IPGRI

# Report of a Working Group on Barley

Fifth meeting - 10-12 July 1997 - Alterode/Gatersleben, Germany

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ECP/GR

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

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of the Consultative
Group on International
Agricultural Research
(CGIAR)

The International Plant Genetic Resources Institute (IPGRI) is an autonomous international scientific organization, supported by the Consultative Group on International Agricultural Research (CGIAR). IPGRI's mandate is to advance the conservation and use of genetic diversity for the well-being of present and future generations. IPGRI's headquarters is based in Rome, Italy, with offices in another 15 countries worldwide. It operates through three programmes: (1) the Plant Genetic Resources Programme, (2) the CGIAR Genetic Resources Support Programme, and (3) the International Network for the Improvement of Banana and Plantain (INIBAP).

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# Part I. Discussions and Recommendations

## Introduction

### Opening and Welcoming address

Professor Konrad Bachmann, acting Head of the Genebank of the Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Gatersleben, welcomed the participants and gave a brief introduction of the history of the institute and its current activities. He emphasized that IPK is located in an area (Magdeburg) in which seed production and plant breeding have a long-standing tradition. The Genebank is an important department of the Institute which has the overarching mandate to develop science and technology as a basis for crop improvement. The Genebank holds close to 98 000 accessions and responds annually to about 20 000 requests (status in 1996). All regeneration activities are carried out by the institute itself (about 10 500 accessions annually, including 1230 accessions of Barley). Recently more emphasis is being placed on the assessment of diversity and the characterization of the collections using molecular techniques. Barley is a model crop for such work, as will be illustrated later during the meeting by the presentation of IPK's new Research Programme 'Plant Genome Resource Centre' focusing on barley.

### Information on ECP/GR

Lorenzo Maggioni, ECP/GR Coordinator, thanked Dr Helmut Knüpffer and Prof. Karl Hammer of IPK for the excellent organization of the meeting. He then welcomed all the participants on behalf of IPGRI. He noted with pleasure the presence of observers from the Vavilov Institute (VIR), Russian Federation, from ASSINSEL and from various German institutes. He mentioned that invitations were sent to Dr Theo van Hintum of CGN (Centre for Genetic Resources, the Netherlands) and Dr Jan Valkoun from ICARDA, who were unable to attend. He added that members from Hungary, Portugal and Turkey had corresponded with IPGRI regarding the present meeting, briefly informing about the status of their national collections and confirming their interest in the outcome of the meeting (a report received from Turkey is included in Part II of the present report).

Since the Group had met for the last time in 1993, before the beginning of the present Phase V of ECP/GR, L. Maggioni illustrated the objectives and the new structure of ECP/GR, defined during the Technical Consultative Committee (TCC) meeting of September 1995 in Nitra, Slovakia. He summarized the activities of ECP/GR during Phase V, with specific reference to the Cereals Network and to the recent workshops of the Documentation and Information Network, held in Budapest, Hungary (October 1996) and in Bonn, Germany (June 1997). In particular, he showed the structure of the European Information Platform on Crop Genetic Resources, prepared in collaboration with CGN, Nordic Gene Bank and ZADI (Centre for Agricultural Documentation and Information, Bonn, Germany) and recently made available by IPGRI on the Internet. He explained that the Platform offers direct access to the on-line ECP/GR Central Crop Databases, including the European Barley Database (EBDB). In view of the Steering Committee meeting of ECP/GR in June 1998 and of a possible new Phase VI of ECP/GR, starting in 1999, L. Maggioni suggested to the Barley Working Group the opportunity to formulate recommendations for its future role as well as for the continuation of ECP/GR.

### The Chair's report

Karl Hammer provided a brief outline of the former meetings of the ECP/GR Barley Working Group, with special reference to the fourth meeting of the Group held in Gatersleben in 1993. The objectives of that meeting had been to review the progress made by the Group during Phase IV of ECP/GR (1989-93) and to formulate a workplan for the next period. Main topics discussed were the accessibility of data to users, the identification of duplicates, safety-duplication of base collections, the inclusion of evaluation data into the EBDB, the use of wild relatives and landraces in breeding programmes, the barley core collection, cooperative evaluation projects, molecular approaches and accelerated multiplication.

### *Implementation of the workplan and recommendations*

- The European Barley Database is the backbone of the work of the Group. Following the recommendations to seek an EBDB coordinator, many efforts were made to obtain the necessary funds for such a position at IPK. These include approaches at the local and national level as well as the submission of a project to the EU genetic resources programme EC 1467/94. Financial support for this position over a limited period has been provided by IPK since the beginning of 1997. This allowed the initation of the updating and upgrading of the EBDB. A prototype of the new version of the EBDB has recently been presented at an ECP/GR-ZADI Training Workshop for Central Crop Database Managers and is accessible via Internet at <**http://www.dainet.de/eccdb/barley/**>. A list of presumably unique accessions will be sent to curators of genebanks in due course.
- The European part of the Barley Core Collection has been created under the coordination of Prof. Fischbeck at the Technical University of Munich. This material has been physically transferred to the IPK Genebank where it is being multiplied and will soon be available for distribution.
- Progress has also been made in the development of mechanisms to extend genetic characterization to the molecular level and to further evaluate the barley collections in national programmes.
- East European genebanks have been given support in several projects. They consider the European Barley Working Group as an important platform for the work with barley germplasm. Passport data (excluding wild barley species) have recently been received from the Vavilov Institute for inclusion in the EBDB.
- Overall the European Barley Working Group made good progress during Phase V of ECP/GR, considering the tremendous amount of accessions and respective data. At the time of the meeting, the database contains data of 72 000 accessions from about 20 European Countries.

K. Hammer asked all the participants, many of whom were attending an ECP/GR meeting for the first time, to briefly introduce themselves.

## The European Barley Database (EBDB)

### Status of the EBDB

Helmut Knüpffer presented the status of the European Barley Database. In March 1997 IPK hired Mr Luis López for six months to assist IPK's genebank in the updating of the European Barley Database. The database managers contacted more than 90 institutions by email, fax or letter, asking for their barley passport data. The address list was received from IPGRI. Until the time of the meeting, contributions from 28 institutions in 22 countries were received, with a total of approximately 80 000 accessions. Data of 37 231 accessions from 12 institutions were already included in the database. For the rest of the data, some clarifications of descriptors definitions or coding schemes were still needed before inclusion. Some participants handed their data over to the EBDB managers during the meeting. It is expected that by September 1997 more than 100 000 accessions will be included. Incoming data sets were subjected to a thorough analysis of the data structure, the coding schemes, and questions were sent to the contributors when necessary. Data were received in various formats (DBF, Excel, ASCII, few on paper), largely via email.

The structure of the new EBDB (field names and descriptor definitions) is based on FAO/IPGRI's *Multicrop Passport Descriptors List*, extended by a few additional passport descriptors found in the data received. For institution acronyms, the INSTCODE.DBF maintained by FAO (J. Serwinski) is taken as the basis.

H. Knüpffer also reported about the previous version of the EBDB which was finalized in 1987, and about its use in identifying duplicates between European collections. Owing to lack of personnel resources in IPK, the EBDB was not updated until the beginning of 1997. By the end of September 1997, when L. López left IPK, the number of accessions included in the EBDB was 88 996, belonging to 29 institutions in 24 countries. Details about the EBDB are given in Part II of this report (see p. 18)."

*The Group thanked IPK for its long-standing commitment to the development of the EBDB as an input in kind to ECP/GR. It also recognized how essential it is that the European database be as complete as possible, in order to be utilized to its full potential. A screening of the collections in Europe, made to identify unique samples or to locate duplicates, is a clear example of where wide coverage and completeness of data is needed. The Group therefore recommended that all members ensure that the passport data from barley collections of their respective countries be sent to the EBDB manager. These should be forwarded no later than 31 October 1997, in electronic format using the agreed descriptors as far as possible.*

*The Group recommends looking into the possibility of hiring a full-time EBDB manager to ensure the continuing development and management of the Barley Database.*

### *EBDB additional recommendation*

*It was agreed that the following tasks, some of which were identified during the fourth meeting of the Group, should be included in the Group's workplan:*

| ***Task*** | ***Task leader*** | ***Time frame*** |
|---|---|---|
| *Request from genebanks, by the end of August 1997, passport data about the national collections, to be included in the EBDB (including data about the breeding institute, environmental descriptors of collecting site, minimum characterization, principal attributes, and location and date of safety-duplicate) (see Appendix I).* | *EBDB manager and all Group Members* | *December 1997* |
| *Coordinate the data verification by national experts.* | *EBDB Manager* | *ongoing* |
| *Identify possible duplicates and unique accessions (in the subset of cultivars bred in Europe), and circulate a report to the Working Group Members.* | *EBDB Manager* | *July 1998* |
| *Request from genebanks, by the end of August 1997, by way of a questionnaire, meta-data about evaluation and characterization.* | *EBDB Manager and all Group Members* | *December 1997* |
| *Establish technical solutions to solve problems of linking evaluation and characterization data to the EBDB.* | *ZADI/EBDB Manager* | *July 1998* |
| *Assist upon request in the drafting of safety-duplication agreements.* | *IPGRI* | *ongoing* |

## Multicrop passport descriptors

L. Maggioni introduced the subject of multicrop descriptors and the background leading to their compilation. As reported by Hazekamp *et al.*[1] the process of developing descriptors at IPGRI over the last 20 years was characterized as constantly evolving. This has led to a situation where some common descriptors are defined in different ways for different crops. A request was then made, by a number of documentation specialists, that IPGRI harmonize the passport descriptors in a multicrop passport list. This would facilitate the documentation management, especially in cases of genebanks dealing with several crops. A Multicrop List was drafted by IPGRI, in collaboration with FAO and presented at the Workshop in Budapest (1996); a revised list was adopted there and a final version was published in the report of the Workshop. The list is intended for use in all future IPGRI crop descriptors and is proposed as a standard format for data exchange. L. Maggioni then reported on the generally favourable acceptance of the *Multicrop Passport Descriptors List* by other ECP/GR Working Groups. The *Prunus* Working Group adopted the list for the European *Prunus* Database and decided to include additional passport and characterization data.[2] The *Brassica* Working Group accepted the list in November 1996, to be used as a standard format for data exchange. The Forages Working Group decided in March 1997 to extend the passport list with a number of additional descriptors, in particular including environmental information. The *Malus/Pyrus* Working Group approved the list and agreed to extend it with two passport descriptors, PLANT USE and PARENTAGE, and together with a number of additional characterization descriptors, to be used for data exchange.

