeping.

Documentation.

The documentation of the BCC will comprise of passport data, evaluation data and literature references. Passport information should be compiled during the creation of the BCC, the remaining information will be compiled on the basis of feedback from users. The availability of all information to all users has to be ensured. One center should have a coordinating task in bringing all information together and distributing it to the other centers, who, in turn, supply new information to the coordinating center. The centers maintaining physical BCC's should be part of this information network.

Maintenance of the reference material.

Herbarium, spike and seed collections should be available for quick reference. Such dead collections can be maintained by the institutions holding the base or an active collection. A reference seed collection will have to be maintained by the institutes involved in the seedhandling.

Coordination.

The coordination of the activities should be done by a coordinating committee meeting on a regular basis. This BCC Coordinating Committee could be closely allied to either the ECP/GR Barley Working Group or the world barley network. Topics like the effectiveness and eventual expansion of

the BCC should be discussed by this group.

Financial inputs

The basis of the BCC is the free availability of seed and information. Many of the tasks mentioned previously can be inputs in kind from the contributing institutes, given the mutual interest in the project. Even though, some financial inputs will be needed, e.g. for meetings of the coordinating committee, or publication of a 'catalogue'. Sources for these limited inputs will have to be located.

Conclusion

The BCC Working Group has worked out an applicable concept for the establishment of an international Barley Core Collection, which could

- increase the accessibility of existing barley germplasm collections,
- stimulate barley research via standardization and increased knowledge of the basic material,
- act as a model for second generation germplasm management.

The efforts necessary for the establishment of a BCC are considerable, but via task sharing within a framework like the ECP/GR Barley Working Group or an International Barley Germplasm Network this could be a uniting project. These frameworks could also act as a source or mediator for the funding which will be necessary.

Recommendations from this International Workshop on Barley Genetic Resources supporting the ideas presented here would help in the establishment of the Barley Core Collection. Commitments for cooperation in setting up and running a Barley Core Collection are indispensable.

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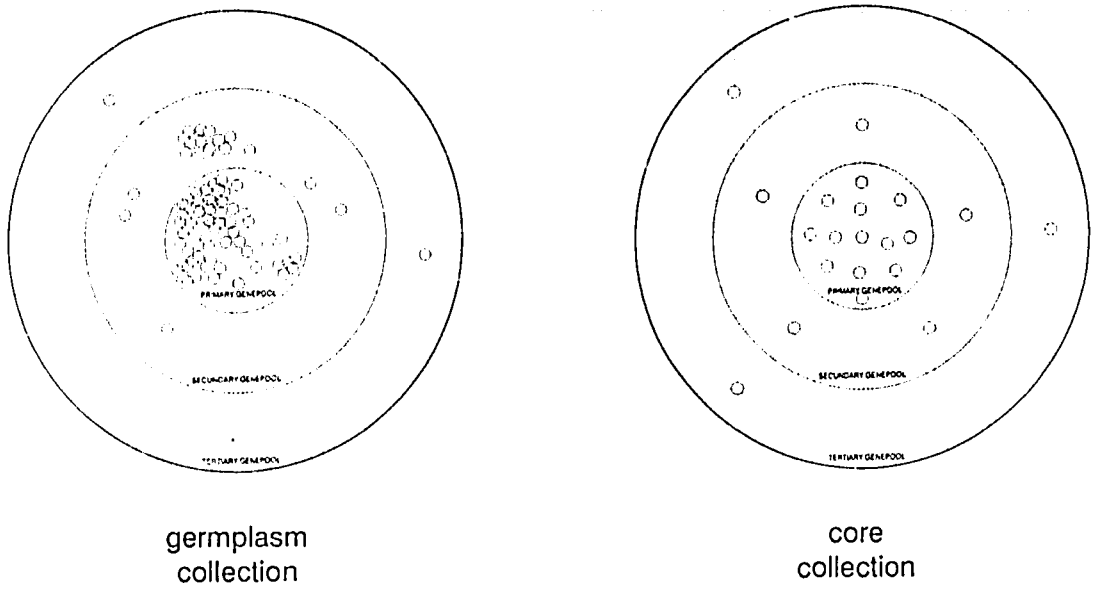

Fig. 1. Genetic diversity in an ordinary germplasm collection with 85 accessions (left) and in a core collection with 21 accessions (right).