A group on Potato genetic resources, during the coordination meeting of the EC project CT95-34 in February 1997, also decided to consider the use of the *Multicrop Passport Descriptors List* for the definition of descriptors to be included in the European databases on potato varieties and wild species.

L. Maggioni concluded that the trend in Europe is for the general adoption of the Multicrop List, as a whole or with the inclusion of descriptors considered essential to specific crop groups. This tendency is expected to improve the management of plant genetic resources documentation in Europe and to make data exchange faster and easier.

*After a plenary discussion, a small task group met in a separate session and reached the following conclusion with regard to the Multicrop Passport Descriptors List:*

- *The* Multicrop Passport Descriptors List *should be adopted for data exchange.*
- *A reference to genetic stocks is important. This can be added under descriptor 14 'Status of sample', by using a separate state 6.*

*Given the importance of the status 'genetic stock' for several crops, it is proposed that the documentation specialists amend the multicrop list as follows:*

*1. Wild*
*2. Weedy*
*3. Traditional cultivar/Landrace*
*4. Breeder's line*
*5. Advanced cultivar*
*6. Genetic stock*
*0. Unknown*
*99. Other*

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[1] Hazekamp, Th., J. Serwinski and A. Alercia. 1997. Multicrop passport descriptors. Pp. 35-39 *in* Central Crop databases: Tools for Plant Genetic Resources Management (E. Lipman, M.W.M. Jongen, Th.J.L. van Hintum, T. Gass and L. Maggioni, compilers). International Plant Genetic Resources Institute, Rome, Italy/CGN, Wageningen, The Netherlands.

[2] L. Maggioni, A. Zanetto, F. Dosba and T. Gass, compilers. 1997. Report of an extraordinary meeting of the ECP/GR *Prunus* Working Group and the First Coordination meeting of the Project GEN RES 61, 28-30 October 1996, Rome, Italy. Unpublished report, IPGRI Regional Office for Europe.

***The*** **Multicrop Passport Descriptors** ***should include the following additional descriptors:***

- *'Breeding institute' (BREEDINST), following the model proposed by the Working Group on Forages.*
- *'Pedigree' (PEDIGREE) (topic addressed by a subgroup – see below).*
- *The 'Principal attribute' or value of the accession (valid for all crops), for example, 'translocation 6-7', 'mildew-resistant', 'drought-tolerant', 'mutant brachytic', etc.*
- *The location and date at which the safety-duplicate was made.*

***In addition, the Group feels that all records for barley should include the following descriptors:***

- *Barley-specific attributes (basic management tools)*
    - *Row number (2-row; 6-row; other)*
    - *Seasonality (winter or spring type)*
    - *Kernel covering (naked or hulled)*

***The Group approved the above recommendations (see the Barley Passport Descriptors list in Appendix I).***

***A subgroup met to discuss the issue of compiling pedigree information and formulated recommendations. These were adopted by the Group as follows:***

*The Group recognized the importance of pedigree information relating to the documentation of plant genetic resources. The development of pedigree information was seen as an important additional tool complementing the EBDB and the German EVA initiatives (see below) and providing added value in enabling the tracking and identification of lineages, traits and alleles as well as in relation to diversity and structure of the cultivated genepool. It will also be important to include information concerning selection from landraces or local varieties.*

*The Group recognized a number of additional factors that were relevant in considering how pedigree data should be approached.*

*i.* *The problem is not barley-specific but important to the majority of crop species.*
*ii.* *There are two different main notation systems in use and a survey of the different systems and their relative merits should be considered.*
*iii.* *The collation and standardization of pedigree information is a significant undertaking requiring independent coordination in the initial phase and close cooperation with the CCDB managers, with members of other Working Groups and with initiatives such as SINGER (CGIAR) and ISIS (CIMMYT). In addition, it would be desirable to include information about pedigrees collated by previous initiatives (e.g. Arias* et al. *1983, Baum* et al. *1985*[3]*). There is also a database system for wheat pedigrees (S. Martynov, Saratov, Russia, in cooperation with Prague-Ruzyně, Czech Republic).*
*iv.* *A link between the pedigree database for cultivars and the EBDB must be made.*

*The Group recommends the initiation of a small task group representing a range of ECP/GR Working Groups to undertake the following:*

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[3] Arias, G., L. Reiner, A. Penger and A. Mangstl. 1983. Directory of Barley Cultivars and Lines. Ulmer, Stuttgart.

Baum, B.R., L.G. Bailey and B.K. Thompson. 1985. Barley register. Agriculture Canada Publ. No. 1783/B. Biosystematics Research Institute, Ottawa, Ontario, Canada.

- ***Aims***

v. *To collate information on what is available and the notation and structure used. This information could be included in the ECP/GR Platform on the Internet as an interim measure.*

vi. *To evaluate long-term possibilities of creating an ECP/GR-wide unified approach including subroutines/procedures to utilize standardized data to produce pedigree trees and pedigree analysis.*

- ***Mechanism***

vii. *Initiate discussions with IPGRI to contact the Chairs of the ECP/GR Working Groups and CCDB managers, inform them of the initiative and invite participation in this task group.*

viii. *Key specialists in the area of Barley pedigree should also be coopted to help with the tracing and validation of information. A first group of suggested people include:*

*Dr J. Spunar (ARI Kroměříž, Czech Rep.)*
*Dr L. Jestin (INRA, France)*
*Dr J.L. Molina-Cano (IRTA, Spain)*
*Prof. G. Fischbeck (University Munich, Germany)*
*Dr G. Persson (Svalöf Weibull AB, Svalöv, Sweden).*

*M. Ambrose agreed to initiate first steps as outlined above and will endeavour to assemble a task group. The group could communicate via email.*

***Tentative workplan:***

- *Collate information and draft document of findings, options and strategies relating to pedigree data by the end of December 1997.*
- *Develop a discussion document with proposals by the end of May 1998 for presentation to the Steering Committee meeting of 1998.*

*The Group suggests that this initiative could form the basis of a concerted action submission to EC Regulation 1467/94.*

## EU Barley project and opportunities for resubmission

Karl Hammer reported on the outcome of the project proposal on 'Barley database, characterization and evaluation', submitted to the first call for proposals within the framework of EC Regulation 1467/94 which had been coordinated by H. Knüpffer. The project aimed at a coordinated and complementary evaluation of barley accessions for resistance to pathogens important in EU countries; upgrading of the existing European Barley Database with inclusion of missing data sets and of new characterization/evaluation data; identification of duplicates, gaps and unique accessions; and urgent multiplication and characterization.

The project received an overall impression rate C and therefore was unsuccessful. Positive comments were made by the Commission, with respect to the very comprehensive partnership proposed, the detailed coordination plan and the well-thought-out and quantitative details provided. However, the identification of the 'nature of resistance' (which was not part of the proposed project) was considered a research programme incompatible with the requirements of EC regulation 1467/94. Also, novel aspects which conform to the priorities of this EU programme, such as the prospects of improving diversification/product quality, were considered too limited, although the contribution to take better care of the environment by use of fewer pesticides was acknowledged.

The Commission considered the inclusion of funding for non-EU partners in the project as not in accordance with the Regulation and also raised the question of ownership/utilization potential of germplasm in non-EU member states.

In view of a third call for proposals from the EC, expected for the autumn of 1997[4], the Group considered it worthwhile to formulate a new application proposal. Possible interested partners for a new project are H. Knüpffer (IPK-Gatersleben, Germany), R. von Bothmer (Sweden), J. Spunar (Czech Republic), A. Jahoor (Risø, Denmark), U. Walther (BAZ-Aschersleben, Germany), L. Jestin (INRA, France), J.L. Molina-Cano (IRTA, Spain), F. Debre (Slovakia) and C.E. Ciotir (Romania).

*A subgroup of the meeting met to discuss the strategies of a new application for an EU barley project for the third call within the EC regulation 1467/94.*

*The following points were agreed upon:*

- *The new project should be clearly distinct from the previous one. The title should be 'Evaluation and Conservation of Barley Genetic Resources to improve their accessibility to breeders in Europe'. The project duration will be three years.*
- *It will consist of three subgroups:*
  - *i. evaluation for biotic stresses,*
  - *ii. evaluation for abiotic stresses, and*
  - *iii. overall coordination and work related to the development of a European barley information system, such as identification of duplicates, recommendations for responsibility-sharing in conservation, identification of unique accessions, questions of safety-duplication, including links to characterization and evaluation data gathered within the project and from other sources, and establishment of an Internet searchable information system.*

*The group considered that in the evaluation work, emphasis should be given to the international Barley Core Collection, landraces and* Hordeum vulgare *L. subsp.* spontaneum *(C. Koch) Thell. The project should be extended to include partners from all European countries significantly involved in the barley crop.*

*A small group consisting of Helmut Knüpffer (overall coordinator and information system), Ursula Walther (subcoordinator for biotic stresses), Louis Jestin and Mike Ambrose will draft the new project. A subcoordinator for abiotic stresses will have to be identified.*[5]

*H. Knüpffer and U. Walther will prepare the first draft and distribute it by end of July 1997 to the other members of this group and a few other volunteers for comments. The revised draft will then be circulated to potential partners together with a letter asking about their willingness to participate. The potential partners will include all partners of the first application, participants of the Barley Working Group meeting who had expressed their interest, and other possible partners.*

*Patrick Heffer from ASSINSEL offered to inform members of his organization about the project and possibly identify breeding companies willing to contribute to the evaluation work.*[6]

*Improved ways of inclusion of non-EU partners have to be sought. The group recommended to approach ECP/GR for possible co-funding for these partners. Other options to be investigated include the EU programmes INTAS and INCO-Copernicus which support joint projects between EU and non-EU members. Non-EU participants clearly expressed their willingness to participate*

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[4] The Third call for proposals for the Community programme on the conservation, characterization, collection and utilization of genetic resources in agriculture was published on 9 April 1998 (closing date for proposal submission 9 July 1998).

[5] Michele Stanca, Italy, Member of the Barley Working Group, was approached immediately after the meeting and agreed to be subcoordinator for abiotic stresses.

[6] A circular letter distributed by P. Heffer immediately after the Working Group meeting resulted in expression of interest by several breeding firms and research institutes which were subsequently included as evaluation partners in the project.

*in the project, e.g. doing extensive evaluation work, if sufficient funds for their participation can be provided. However, co-financing by ECP/GR would be the most suitable option, since the other EU programmes supporting the cooperation with non-EU countries are research-oriented.*

*The project will conduct one meeting at the beginning. The second meeting will be organized at the same venue as the next ECP/GR meeting, just prior to the meeting. A final meeting will be held some months before the end of the project, in order to finalize findings and results and to define objectives and opportunities for future initiatives.*[7]

# The status of national collections

*(for more detailed information see also Part II, Presented Papers)*

## The Austrian barley collection

Rudolf Schachl reported on the Austrian *ex situ c*ollection, maintained in three genebanks in Vienna, Linz and Rinn. The collection comprises 905 accessions in total (786 spring types, 119 winter types), including 329 accessions of landraces and 576 of cultivars (160 accessions of Austrian-bred cultivars and 166 accessions of German bred-cultivars). The presentation concentrated on landraces, describing their development during the last 150 years, the mechanisms of their spreading and their genetic variability, found to be lower than expected in a gene centre.

## The Bulgarian barley collection

Zapryanka Popova informed on the basic collection of barley in Bulgaria maintained in IPGR-Sadovo, comprising a total of 5120 accessions. There are small collections, mainly selection lines, in the Institute of Barley in Karnobat and in the Agricultural Institute in Plovdiv. A working collection contains 1425 accessions originating basically from Ethiopia. The Gene Bank in Sadovo holds collections in long-term (-18°C) and medium-term (6°C) storage. Evaluation is being carried out.

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[7] The project under the title "Evaluation and Conservation of Barley Genetic Resources to Improve Their Accessibility to Breeders in Europe" was submitted to the European Commission in June 1998. The project coordinator was informed in October 1998 that the project was selected for funding. The project is supposed to start on April 1, 1999.

The project aims at coordinated and complementary evaluation of several hundred to several thousand barley accessions for resistance to various pathogens and pests (fungi, viruses, aphids) and environmental stresses (drought, cold, heavy metals, salinity, etc.), using agreed-upon evaluation methods. Accessions to be evaluated will jointly be selected from the International Barley Core Collection (BCC) as well as from partners' genebanks. The project uses the existing European Barley Database managed by the coordinator (IPK). It will include also existing characterization and evaluation as well as those resulting from the project. Other activities include: identification of duplicates, providing information on gaps and unique accessions; identifying needs for urgent multiplication and characterization; provision of promising material to interested breeders, some of them already participating in the project. Information will be disseminated using Internet and other media. Availability of resistant material from this project with diverse genetical background and accessibility of information should eventually lead to better utilization of existing germplasm in breeding with lower agrochemical inputs.

The 28 project partners include eight genebanks, eleven public research institutes, nine private breeding companies and one non-governmental organization from EU Member States. Up to seven countries not belonging to the EU may join the project with ECP/GR financial support to their participation in annual coordination meetings.

## National collection of winter and spring barley in Croatia

Josip Kovačević presented the barley breeding activities in Croatia, which have a long tradition, starting at the beginning of this century. A Dalmatian barley population had an important role for breeding in Europe, since from it the famous variety of two-row spring barley 'Ragusa' was selected by German breeders in 1929. The Osijek Agricultural Institute maintains collections of 38 varieties and lines of winter barley and 65 varieties and lines of spring barley of Croatian origin. The new buildings of the Osijek Agricultural Institute were completely destroyed during the war; therefore storage facilities are not available and the material is continuously multiplied. The National Programme requires national capacities for collecting, conservation and utilization of local germplasm to be strengthened.

## The barley collection in Cyprus

Andreas Hadjichristodoulou illustrated the considerable progress made in Cyprus in collecting germplasm of local landraces of barley, collecting and evaluating wild barley germplasm, and finally its use in breeding programmes, aimed at developing improved barley cultivars for drylands. The ARI Genebank in Cyprus holds 26 accessions of barley collected in 1978 and 3354 inbred lines (progenies of single spikes collected during regeneration of the 26 accessions). Also landraces, selected in Cyprus for thousands of years, are stored in the genebank. They have recently been evaluated and found very adapted to dry and hot Mediterranean climates.

## The Czech barley collection

Jaroslav Spunar presented the activities in conservation and utilization of barley genetic resources in the Czech Republic, where close collaboration exists between the Agricultural Research Institute Kroměříž, Co. Ltd. which is the main institution involved in barley breeding at the national level, and the Research Institute for Crop Production in Prague which holds the national base collections and coordinates the national plant genetic resources programme. J. Spunar emphasized the value of testing winter barley germplasm in the Czech Republic where temperatures of –12 to –15°C are frequently experienced during winter. He offered to collaborate in regional evaluation trials to which his country could contribute by screening for winter-hardiness and certain disease resistances. From 300 to 500 accessions could be tested annually.

## The French national barley collection

Louis Jestin informed the Group about the way in which the conservation and utilization of barley genetic resources is organized within the French National Programme on Genetic Resources. A collaborative initiative involving national partners from the public and private sectors is being organized around a National Charter for cereals and a National Cereals Database. Currently the national collection includes 78 old landraces, 201 cultivars deleted from the national catalogue, 171 breeder's lines with recognized valuable attributes, and 17 accessions of other material including genetic stocks. L. Jestin expressed France's interest in participating in regional evaluation trials and in a possible re-submission of the EU project.

## The German barley collections at IPK and BAZ

### *IPK*

Karl Hammer gave an overview of the composition of the barley collection of IPK's Genebank. The genebank comprises 12 402 barley accessions, among them 11 470 *Hordeum vulgare* and many wild species. Details of the species composition and the origin of the material were provided, and information about reproduction and storage, characterization and evaluation, documentation, and availability of the material was given. Barley has always been an important crop for IPK, and a detailed review of literature about evaluation, research and other aspects of barley genetic resources of IPK was presented. IPK organized and hosted all ECP/GR Barley Working Group Meetings and some other IBPGR workshops devoted to barley. The European Barley Database and active participation in the development of the International Barley Core Collection are further activities worth mentioning.

### *BAZ*

Lothar Frese presented the Braunschweig Genetic Resources Collection (BGRC), now under the responsibility of the Federal Centre for Breeding Research on Cultivated Plants (BAZ) since July 1996. Currently, the total barley collection amounts to 8892 accessions of which 1294 accessions are temporarily out of collection (material provided by the Ethiopian genebank in the early 1980s with the request to keep safety-duplicates, for which clarification of status is needed). *Hordeum vulgare* L. is the prevalent species with 92% of all material. The collection contains 52, 20 and 16% of landraces, cultivars and breeder's lines respectively. L. Frese provided detailed data on the origin, characterization and evaluation, regeneration status, seed accessibility, availability and quality of accessions. The BAZ genebank cooperates at a national level by participating in the central database PGRDEU developed by ZADI/IGR, and at international level in the EBDB.

## The Israeli barley collection

Abraham Korol informed on the three genebanks conserving barley collections in Israel: Lieberman Germplasm Bank, Institute for Cereal Crops Improvement, Tel Aviv University (8000 *Hordeum spontaneum* lines and 500 *H. vulgare* varieties collected in Israel); Institute of Evolution, University of Haifa (3500 genotypes of *Hordeum spontaneum* from various sources) – in this Institute, studies of genetic diversity are undertaken through RAPD analyses, and the polymorphism of natural populations of *H. spontaneum* through genetic mapping of QTLs for stress tolerance and disease-resistance genes; and the Israeli Gene Bank for agricultural crops, Volcani Center (ARO) – about 700 accessions, including 150 landraces [*H. vulgare* convar. *distichon* (L.) Alef. and *H. vulgare* var. *hexastichon* (L.) Aschers.] and 550 *H. spontaneum*.

## The Lithuanian barley collection

Alge Leistrumaitë indicated that spring barley collections are maintained in three locations: the Lithuanian Institute of Agriculture, Dotnuva (644 accessions), Vilnius University (233 accessions) and the Lithuanian Agricultural University, Kaunas (19 accessions). All accessions are kept in working collections. A recent inventory of the collections showed that there were 12 spring barley varieties of Lithuanian origin. Two old spring barley varieties of Lithuanian origin were lost. Spring barley accessions of Lithuanian origin are kept in long-term seed storage at Nordic Gene Bank for the Lithuanian Institute of Agriculture.

## The Nordic countries barley collection

Jens Weibull gave a brief overview of the barley material available at the Nordic Gene Bank. The number of accessions of cultivated barley, *Hordeum vulgare* subsp. *vulgare* L., amounts to 1634 when excluding duplicated Nordic accessions. About 60% or 985 accessions are of Nordic origin, 16% (262 accessions) have unknown origin and the remaining 24% (387 accessions) are of foreign origin. Two special collections were also mentioned: the barley mutant collection comprising almost 9900 accessions, and the collection of wild *Hordeum* taxa. Additional information was given on recent evaluations/descriptions of particular interest, and on two research projects: a joint Nordic project on development of molecular markers, ended in 1997; and a project of the Cereal Working Group at the Nordic Gene Bank initiated in 1997 to study the processes and problems associated with repatriation of germplasm for which barley was selected as a pilot crop.

### The Romanian barley collection

Claudia Ciotir presented the Romanian barley genetic resources activities which involve three separate national institutes under the coordination of ICCPT Fundulea. All three institutes have active breeding collections which are regularly regenerated. The national base collection is maintained at the Suceava Genebank and includes 1014 accessions of which 180 are of indigenous origin. C. Ciotir expressed Romania's pleasure in being represented in the Working Group and the country's strong interest in collaborating with the other barley programmes in Europe in initiatives such as the EU project.

### The Slovak barley collection

Frantisek Debre explained that the Slovak barley collection is an integral part of the National Programme of 'Conservation of Cultivated Plant Genetic Resources', presently coordinated by RIPP Piešťany. The new genebank, opened at Piešťany in 1996, hosts 1470 accessions of spring and winter barley, fully documented with passport data. Characterization of morphological traits and evaluation for quality and disease resistance is regularly carried out. The most promising accessions are handed over to plant breeders for inclusion in their breeding programmes. The genebank is also developing expertise in molecular techniques, to be applied in the identification of accessions and duplicates, as well as in genetic and diversity studies.