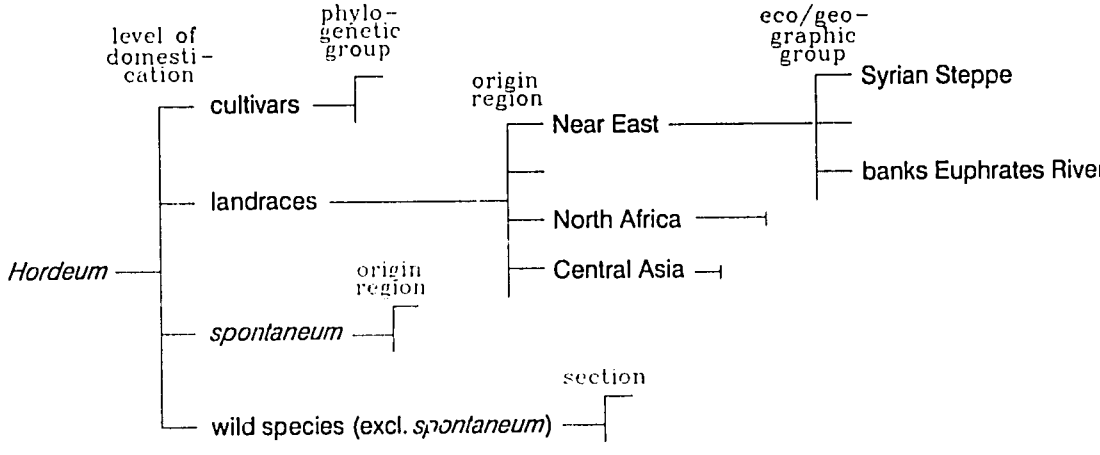

Fig. 2. Simplified part of the 'barley genetic diversity tree'.

DATABASE FOR BARLEY GENES
I
THE INTERNATIONAL BARLEY GENE NETWORK

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This survey is presenting some items about the construction of the international barley gene network and the importance of the genetic diversity for plant genetic resources.

Being an important crop world-wide, barley is under intensive studies both genetically, taxonomically and from evolutionary points of view. Large collections have been brought together all over the world and with a high degree of duplication amongst them. Thus, several meetings have discussed the introduction of the core concept in barley in a network approach for conservation and utilization of genetic resources.

The international network of barley gene investigations is organized as follows:

Already at the First International Barley Genetics Symposium the need for an international barley genetics newsletter and the need for coordinators for genetic stocks, chromosomes and linkage groups were discussed. During the second Symposium in 1969, it was decided that a Barley Genetics News Letter should be published yearly. The News Letter was asked to publish reports of the genetic marker stock lists and new information from linkage studies of the different chromosomes. Also a complete up-dated linkage map of the genetic markers and the translocation breakage points should be published in every issue.

Coordinators for the main stock center at Fort Collins, for special gene collections, for the seven chromosomes, and for various chromosomal variations were appointed. An Overall Chairman for the Chromosome/Linkage Groups and Collections is serving the different coordinators and arranging the reports for publishing in Barley Genetics Newsletter. Both the Overall Chairman and the different coordinators are appointed by the International Committee of the Barley Genetics Symposium. It was and is still the coordinators' duty and responsibility to maintain current information concerning their area and to serve as sources of information. Annual reports are published in the Barley Genetics Newsletter. The coordinators are also asked to maintain seed stocks for the different areas where they have carried out research, and in case of referring to current literature, the original author is obliged to keep the seed stock available for every barley researcher.

Concerning the nomenclature and the gene symbols in barley two systems of symbols are in use. The classical genes on the map are designated with one- or two-letter symbols based on descriptions in English language. Large groups of polymeric genes containing many allelic members each have been identified with the aid of induced mutants. For these, three-letter symbols based on Latin with an additional letter or number designating the locus are preferred. The latter system adheres more closely to the rules recommended by the International Committee on Genetic Symbols and Nomenclature in observing the preference of higher internationality and the recommended symbolization of genes having phenotypically similar affects. In order to establish the identity of loci in the two systems, it is necessary to make allelic tests; only after that a revision and standardization of the gene symbols is possible.

For assigning gene symbols an Overall Coordinator together with different coordinators are assigning a symbol according to the character after description of the mutant or gene and after the obtained genetic data. To-day the Overall Coordinator for the Nomenclature and the Gene Symbols is not the same person as the Overall Chairman for the Chromosome/Linkage Groups and Collections. The coordinators are asked to follow the rules which are recommended by the International Committee for assigning gene symbols and published in the first issues of Barley Genetics Newsletter and in Barley Genetics IV.

By a call to all barley coordinators of to-day at the end of March 1991, the following information was

tried to be inquired:

[1] Are most of the yearly coordinators' reports in Barley Genetics Newsletter based on literature studies or based on own research work?

[2] Are the reported results and descriptions available on magnetic media, and which systems have been used?

[3] Are the materials which are reported on, still available in own collections, gene banks or the Main Stock Center?

The result of this call was pretty good; unhappily there was no response from the Main Stock Center, and there was no reaction from any of the molecular gene coordinators.
The reports are based both on literature studies and own research, depending, if the coordinator is able to do some research in the subject. Most of the results are kept on magnetic media, either on word-processing documents or databases. There are some exceptions by the older coordinators which have their results written by hand in their field-books. Many of the stocks are available either in the places they have been investigated, in national gene banks or at the Main Stock Center. But many of the very old genes reported on are missing. This statement is made by many barley researchers. Unhappily, a complete collection's register with different stock source places does not exist.

As an example of the large diversity that exists in barley, the large Swedish collection of mutants with its about 10.000 different accessions, which are incorporated in the Nordic Gene Bank, will be discussed here. This collection is the result of a sixty years intensive research in barley in Scandinavia and consists of a large number of different types of mutants induced by different types of mutagenic treatments. The genetic analyses of these mutants have added to our understanding of the mutation process and the genetic architecture of the different characters.

It is possible to divide this large diversity into 10 different mutant categories with altogether 94 different subtypes of mutants. About half the total number of mutants have been studied genetically in more or less deepgoing details, but these mutants form only a minor part of the range of different mutant types.

In the following survey the different categories are described; and some examples will be given for each category.

A. Mutants with changes in the spike and spikelets;
dense and lax spikes, six-row and intermedium types, calcaroides, *bracteatum*, lemmalike glumes etc. Totally 24 subtypes.

B. Mutants with changes in culm length and culm composition;
e.g., short and long culm, dwarfs, densinodosum, uniculme, giant plant, etc. Totally 15 subtypes.

C. Mutants with changes in growth type;
e.g., rapid growth, prostate type, viviparoides, etc. Totally 5 subtypes.

D. Physiological mutants;
e.g., early heading, late maturity, *eceriferum*, rich wax coating. Totally 4 subtypes.

E. Mutants with changes in awns;
e.g., short awns, smooth awns, etc. Totally 8 subtypes.

F. Mutants with changes in seed size and shape;
e.g., globe-shaped grains, size of the seeds, semi-naked caryopsis etc. Totally 5 subtypes.

G. Mutants with changes in leaf blades;
e.g., narrow, broad, curled leaf blades etc. Totally 14 subtypes.

H. Mutants with changes in the anthocyanin and colour;
e.g., anthocyanin-less, necroticans etc. Totally 18 subtypes.

I. Mutants resistant to barley powdery mildew;

J. Translocation lines.

In this survey some characters may be picked out to demonstrate the different numbers of genes that can be involved in the specific character.

	Number of	
Mutant group	Mutants	Loci
Praematurum (early heading)	172	9
Erectoides (dense spike)	205	26
Breviaristatum (short awns)	140	17
Eceriferum (waxless)	1580	79
Intermedium (intermedium spike)	103	11
Hexastichon (six-row)	41	1
Macrolepis (lemmalike glumes)	40	1
Bracteatum (third outer glume)	28	4
Calcaroides (partially hooded)	18	4
Mildew resistance	77	several
Exrubrum (anthocyanin-less)	about 500	about 27

Several of the mutants mentioned above have been tested against the genetic marker stocks collected at the Barley Stock Center in Fort Collins, USA. Generally allelism has been the outcome.

The induction of mutant genes is undoubtedly an important tool to contribute to the pool of genetic diversity. It is of importance to coordinate the different collections to make them usefully available for barley researchers and plant breeders. No doubt the collections of barley mutants with their well defined origins of mutant genes will form a major input for future gene mapping, and will be immensely valuable for molecular genetical analyses of cloned mutant genes.