### The Spanish barley core collection

José Luis Molina-Cano reported that the National Germplasm Bank (BNG) at the Centro de Recursos Fitogenéticos (CRF-INIA) in Alcalá de Henares holds a collection of 2000+ barley accessions, mostly landraces collected in Spain. To facilitate the study of the genetic diversity and its use by barley breeders, a core collection was built. The different steps followed in this process were described.

### Other barley collections

Additional information was received from Ireland, Poland, Russia and Turkey.

## Sharing responsibilities for conservation

T. Gass introduced the subject by informing the Group about the discussions that have been held to date within other ECP/GR Working Groups.

The sharing of responsibilities in conserving and making genetic resources available to users has increasingly become an issue in the following context:

- Europe is a large region including over 30 different countries which all have an interest in plant genetic resources
- National Programmes within the region vary widely in their structure, mode of operation and level of development
- Genetic resources programmes are frequently affected by the general reduction in funding to agricultural research
- At the regional level, a high potential exists for the risk of a duplication of efforts as well as for neglecting to conserve and adequately make available genetic resources
- The globalization of economy and agriculture has emphasized further the interdependence of countries with regard to genetic resources.

It is assumed that:

- The long-term conservation is primarily a public sector responsibility

- A restriction of access to the genetic resources conserved in genebanks throughout Europe would seriously impede the efforts of breeders
- The economic constraints facing national programmes call for clear prioritization of genebank activities and the sharing of responsibilities
- ECP/GR is the platform to facilitate the implementation of the Global Plan of Action on Plant Genetic Resources for Food and Agriculture (TCC, Nitra 1995; GPA, Leipzig 1996).[8]

This implies that ECP/GR should move to play a role in formalizing the sharing of responsibilities for the conservation and promotion of the use of crop genetic resources. This could include mechanisms such as the establishment of centralized or decentralized regional collections. The establishment of such collections would need to give appropriate consideration to aspects such as the scope of the collections (species coverage, type of accessions and status of accessions). Each country would need to accept responsibility for accessions of national origin after they have been identified and accepted as primary holdings. Furthermore, the role of the different parties concerned by these collections (the collection holders, the hosts of the safety duplicates, the manager of the Central Crop database and the respective ECP/GR crop Working Group) needs to be clearly defined.

*The Group took note of the recommendations developed by the ECP/GR Working Group on Forages and agreed to establish a task force consisting of J. Weibull (coordinator), F. Debre, Th. van Hintum (to be confirmed), O. Kovaleva, M. Miklis and E. Ciotir, to study the implications of a mechanism*[9] *for the conservation of barley genetic resources in Europe. It was agreed that the task force would circulate a discussion document and a draft action plan by the end of October 1997. A revised document could then be included in the present report in time for publication.*[10] *This document would also be submitted to the Steering Committee of ECP/GR.*

## Promoting the use of barley genetic resources

### Information on the International Barley Core Collection

Helmut Knüpffer provided brief information about the present state of the International Barley Core Collection (BCC). He reminded the participants that the idea to create a European 'synthetic' barley core collection, based on European holdings of germplasm, was presented to the third meeting of the Barley Working Group (1989) by Th. van Hintum. The concepts of a BCC were developed by a small group consisting of Th. van Hintum, G. Fischbeck, R. von Bothmer and H. Knüpffer. The Sixth International Barley Genetics Symposium recommended in 1991 to extend the scope of the BCC into an International BCC, and an international BCC Coordinating Committee was established. Members of this committee as well as specialists from different regions were made responsible for creating subsets of the BCC. At the Seventh International Barley Genetics Symposium (Saskatoon,

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[8] Gass, T., G. Kleijer, M. Waldman and E. Frison, editors. 1995. Report of the Technical Consultative Committee. Sixth Meeting, 21-23 September 1995, Nitra, Slovakia. European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR). International Plant Genetic Resources Institute, Rome, Italy.
FAO. 1996. Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture and the Leipzig Declaration adopted by the International Conference on Plant Genetic Resources, Leipzig, Germany, 17-23 June 1996. FAO, Rome, Italy.

[9] See pp. 12-15 (The European Forages Collection) *in* Maggioni, L., P. Marum, R. Sackville Hamilton, I. Thomas, T. Gass and E. Lipman, compilers. 1998. Report of a Working Group on Forages. Sixth meeting, Beitostølen, Norway, 6-8 March 1997. International Plant Genetic Resources Institute, Rome, Italy.

[10] A discussion document prepared by the task force is included as Appendix II of this report.

Canada, 1996), the status of the BCC was presented.[11] Some parts of the BCC are ready for distribution to the four active BCC centres. The European part of the BCC was handed over to IPK for initial multiplication; IPK also received 380 East Asiatic accessions belonging to the BCC. Other subcoordinators reported that they are well on the way. A paper giving some background information about the BCC has been published elsewhere.[12] The BCC will be an important tool in the standardization of research on barley.[13]

## Molecular characterization of the Barley Core Collection

Ahmed Jahoor indicated that the national research centre (National Laboratory Risø, Denmark) has a long tradition for the evaluation of genetic material for different biotic and abiotic stresses. Many different disease resistances have been identified for wild barley. The sources have been incorporated to enlarge genetic polymorphism in cultivars.

## The breeder's perspective on barley genetic resources

Jens Weibull addressed this issue by taking as an example an American survey conducted in 1984 on five 'big' crops: maize, wheat, sorghum, soybean and cotton. Some of the trends highlighted by that survey may apply equally well in a European situation. He then referred to a similar study undertaken by the ECP/GR Barley Working Group, in the mid-1980s, by sending out a questionnaire to 150 European breeders to assist in developing a strategy for the European Barley Database. European breeders seem to behave remarkably similarly to their North American colleagues in the search for novel disease resistance genes. J. Weibull pointed out that there is still a critical lack of information on evaluation data on pest and disease resistance. Cooperation between genebanks and breeders should be increased in areas such as evaluation, pre-breeding programmes, and in relevant research; and the knowledge of breeders about varieties and plant characters should be better valorized, e.g. in training activities.

## Wild relatives

Roland von Bothmer gave a presentation about the importance of conserving wild barley genetic resources and about their potential utilization. He reminded the Group how time-consuming, laborious and costly it is to utilize exotic germplasm in conventional breeding programmes. For this reason practical breeders are reluctant to use these gene sources. This leads to an increasing gap between genebanks and the breeding industry. However, public sector resources should be invested in the organization of pre-breeding programmes in order to broaden the genetic base of the crop and in this way act as an interface between genebanks and the practical breeding.

### ***Hordeum vulgare* L. subsp. *spontaneum* (= *H. spontaneum*)**

*H. spontaneum* has great potential for breeding purposes. It is highly variable and belongs to the primary genepool of barley as there are no biological sterility barriers in crosses with the crop. It is at present underutilized as a gene source in breeding programmes. Effort is required to identify gaps in existing *ex situ* collections and to carry out collecting in target

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[11] Draft Report of the Barley Core Collection Meetings held before and during the VIIth International Barley Genetics Symposium (by H. Bockelman, R. von Bothmer, G. Fischbeck, Th. van Hintum, A. Jaradat, T. Konishi).

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

[13] IPK, as one of the active BCC centres, received the North and South American BCC in 1998. First material of the European, South & East Asian, and North & South American BCC subsets (samples of 25 seeds each) was already distributed to evaluation partners of the EU project GENRES CT98-104 and other interested users.

areas. *In situ* conservation programmes established in Israel, Turkey and Syria should be followed and the establishment of similar initiatives in other countries such as Greece and Cyprus should be supported.

### *Hordeum bulbosum* L.

The species is the only one belonging to the secondary genepool of barley. Previous interest was shown in *H. bulbosum* for utilization in breeding for haploid production (chromosome elimination). It has received renewed interest as a gene source owing to the recent breakthrough in successful backcrosses to barley. *H. bulbosum* from Europe is underrepresented in *ex situ* collections (specifically from France, Italy and the Balkan region). Efforts should be made to identify gaps in existing collections and to initiate collecting in these areas. This is of importance for optimal representation of genetic diversity of the species as well as for the Barley Core Collection. *H. bulbosum* is probably adequately preserved *in situ* in most countries of its distribution at present. Special attention should be given to those countries where the species is rare.

### Other wild *Hordeum* species

Around 30 wild species (in total about 50 different taxa and cytotypes) belong to the tertiary genepool of barley and are at present not available for breeding purposes but are known to contain valuable genes of interest for breeding. Most species are at present well preserved *in situ* and are also fairly well represented in *ex situ* collections even though some gaps are evident. In Europe the single species *H. secalinum* Schreb. is drastically decreasing in many areas and should be the concern for national programmes in the following countries (Sweden, Germany, Spain, etc.). Six American taxa or cytotypes are rare or threatened and need special actions.

### Recommendations

- *Encourage national programmes to increase their efforts in the conservation, evaluation and utilization of wild barley species*
- *Encourage the further development of breeding techniques for wide crosses in barley together with pre-breeding programmes to improve utilization of the extended genepools*
- *In the case of* H. spontaneum *(and barley landraces), this could be achieved through initiation of composite cross programmes ('dynamic genepools')*
- Hordeum spontaneum *(together with barley landraces) should also be the main object of evaluation in the new EU project proposal (see above).*

For the first part of the sixth session the Group moved to IPK-Gatersleben where it was welcomed by Prof. Ulrich Wobus, Director of the Institute. Prof. Wobus presented IPK's objectives, the role the Genebank plays within the overall structure of the Institute and the new focus on the development and application of molecular techniques. The Group was also provided with a short visit to IPK's genebank facilities, guided by K. Hammer.

## Barley genome research at IPK – the Plant Genome Resources Centre

Andreas Graner presented the IPK Plant Genome Resources Centre (PGRC), a platform for the generation of biological resources and the development and application of DNA-technology. Its major goal is to maintain and provide biological resources such as probe repositories, DNA libraries and mapping populations together with the appropriate technology including the development of molecular markers, the refinement and application of megabase technologies for map-based cloning, and the production of transgenic plants. Research activities at the PGRC mainly concentrate on cereals, particularly barley, mainly because its cultivated form (*Hordeum vulgare* L.) and its wild ancestor (*Hordeum spontaneum*) represent one of the major collections of the Genebank comprising more than 12 000 accessions. The integrated structure of the PGRC will facilitate genetic research extending from the analysis of a phenotypic trait to the isolation of the corresponding gene. The close interaction with plant breeders will facilitate a rapid transfer of know-how and technology and provide new avenues to access barley germplasm maintained at the Gene Bank for genetic studies and breeding purposes.