DATABASE FOR BARLEY GENES
II

A PROPOSAL FOR AN INTERNATIONAL DATABASE FOR BARLEY GENES AND GENETIC STOCKS

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OBJECTIVE

The objective of the proposed International Database on Barley Genes and genetic stocks (IDBG) is to provide the international research community with reliable information about the known barley genes, the genetic stocks possessing these genes and the literature describing them. The database may be extended by adding linkage data etc and thus form the basis for constructing objective linkage maps for the seven barley chromosomes.

STRATEGY

In view of:

- the main objective given above,
- the organization of the international network of barley genetics coordinators, and
- the fact that for compilation, revision and distribution of the database some experience in the exchange of computerized data and in relational database management is required,

the following strategy is proposed:

- The database should be a cooperative venture between
  - the overall coordinator for barley genes, who is appointed by the International Barley Genetics Symposium, and
  - an information officer in a genebank or institute participiating in the proposed International Barley Genetic Resources Network.
- The database should be based on the nomenclature used in the Barley Genetics Newsletter (BGN).
- The database should be compiled using the published information made available by the barley genetics coordinators. Databases available elsewhere should be included whenever possible.
- The database should use the IBM family of Personal Computers running MS/PC-DOS.
- The database should be integrated with the proposed International Barley Documentation System.
- The database should be updated and revised using the annual reports of the barley genetics coordinators in the BGN. A report on the status of the database should be given in every volume of the BGN.
- New versions of the database should be distributed annually to institutes participating in the Global Barley Genetic Resources Network. It should be made available upon request to users by these institutes and the central institute.

STRUCTURE OF THE DATABASE

The database should be a relational database. A relational database includes data tables containing items with the same type of information. The items are arranged in the rows of the table (the records) with the units of information (descriptors) in the columns (the fields).

The main tables to be included in IDBG are described below. Figure 1 shows how the tables can be organized into a relational database.

The Gene table

In this table, genes and cytological markers, are the items. For each gene there is one record. The fields contain the information specific to each gene such as:

- the valid locus symbol
- the chromosome number or the plasmid name
- short description of the effect
- unstructured text (a memo field)

The Allele table

Here, the different alleles at each locus are the items. The fields contain information about the mode of inheritance (recessive, co- or semi-dominant, dominant etc), and other information related to the allele.

The Effect table

An allele may have other effects in addition to its main effects. These are important for the users of the database so one table is included for the genes and all the effects. This table has one record for each gene/effect combination. The information is coded to make sorting easier.

The Synonym table

This table contains only two fields, one for the valid gene designation and one for a synonym. For each gene there are as many records as there are synonyms.

The Stock table

In this table the identification and description of the genetic stocks is found. Among other things it contains:

- A code for the holder of the stock (the genebank)
- The unique number which identifies the stock within the collection
- The number identifying the stock in the proposed International Barley Documentation System when this becomes operational.

By including the last field above, the database can be integrated into the International Barley Documentation System and related to databases kept by the holders of the stocks. In these databases, additional information about the stocks can be found. Some characteristics which are useful for the users of IDBG should be transferred from these databases and also stored and distributed with IDBG. Information about structural rearrangement of chromosomes and other cytological characters is essential for example. The method used to develop the stock (mutation, cross(es)) is also an important descriptor. For mutants, information about both the variety or line from which the mutant originates, and the mutagen applied, is desirable.

The Reference table

The reference table includes the references to the genes and the stocks. It includes the name of the author and other bibliographical information.

The Institute table

Here, the full name of the genebank holding the stock is included together with the address, the communications links (phone, telefax, Email) and the name of the curator.

One additional table is included in Figure 1. The purpose of this table is to establish a relationship between the other tables. By using this structure, the complexity of the information is accounted for so that

- any one stock and/or gene is described in many references;
- one reference describes many stocks and/or genes;
- one gene is available in many stocks;
- one stock has multiple markers.

DISTRIBUTION

Two possible methods of distribution are:

1) Distribution as ASCII files. The format should follow the recommendations for the exchange of data issued by IBPGR. This means that the institute receiving the database has to use a relational DataBase Management System (DBMS). Those institutes using the same DBMS as the institute holding the database can receive the data directly as a copy of the database files.

2) Distribution of database files together with a compiled application for managing the information in the database (sorting, searching and printing, but not editing).

If people who are not experienced information officers are to use the database, then the latter method is to be preferred.

IMPLEMENTATION: TIMETABLE AND PERSONNEL REQUIREMENTS

The following timetable is proposed:

1992 Preparatory work

- Choosing a genebank/institute to compile the database
- Identifying sources of finance
- Other preparatory work, such as making agreements with institutes and participants etc.

1993-1994 Compilation of the database

The database will be compiled from the reports of the barley coordinators, as they are published in the BGN. Many of these are available on magnetic media.

During this phase, I estimate that the overall coordinator and the information officer, or people delegated by them, will need to devote 50% to 75% of their time to the project. However, if already existing databases on barley genes are made available to the project, the work load on the information officer can be reduced. Many comprehensive databases already exist, such as databases for

- barley genes and chromosomes, at the Carlsberg Laboratory in Denmark
- genes for reaction to mildew, at the Riso National Laboratory in Denmark
- mildew resistance genes in European barley varieties, at the Cambridge Laboratory in UK and the Riso National Laboratory in Denmark
- the barley mutant collection at the Nordic Gene Bank

Development of software for data retrieval requires some months of work by an information officer who is an experienced programmer.

from 1995 Revision, maintenance and distribution of the database.

In this phase, the database will be revised by using the annual reports of the barley coordinators. These reports (and any other new data) should be sent to the overall coordinator, preferably on magnetic media. After revising the database, the new version will distributed to the institutes in the barley network.

By this stage, the overall coordinator and the information officer, or people delegated by them, will need to devote 25% to 50% of their time to the project.

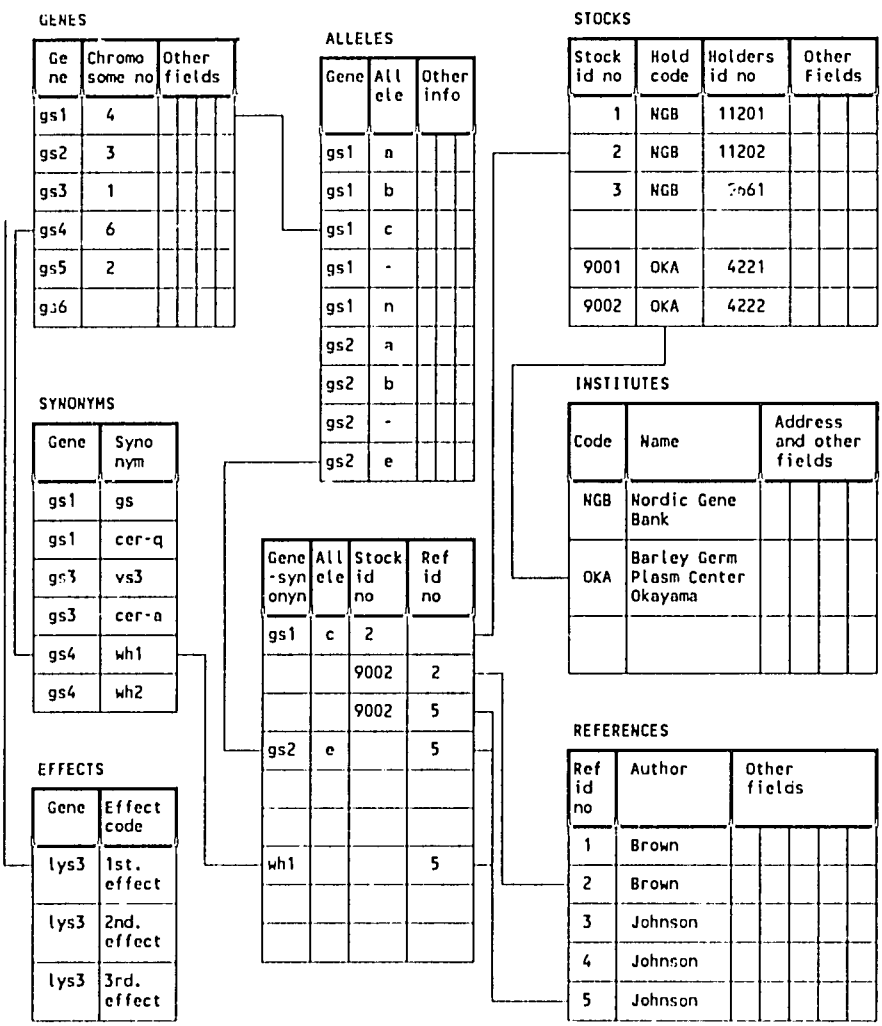

Figure 1. Structure of the proposed International Database for Barley Genes.