## Internet presentations – European Barley Database and IPK Genebank passport data

Helmut Knüpffer presented two databases searchable on-line. A prototype of the European Barley Database **<http://www.dainet.de/eccdb/barley>** was made searchable on-line by ZADI, in close cooperation with the EBDB managers, before the ZADI-ECP/GR Workshop on Central Crop Databases (Bonn, June 1997). It allows searching for many descriptors, and some of its search functions were demonstrated. The prototype contains only about 30 000 accessions. When the update of the EBDB is finished (September 1997), the full database will be forwarded to ZADI. Some remarks of users concerning the appearance of query results will be taken into consideration when re-designing the WWW database. For example, coded information should not appear as output. The on-line EBDB is linked with the ECP/GR information platform **<http://www.cgiar.org/ecpgr/platform/Index.htm>**.

Another presentation was devoted to the passport database server of IPK's genebank **<http://fox-serv.ipk-gatersleben.de>** which was developed by two computer-science students from the Leipzig University.[14] Selected descriptors from IPK's passport database can be retrieved for about 84 000 accessions of the genebank. There are three search possibilities: (1) for accession numbers; (2) for scientific names and/or countries of origin; (3) flexible search – combined search for up to four descriptors to be chosen from a total of 15 searchable descriptors, with the possibility of using wildcards for search strings. The output format for the search results is rather compact. Particular attention was paid to proper handling of characters with diacritical marks. The possibility of downloading the results of the actual search was a novel feature for plant genetic resources databases. This database is increasingly being used as a basis for requesting accessions.[15]

## Information system for evaluation data for barley genetic resources

Siegfried Harrer informed about a project named EVA, Information system for evaluation data of plant genetic resources. This is a cooperative project involving four German institutions. EVA aims at making evaluation and characterization data of barley (and fruit trees and potatoes) available in a centralized German information system. The project partners are: the Centre for Agricultural Documentation and Information (ZADI) in Bonn as overall coordinator and information system developer, the genebank of the Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) in Gatersleben and its branch stations for fruit trees and potatoes, the Institute for Epidemiology and Resistance (IfEu/R) of the Federal Centre for Breeding Research on Cultivated Plants (BAZ) in Aschersleben, and the Biometrics and Data Processing Group of the Institute of Crop Science of the University of Halle-Wittenberg in Bad Lauchstädt. The genebank of the BAZ in Braunschweig is an associated partner.

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[14] Knüpffer, H. 1997. Options and approaches to providing on-line access to databases. Part III. FoxPro on-line databases on an institution server. Report, European Central Crop Databases (ECCDB) On-line Databases Training Workshop, 8-10 June 1997, Bonn, Germany. ECPGR & ZADI <**http://www.cgiar.org/ecpgr/platform/ECCDB1/Fox-serv.htm**>

[15] The WWW server for passport data has been accessed approximately 430 times per month between March 1997 and December 1998, among them 77% from outside IPK. About 21% of the seed requests for genebank accessions were based on previous database searches by the requesters.

EVA will be an on-line database with worldwide access via Internet. Different data sources will be combined in the system, and links established to other relevant data (e.g. literature, research projects, etc.). Most of the evaluation data relevant for the project have to be registered electronically.

IPK-Gatersleben contributes observation, characterization and evaluation data of its more than 12 000 accessions of barley. IfEu / R-Aschersleben is responsible for recording detailed race-specific resistance data of IPK's barley accessions. The BAZ genebank in Braunschweig contributes computerized data of about 7500 barley accessions. Data from official barley performance trials are being made available by the group from the Halle University. Also the re-analysis of performance trials and the development of statistical procedures for combining and evaluating all data will be done there.

The project started in May 1996 and is funded by the German Ministry of Food, Agriculture and Forestry.

Prof. M. Neumann, Director of the Federal Centre for Breeding Research on Cultivated Crops (BAZ) welcomed the Group to the Head Office of this centre in Quedlinburg, where the second part of the sixth session of the meeting was held. Prof. Neumann presented the Centre, its objectives and structure. The Centre was established in 1992 as part of the research sector of the Federal Ministry of Food, Agriculture and Forestry. It includes ten institutes as well as the Genebank in Braunschweig. BAZ produces the scientific basis to aid political and administrative decisions by the Ministry of Agriculture and promotes the agricultural policy for an ecologically compatible and sustainable agriculture. BAZ also supports private plant breeders through the development of new methods and by providing plant breeding material.

### Evaluation of IPK's barley germplasm for disease resistance for exploitation in breeding

Ursula Walther reported about the evaluation work for disease resistance on the barley collection of IPK's genebank carried out by herself and her colleagues during three decades, before and after the establishment of the BAZ in 1992. Before 1991, in research institutions of the former Academy of Agricultural Sciences of the GDR, many accessions of the barley collection were tested for race-specific resistance to a number of diseases, such as mildew, leaf rust, stripe rust, net blotch, barley yellow mosaic viruses and barley yellow dwarf virus. For some of these diseases, several thousand accessions were tested, resulting in accessions with different field- and race-specific resistances. At present this work is being carried out for viruses (BYDV, BaMMV, BaYMV-1, BaYMV-2), fungi [*Puccinia hordei* Otth., *Pyrenophora teres* (Sacc.) Drechs., *Puccinia striiformis* West., *Erysiphe graminis* DC.] and aphids [*Rhopalosiphum padi* L., *Sitobion avenae* F., *Metopolophium dirhodum* (Walker), *Rhopalosiphum maidis* (Fitch)]. Results of evaluation are given in detail in Part II of this Report (p. 93).

## Conclusion

The Barley Working Group has been successful in bringing together scientific and technical expertise in genetic resources throughout Europe as a region. The forum has proved useful at the practical level for sharing information, development of common work programmes and coordination of a number of joint projects. The development of the EBDB has been an important exercise in centralizing and standardizing information on barley and in improving access and awareness of barley genetic resources. The Group's contribution to the development of the Barley Core Collection, particularly relating to European accessions, will continue with the initiation of evaluation of the material for winterhardiness in the Czech Republic. This will add to the identification and utilization of useful traits as well as extending the data and value of the collection.

Both the EBDB and Core Collection initiatives have raised awareness within the group of successes and difficulties and the necessity of shared responsibilities. The Group supports the initiative of sharing responsibilities and is actively involved in contributing to these discussions.

The Group will increase its focus on the conservation and evaluation of wild relatives of cultivated barley, in particular *H. spontaneum* and *H. bulbosum,* with reference to biotic and abiotic stresses. The Group will strongly promote the importance of pre-breeding efforts in improving access and utilization of these diverse genepools.

The primary objective of the Group remains the completion of the EBDB and its use in addressing questions related to identification of duplicates, primary country holdings and gaps in collection. If personnel capacities become available, the EBDB will also be extended by developing links to available evaluation data.

The Group therefore strongly recommends the continuation of the Barley Working Group in order to complete the work it has started and realize the potential from these developments in terms of genetic resources management and their utilization.

*The draft report was presented to the Group and adopted with some modifications.*

## Election of the Chair

Roland von Bothmer was elected Chair until the end of the next Barley Working Group meeting.

## Closing remarks

Karl Hammer thanked the Group and IPGRI for their input in the meeting and throughout his time as Chair of the Group. R. von Bothmer, on behalf of the Group, expressed his thanks to the local organizing committee for the warm hospitality and the selection of a lovely and peaceful venue for the meeting. He also expressed his sincere thanks to K. Hammer for his achievements on behalf of the Barley Working Group.

# Part II. Presented papers

## Status report on the European Barley Database (EBDB)

***Helmut Knüpffer and Luis López***

*Genebank, Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany*

### *Introduction*

The first version of the European Barley Database was built up by the Genebank of IPK Gatersleben from 1984 to 1987 (Knüpffer 1988). Meetings of the ECP/GR Barley Working Group (held in Gatersleben in 1983, 1986, 1989 and 1993) formulated its objectives, and status reports were given (e.g. Anonymous 1986; Knüpffer 1989a, 1993). In 1987 a catalogue, the European Barley List (EBL), was published (Knüpffer 1987). An international meeting of barley database managers organized by IBPGR was held in Gatersleben in 1993 to investigate the possibilities of creating an international barley database.

Owing to the large size and number of European barley collections, and based on previous experience, it was expected that the establishment of a second, completely new version of the EBDB would be time-consuming, and, therefore, would require a full-time database manager, at least for a certain period. Attempts to obtain an EU project grant for this failed[16] and IPK kindly provided funds to hire a specialist for six months (April-September 1997) to create the new EBDB. The first achievements were presented at the Fifth Meeting of the ECP/GR Barley Working Group. The work was continued until September 1997.

### *Identification of duplicates*

In 1988 and 1989, extensive work was carried out to identify possible duplicates within the EBDB, using the so-called KWIC (key word in context) index approach, details of which are given by Knüpffer (1988). A large number of potential duplicates was identified, based on identical or similar accession names, numbers, etc. The approach also allowed duplicates such as 'Weibulls Herta' and 'Herta' to be found. This resulted in a tentative grouping of accessions into "duplicate groups". The approach was further elaborated by van Hintum and Knüpffer (1995).

The Working Group considered in 1989 that for verifying and refining the duplicate groups of named accessions, experts from different countries would have to be involved. The aim was, for cultivars released after 1950, to identify two or three "most original" accessions representing each group.

No efforts have been made so far to identify duplicates in the new version of the EBDB. The duplicate groupings identified in version 1 could be transferred to version 2, as a starting point. Continuation of these activities is planned within the EU project mentioned.

### *Updates*

In 1989 the Working Group recommended to update the EBDB every three years. EBDB extracts should be sent to contributing genebanks for corrections and additions. It was hoped that this would enable curators to improve their own documentation systems.

Furthermore, the group recommended to include additional descriptors for cultivars, such as Year of Registration and/or Year of Release. This would add to the EBDB some

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[16] Updating the EBDB and inclusion of characterization and evaluation data is part of the re-submitted EU project GENRES CT98-104 which is expected to start in April 1999 (see Part I, p. 6).

functions of a variety register. It would justify requesting data from existing variety registers for barley. Principal attribute was also considered important.

### Distribution of the EBDB

The first version of the EBDB was sent in electronic form to many users on request, especially after the 1989 meeting and the Sixth Barley Genetics Symposium in 1991. Other users requested the printed catalogue (now out of stock), or specific selections from the database. A prototype of the second version, including data from three institutions, was made searchable on-line in cooperation with ZADI: **<http://www.dainet.de/ecpgr/barley>**.

There was some feedback from users of the EBDB and the EBL who reported that they used it to locate genebanks keeping desired material, or to improve their own documentation system by comparing their data with those for the same accessions from other collections represented in the EBDB. A few users also reported on errors which they had detected in the EBDB.

### Publications

Following the recommendation of the 1989 group meeting, information about the EBDB was published in different journals and newsletters (Barley Newsletter, Rachis, see Knüpffer 1989b, 1990a, 1990b), and presented at conferences (Knüpffer 1991a, 1991b).

### Version 2 of the European Barley Database

During the first half of 1997, 91 institutions from 34 countries in Europe and Israel dealing with barley genetic resources (based on an address list provided by ECP/GR) and holding a total of about 157 000 barley accessions, as well as those which had contributed to the first version of the EBDB, were approached by letter, fax and email. By 30 September 1997, 36 institutions from 25 countries had sent their data (Table 1). A breakdown of contributing institutions with number of accessions is given in Table 2. The last column gives a comparison with the first version of the database (1987). It can be seen that some important institutions which had participated in the first EBDB did not send their data in 1997 (Table 3). Some contributions were not yet included in the database because they arrived too late (just before or after end of September 1997), or because requests for clarifications of questions remained unanswered.

**Table 1.** Overview of contributions to the EBDB

| | **7 July 1997** | | | **30 September 1997** | | |
|---|---|---|---|---|---|---|
| | **Institutions** | **Countries** | **Accessions** | **Institutions** | **Countries** | **Accessions** |
| Contacted | 91 | 34 | 157 400 | 91 | 34 | 157 400 |
| Data received | 24 | 20 | 72 000 | 36 | 25 | 91 000 |
| Data announced | 12 | 8 | 15 800 | 4 | 4 | 14 000 |
| Reply: no data, or data included in another database | 15 | 10 | | 16 | 12 | |
| No reply | 41 | 25 | | 36 | 22 | |

**Table 2.** Institutions contributing to the EBDB until 30 September 1997

| Country | Institute | Accessions received, but not included | Included in EBDB 2 | EBDB 1 (1987) |
|---|---|---|---|---|
| AUT – Austria | BVAL Linz | – | 716 | 298 |
| | Bundesamt u. Forschungszentrum für Landwirtschaft, Wien | – | 243 | – |
| | Arche Noah, Schiltern | 103 | – | – |
| | Landesanstalt Rinn/Tirol | 146 | – | – |
| BEL – Belgium | CRA Gembloux | – | 146 | 289 |
| | 2 collections: Clovis-Matton, Heverlee | – | – | 494 |
| BGR – Bulgaria | IIPGR Sadovo | – | 5120 | 506 |
| CHE – Switzerland | Changins, Nyon | – | 794 | 748 |
| | Pro Specie Rara | – | 8 | – |
| | Sortengarten Erschmatt | 43 | – | – |
| | SAVE | 3 | – | – |
| CYP – Cyprus | ARI Nicosia | – | 26 | 26 |
| CZE – Czech Republic | RICP Prague-Ruzyne, and Cereal Inst. Kromeriz | – | 3748 | 1278<br>+907 |
| DEU – Germany | BAZ Genebank Braunschweig | – | 7467 | 8274 |
| | IPK Genebank Gatersleben | – | 12360 | 10266 |
| ESP – Spain | INIA Madrid | – | 2333 | 1004 |
| EST – Estonia | Jogeva | – | 488 | – |
| ETH – Ethiopia | PGRC/E Addis Ababa | – | – | 5335 |
| FRA – France | INRA Clermont-Ferrand | – | 3387 | 1674 |
| | GEVES La Minière | – | – | 873 |
| GBR – Great Britain | Scottish Agric. Sci. Agency Edinburgh | – | 1647 | – |
| | (PBI) John Innes Institute | – | – | 9458 |
| | RBG Kew | – | – | 14 |
| GRC – Greece | Cereal Inst. Thessaloniki | – | 112 | 721 |
| | Greek Gene Bank | – | 133 | 64 |
| HUN – Hungary | RCA Tápiószele | – | 2738 | 2207 |
| IRL – Ireland | Backweston | – | | 20 |
| ISR – Israel | Israel Gene Bank, Bet Dagan | – | 232 | 102 |
| | Tel Aviv University | – | 6652 | – |
| | Haifa University | – | 1442 | – |
| ITA – Italy | Ist. Germoplasma Bari | – | 2102 | 1242 |
| | Cereal Institute, Fiorenzuola d'Arda | 489 | – | – |
| LTU – Lithuania | Lit. Agric. Inst. | – | 656 | – |
| LVA – Latvia | Inst. Biol. Salaspils | – | 1548 | – |
| NLD – The Netherlands | CGN Wageningen | – | 3466 | 2912 |
| POL – Poland | IHAR Radzikow | – | 5946 | 2321 |
| | Bot. Gard. Powsin | – | – | 116 |
| PRT – Portugal | ENMP Elvas | – | – | 46 |
| ROM – Romania | Genebank Suceava | – | 1014 | – |
| RUS – Russia | VIR St. Petersburg | – | 19437 | – |
| SVK – Slovakia | Genebank Piestany | – | 1473 | – |
| SWE – Sweden | Nordic Gene Bank (representing 4 barley collections in Denmark, Finland, Norway) | 1188 | – | 968 |
| | Scandinavian *Hordeum* Collection Svalöv | – | – | 1861 |
| TUR – Turkey | AARI, Izmir | – | – | 685 |
| UKR – Ukraine | Inst. Plant Breed. Kharkov, Inst. Genet. and Sel. Odessa | – | 3415 | – |
| YUG – Yugoslavia | Inst. Small Grains Kragujevac | – | – | 660 |
| | Maize Res. Inst. Zemun | – | 149 | – |
| **Total** | | **1972** | **88998** | **55369** |

**Table 3.** Summary of institutions which have not sent data

| Country | Data announced but not sent | No data, or data not public, or data included in another database | No response |
|---|---|---|---|
| ALB – Albania | – | – | 2 |
| AUT – Austria | – | 1 | – |
| BEL – Belgium | – | – | 2 |
| DEU – Germany | – | 1 | 1 |
| ESP – Spain | – | 2 | 3 |
| FIN – Finland | – | 1 | – |
| FRA – France | 1 | 1 | 1 |
| GBR – Great Britain | – | 3 | 3 |
| HRV – Croatia | – | – | 1 |
| HUN – Hungary | 1 | 1 | 3 |
| IRL – Ireland | – | 2 | 1 |
| ITA – Italy | – | – | 1 |
| LTU – Lithuania | – | 1 | – |
| LVA – Latvia | – | 2 | 1 |
| MLT – Malta | – | – | 1 |
| NOR – Norway | – | – | 2 |
| POL – Poland | 1 | – | 1 |
| PRT – Portugal | – | 1 | 1 |
| ROM – Romania | – | – | 2 |
| SVK – Slovakia | – | – | 1 |
| SWE – Sweden | 1 | – | 1 |
| TUR – Turkey | – | – | 1 |
| UKR – Ukraine | – | – | 4 |
| YUG – Yugoslavia | – | 1 | 2 |

## *Descriptors included in the European Barley Database*

The completeness of the data provided by different donors and the original structures varied. Managers of different Central Crop Databases reported in detail about this fact elsewhere. Part of the data were received in a structure based on the Multicrop Passport Descriptors, others used their own descriptor system. Among the different formats there were DBF tables, EXCEL spreadsheets, tables or plain text in ASCII or in word-processor formats. Most of the descriptors, as far as they belonged to passport or the "barley-specific additional descriptors" as defined in Appendix I, were transferred to the EBDB. Some contributions contained data which were difficult to interpret, or were in local languages, or belonged to descriptors initially not included in the EBDB. This needs further investigations. Table 4 gives an overview of the descriptors in the present version of the database, with reference to the barley descriptors.

The species composition of barley accessions represented in the EBDB is given in Table 5. No attempt was made to standardize the species concepts used by different donors of data. In addition, the species composition is heavily biased towards cultivated barleys because at least two important wild species collections are not yet included, namely the Scandinavian *Hordeum* Collection, and the wild species collection of the Vavilov Institute, St. Petersburg, which has not been computerized at all. Infraspecific names at different levels (subspecies, convarietas, varietas) are given for 28 868 accessions, among them only 392 accessions of wild species. After modest standardization of infraspecific names provided (standardization of spelling, author abbreviations, capitalization), there seem to be 33 different infraspecific taxa in wild species and 238 in *Hordeum vulgare*. Some may turn out to be synonyms of others. Barley taxonomic expertise was not available at the time of compiling the database.

The most frequently represented countries of origin are given in Table 6. The table lists 58 countries with at least 200 accessions. In total there are 127 different country acronyms, including some needing further clarification from the data donors. According to the seasonality, there are 44 456 spring and 12 874 winter barleys, 2120 intermediate forms and 90 perennials; 29 083 records do not contain seasonality information, and 373 accessions have other states. Other descriptors, such as Collecting Source, Status of Sample, Row Number, or Kernel Covering, have too few values, and therefore an analysis would not make much sense.