Enhancement of use of barley germplasm

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As with in other crops, the use of barley collections by breeders and other users is considered unsatisfactory because of the different constraints on both the user and curator. In the present paper an attempt is made to identify the major limitations to the use of barley germplasm held in gene bank collections and indicate a role that a collaborative network could play in enhancement of the utilization of the barley germplasm. Finally, ICARDA's contribution to this effort is outlined.

The constraints to germplasm use can be defined as follows:

A. User side

1. Lack of interest since sufficient diversity is believed to exist in improved germplasm breeder's working collections,

2. Little knowledge of useful genetic diversity in germplasm collections,

3. Heterogeneity of wild species and landrace populations,

4. Difficulties associated with utilization of landraces, wild species or exotic germplasm in conventional breeding programs.

B. Germplasm curator side

1. Lack of relevant germplasm in the collection,

2 Incomplete passport information,

3. Lack of evaluation data,

4. Insufficient interaction with the users.

A collaborative network might be a means to address most of these issues. In its strategy the breeder's needs should be identified and the future demands anticipated, taking into account shifts in breeding objectives (sustainable agriculture, ecological concerns, biodiversity) and methodology (biotechnology).

It is generally agreed that the major bottleneck in the use of gene bank materials is the lack of evaluation data. Thousands of barley germplasm accessions conserved in cold stores have never been properly evaluated. Evaluation is costly and site-dependent, but structuring germplasm collections by their geographical origin, selecting "core" collections, which represent the total diversity, and evaluating germplasm in collaborative projects developed by the network may improve the present situation.

To assess the actual potential of the germplasm, the evaluation should be conducted in adequate environments, done with breeders participation, when possible, in the country or region of origin. The data would be shared among the network participants and published in germplasm catalogs for the world-wide user community. In addition, a data base of evaluation data would be developed and distributed upon request.

Evaluation of heterogeneous accessions, such as wild species and landraces, may pose a problem. In that case, lines derived from single plants can be produced and evaluated for specific traits, e.g. disease resistance.

Although it is recognized that characterization of germplasm according to standard international descriptors and preliminary evaluation is the responsibility of gene banks and germplasm curators, it is highly desirable that breeders and scientists are directly involved in the detailed "in-depth" evaluation, possibly as network participants.

Development of elite lines from wild and primitive forms or unadapted germplasm through collaborative germplasm enhancement programs would greatly facilitate utilization of this "exotic" germplasm in the conventional barley breeding.

It is believed that in a developing-country region like West Asia and North Africa (WANA), a regional network for collaboration in genetic resources activities may better serve the needs of the national agricultural research systems (NARS) than global crop networks and it could be complementary to the current crop network system.

In recognition of the urgent need to enhance the use of barley germplasm collections, ICARDA is ready to participate in the global effort through the international barley crop network. However, because of its mandate, the Center is also strongly involved in the regional genetic resources activities in WANA. In fact, there is no contradiction between the two spheres of interest, since the global and regional function are complementary.

In response to the constraints listed above, ICARDA wishes to adhere to the following specific guidelines for enhancement of the use of barley germplasm with particular reference to WANA region:

A.1. Focus on demands of users from WANA region,

A.2. Evaluate barley germplasm for resistance to stresses in the WANA region for adaptation to the region,

A.3. Develop homogeneous lines from populations of WANA origin,

A.4. Conduct germplasm enhancement activities,

B.1. Serve as both an active and base collection for germplasm originating from WANA. In cooperation with NARS, organize joint collection missions to underexplored areas or sites of special interest in WANA,

B.2. Develop and maintain a database of passport information on barley germplasm of WANA origin,

B.3. Compile catalogs with characterization and evaluation data on all barley germplasm held in the Genetic Resources Unit of ICARDA,

B.4. Enhance interaction with NARS in WANA through a joint IBPGR/ICARDA-coordinated regional genetic resources network.

In conclusion, it should be emphasized that the international collaboration organized through a network system is intended to be an efficient way of enhancing the use of barley germplasm collections.