**Table 4.** Descriptors used in the EBDB. Data on number of different values, number of empty values, etc. are based on 88 998 records already included in the database. The number of different values also includes the value "empty"

| Descriptor | | Empty values | Different values | Remarks |
|---|---|---|---|---|
| 1 INSTCODE | Institute code | 0 | 29 | |
| 2 ACCENUMB | Accession number | 1636 | 79172 | |
| A INTRONUMB | Introduction number | 83577 | 5377 | |
| 3 COLLNUMB | Collection number | 82097 | 5185 | |
| B COLLNAME | Collector | 84982 | 129 | |
| 4 GENUS | Genus | 0 | 1 | constant "Hordeum" |
| 5 SPECIES | Species | 3723 | 41 | after standardization of spelling |
| 6 SUBTAXA | Infraspecific taxa | 60182 | 271 | after standardization of spelling |
| 7 ACCNAME | Accession name | 28991 | 33655 | |
| 8 ORIGCTY | Country of origin | 11294 | 127 | |
| 9 COLLSITE | Collecting site | 50528 | 5545 | |
| 10 LATITUDE | Latitude of collecting site | 85992 | 843 | |
| 11 LONGITUDE | Longitude of collecting site | 85992 | 1115 | |
| 12 ELEVATION | Elevation of collecting site | 86105 | 993 | |
| 13 COLLDATE | Collecting date | 51868 | 639 | |
| 14 SAMPSTAT | Status of sample | 68463 | 9 | |
| 15 COLLSRC | Collecting source | 83012 | 11 | |
| 16 DONORCODE | Donor institute code | 47598 | 1214 | |
| 17 DONORNUMB | Donor number | 64459 | 21776 | |
| 18 OTHERNUMB | Other number(s) | 70576 | 12447 | |
| C BREEDINST | Breeding institute | 84445 | 825 | |
| E PEDIGREE | Pedigree | 85074 | 3189 | |
| F YEAR_RELE | Year of release | 86732 | 36 | |
| 19 REMARKS | Remarks | 86603 | 2393 | |
| 1 ROWNUMB | Row number | 85433 | 4 | This information can also be derived from the name of convarietas, if provided |
| 2 SEASONAL | Seasonality | 29083 | 7 | |
| 3 KERNELCOV | Kernel covering | 85609 | 3 | This information can also be derived from the name of botanical variety, if provided |

**Table 5.** Barley species represented in the EBDB.

| ***Hordeum* species** | **No. of accessions** | ***Hordeum* species** | **No. of accessions** |
|---|---|---|---|
| *agriocrithon* Aberg | 46 | *lechleri* (Steud.) Schenck | 2 |
| *arizonicum* Covas | 1 | *leporinum* Link | 2 |
| *bogdanii* Wilensky | 5 | *marinum* Huds. | 53 |
| *brachyantherum* Nevski | 3 | *murinum* L. | 134 |
| *brevisubulatum* (Trin.) Link | 18 | *muticum* Presl | 4 |
| *bulbosum* L. | 147 | *parodii* Covas | 2 |
| *californicum* Covas et Stebbins | 2 | *patagonicum* (Haumann) Covas | 8 |
| *capense* Thunb. | 2 | *procerum* Nevski | 5 |
| *chilense* Roem. et Schult. | 77 | *pubiflorum* Hook. f. | 1 |
| *comosum* Presl | 4 | *pusillum* Nutt. | 3 |
| *cordobense* Bothmer *et al.* | 7 | *razdanicum* | 1 |
| *depressum* (Scribn. et Sm.) Rydb. | 2 | *roshevitzii* Bowden | 6 |
| *flexuosum* Steud. | 1 | *secalinum* Schreb. | 6 |
| *fuegianum* Bothmer *et al.* | 1 | spec. (species unknown or not specified) | 3723 |
| *geniculatum* All. | 1 | *spontaneum* Koch | 8745 |
| *glaucum* | 1 | *stenostachys* Godr. | 6 |
| *hystrix* Roth | 17 | *tetraploidum* Covas | 1 |
| *intercedens* Nevski | 1 | *turkestanicum* Nevski | 2 |
| *jubatum* L. | 31 | *violaceum* Boiss. et Huet. | 6 |
| *lagunculiforme* (Bacht.) Bacht. ex Nikif. | 45 | *vulgare* L. s.l. | 75874 |

**Table 6.** Composition of the EBDB by countries of origin. Only those countries from which there are at least 200 accessions are listed. Some countries which recently split into several countries are difficult to present in such a table, because often it is impossible or time-consuming to trace back the origin of a sample which is reported to be from, for example, "Soviet Union".

| No. of accessions | Country of origin | Remarks |
|---:|---|---|
| 11463 | Unknown or not stated | |
| 8162 | ETH – Ethiopia | |
| 7932 | ISR – Israel | |
| 6327 | DEU – Germany | incl. 1418 DDR |
| 3831 | USA | |
| 3234 | RUS – Russia | cf. also SUN |
| 2725 | FRA – France | |
| 2586 | ESP – Spain | |
| 2564 | TUR – Turkey | |
| 2094 | CSK – former Czechoslovakia | see also under CZE and SVK |
| 1818 | SUN – former Soviet Union | cf. also under the acronyms of the newly independent states; value includes 170 KAZ (Kazakhstan) |
| 1807 | JPN – Japan | |
| 1715 | SWE – Sweden | |
| 1570 | CHE – Switzerland | |
| 1554 | IND – India | |
| 1471 | UKR – Ukraine | cf. also SUN |
| 1399 | NPL – Nepal | |
| 1350 | CHN – China | |
| 1278 | GBR – Great Britain | |
| 1258 | DNK – Denmark | |
| 1221 | IRN – Iran | |
| 1206 | NLD – Netherlands | |
| 1198 | POL – Poland | |
| 1178 | AUT – Austria | |
| 1111 | MEX – Mexico | |
| 969 | PAK – Pakistan | |
| 913 | BGR – Bulgaria | |
| 895 | CAN – Canada | |
| 815 | GRC – Greece | |
| 796 | ITA – Italy | |
| 792 | HUN – Hungary | |
| 730 | YUG – Yugoslavia | both for former Yugoslavia and present Yugoslavia |
| 728 | ROM – Romania | |
| 697 | AFG – Afghanistan | |
| 448 | AZE – Azerbaijan | cf. also SUN |
| 426 | KGZ – Kyrgyzstan | cf. also SUN |
| 392 | FIN – Finland | |
| 392 | KOR, PRK – Korea | acronym KOR often used in a sense including North Korea |
| 384 | Baltic states | 37 EST, 63 LTU, 184 LVA; cf. also SUN |
| 382 | MNG – Mongolia | |
| 379 | MAR – Morocco | |
| 365 | DZA – Algeria | |
| 362 | SYR – Syria | |
| 351 | BEL – Belgium | |
| 340 | MDA – Moldova | |
| 338 | BLR – Belarus | |
| 332 | UZB – Uzbekistan | |
| 324 | TJK – Tajikistan | |
| 310 | AUS – Australia | |
| 310 | CZE – Czech Republic | see also under CSK |

| No. of accessions | Country of origin | Remarks |
|---|---|---|
| 295 | GEO – Georgia | |
| 294 | ARM – Armenia | |
| 290 | LBY – Libya | |
| 259 | EGY – Egypt | |
| 256 | TUN – Tunisia | |
| 254 | IRQ – Iraq | |
| 244 | ARG – Argentina | |
| 238 | TKM – Turkmenistan | |
| 219 | SVK – Slovakia | see also under CSK |

## *Conclusions*

It is necessary to further develop the EBDB as a tool to identify duplicates, support decision-making concerning safety-duplication of unique material, identify gaps in the collections and make information on European barley holdings, and thus the material itself, better available to the diverse user community. This involves inclusion of data from further institutions and extension by addition of characterization and evaluation descriptors. Identification of duplicates should be carried out as far as possible on a worldwide scale, in order to avoid duplication of efforts between Europe and large non-European collections. The development of the EBDB into an international database is desirable.

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# The status of national collections

## Status of the Austrian barley collection

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The Austrian *ex situ* barley collection, maintained by the three genebanks in Vienna, Linz and Rinn comprises 905 accessions in total (786 spring types, 119 winter types). This includes 329 accessions of landraces and 576 of cultivars (160 accessions of Austrian-bred cultivars and 166 of German-bred cultivars).

We will concentrate here on the landraces since this material is unique and not represented in other collections.

First we have to consider to what extent landraces were collected and maintained, or how much variability was lost. The essential botanical features of the barley landraces can be traced in literature back to 1840. It is necessary to clarify the terms used:

- *Hordeum hexastichon* = *H. vulgare* L. convar. *vulgare*, six-row barley
- *Hordeum vulgare* = *H. vulgare* L. convar. *vulgare*, four-row barley
- *Hordeum distichon* = *H. vulgare* L. convar. *distichon* (L.) Alef, two-row barley, *erectum* and *nutans* types
- *Hordeum zeocriton*, *H. distichon* Pyramidale = two-row barley with triangular ears and fan-shaped spread of awns (Germ. Pfauengerste).

The comparison of the reports given by different authors shows the development of the barley landraces over the last 150 years (Table 1).

**Table 1.** Development of barley landraces during the last 150 years in the Subalpine region (literature review)

| | **six-row barley** | **four-row barley** | **two-row barley (*nutans/erectum*)** | **two-row barley with triangular ears and fan-shaped spread of awns** | **naked barley** |
|---|---|---|---|---|---|
| Sailer 1841 | × | × | × | × | no info |
| Brittinger 1862 | rare | ×; mostly winter type | × | rare | no info |
| Duftschmied 1870/80 | very rare; under 4-row barley | × | × | rare | no info |
| Vierhapper 1885 | rare | × | × | rare | no info |
| Ritzberger 1904 | rare | × | × | rare | no info |
| Werneck 1927 | rare; under 4-row barley | × | × | – | reported not found |
| Burggasser | | | | | |
| 1926 | very rare | × | × | – | reported not found |
| 1955 | – | rare | rare; *nutans* and *erectum* | – | – |
| Schachl | | | | | |
| 1970 | – | rare | rare; *erectum;* missing | – | – |
| 1997 | – | – | – | – | – |
| Alps Mayr 1926 | × | × | × | × | × |
| Styria 1828/1850 | no info (×) | no info (×) | no info (×) | no info (×) | × |

The first exact descriptions have existed since the early 1930s, when local material was collected for plant breeding purposes. At the same time the first Austrian *ex situ* collection was established by Mayr in Rinn, Tyrol, comprising landraces from the Alpine region. In the Subalpine region Werneck was collecting; a few accessions of his collection were recently found by chance and are now being germinated.

While in the Subalpine region of Lower Austria and Upper Austria the six-row barley and two-row barley with triangular ears were lost at the beginning of this century (Werneck reports six-row barley only spread between four-row barley), in Tyrol Mayr could find and collect them. These types are still in our collections today, as Pumper and Fisser barley. The question is whether these six-row and triangular types of the Alps are identical with those previously reported in the Subalpine region. The theory of variety replacement, as developed on wheat landraces (Schachl 1975) implies that older varieties are replaced by newer ones, and pushed down from the intensive lowlands into the extensive mountainous areas, almost following a ring distribution like the waves in a pool (Fig. 1).

Transferring this theory to barley, it can be expected that the Tyrolian types are related to a certain extent to those of the Subalpine region and Danube valley. In this context it might be more correct to talk of groups of landraces consisting of a number of local races with genetic affinity.

We should also consider the spreading mechanism of landraces. Landraces, assuming they are adaptable to a large scale, start from a certain area where they have developed their distinctive properties influenced by farmers' mass selection. Spreading follows along the so-called 'oxen-roads', traditional communication lines exchanging agricultural commodities. These communications are little influenced by borders; such borders did not exist within the Austro-Hungarian monarchy, and the Inn river between Austria and Bavaria never hampered cultural and kinship relations. The example of accessions BVAL 353018 and 353019, called 'dowry barley', illustrates that landraces were even given as marriage dowry and this way could be transferred over long distances, in some cases more than 70 km, a rather big distance in the 1920s.

To what extent can we expect genetic variation in landraces? Landraces previously collected and maintained in genebanks, e.g. in Rinn as well, show high uniformity. Without doubt, one reason can be that originally the material was maintained in genebanks with the aim of plant breeding to make the accessions uniform without taking care of their variability. Referring to the wheat landraces again, but also studying the barley landraces, we found in the early 1970s that they still contain some variability, but that this variability is much less than would be expected, and in any case not comparable with the variation found in a gene centre. The reason for this may be seen on one hand in the previously mentioned mass selection, constantly applied for decades, and on the other hand in the pressure of natural selection getting increasingly stronger with altitude when a landrace migrates deeper into the Alps valleys. Besides, certain events also contribute to reduction of genetic variability. In the second half of the last century, in Bavaria and Western Austria almost all barley landraces were eliminated by catastrophic mildew epidemics; this might also explain the genetic relationship between the local races representing the landraces group. Again in 1926 and 1927, heavy hailstorms damaged the landraces in this region. Farmers did not rebuild their landraces from the surviving plants, but replaced them with cultivars and landraces from other regions, namely Franconia and the Salzburgian Lungau.

With the beginning of plant breeding activities (Pammer 1905-08), special attention was paid to the two-row *nutans* types, such as the 'Böhmerwaldgerste' originating from the area along the Bohemian forest, and the 'Hannagerste', a landrace from Moravia. Whereas the Böhmerwald barley spread into the Danube Valley and formed the basis for the cultivars 'Otterbacher Gerste' and 'Bavaria Gerste', the latter was largely introduced into the European plant breeding programmes.

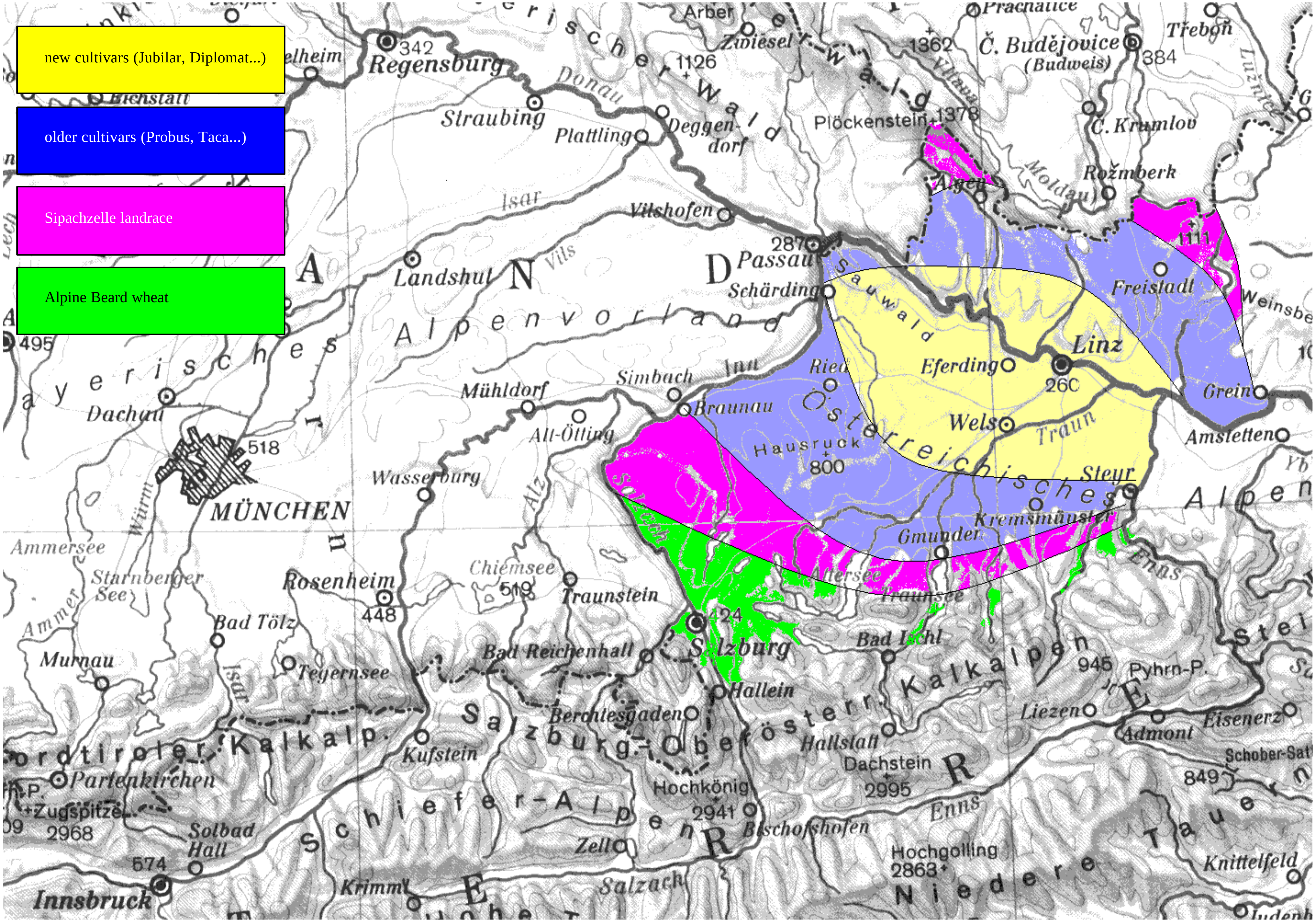

**Fig. 1.** Variety replacement in the Subalpine region.

Himalaya barley, a naked type, can be traced in reports from Styria back to 1828 and is mentioned as identical with the 'Phönix barley' offered around Berlin about 1850. Naked barley did not seem to be of importance for the lower regions like the Danube valley and was not mentioned by the early authors. Only Werneck reports its existence in the mountains but he and Burggasser were no longer able to find it. An accession of Himalaya barley maintained by the Technical University of Munich did not prove identical with that naked type found by Mayr and presently known as 'Tuxer barley' in our collections.

During an evaluation tour organized recently, landraces could no longer be found in the periphery of the Subalpine region where they still existed at the beginning of the 1970s. Considering the results obtained in the past with plant breeding, the reintroduction *in situ* barley landraces conserved *ex situ,* for the sake of a wider biodiversity, is reasonable only when a high level of adaptation to specific environments (climate, soil, production requirements, etc.) is needed.

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# Status of the Bulgarian barley collection

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The basic collection of barley can be found in IPGR-Sadovo with a total number of 5120 accessions. This includes a working collection of 1425 accessions which originate from Ethiopia.

There are small collections in the Institute of Barley in Karnobat and in the Agricultural Institute in Plovdiv, mainly selection lines

Over 3000 accessions are documented for the following characters: morphological (27), biological (5), chemical and technological (3) and a small part of the accessions are documented for 4 characters.

In general the agronomic evaluation of the accessions has been carried out for two years. Accessions that have already shown high economic qualities are still being examined in microexperiments (comparative selection experiments). The last stage is the collection based on qualitative characters. Each year, from 30 to 40 accessions pass through that examination and in the last stage there are about 14-15 accessions left.

After receiving the necessary number of seeds (about 150 g) from a seed probe, accessions are deposited in the Genebank of the Institute under the following conditions:

- long-term storage: –18°C, humidity not controlled, dried seeds packed in laminated foil bags and glass jars
- medium-term storage: 6°C and 50% relative humidity, seeds packed in paper bags; seed dried to 6-7% moisture content.

Classification of the accessions of the barley collection in IPGR-Sadovo according to donor country is shown in Table 1. Germany has the highest number of accessions (1311), followed by Czechoslovakia, USA, Hungary, etc. About 475 accessions have an undefined origin. There are about 39 Bulgarian varieties, 10-15 of which are modern varieties. The 3695 accessions in long-term storage are: varieties (1964), populations or local varieties (384), research material (885), wild relatives (7), not defined (455).

Accessions are also classified according to their growth habit: 994 winter, 1013 spring, 111 facultative, 1577 undefined. They are also distributed into:

- the XIX group – two-row, represented by about 1083 accessions.
- the XX group – multi-row (six-row and intermediate), about 1946 accessions.
- not defined: 466 accessions.

In the collection, naked-grain accessions have been also studied. They are of interest to breeders because of their high protein contents (17-18%) and their lysin content in raw protein over 4%. Two standards are used for the evaluation of the accessions:

- for the multi-row, the Bulgarian variety 'Hemus' and the French variety 'Plaisant'
- for the two-row, the variety 'Alpha'.

The German variety 'Alexis' is the standard for the spring forms.

The species of wild barley that occur in Bulgaria are shown in Table 2.

In 1996, 60 barley accessions were transferred from IPGR-Sadovo to the Institute of Barley in Karnobat and the Agricultural Institute in Plovdiv, and 25 Bulgarian varieties were sent abroad to the Agricultural Institute Osijek in Croatia and the Australian Winter Cereals Collection.

Varieties grown in Bulgaria include: 11 Bulgarian varieties and one French variety 'Plaisant' (Table 3).

**Table 1.** Origin of the accessions maintained at IPGR-Sadovo

| Donor country | Number of accessions |
|---|---:|
| Germany | 1311 |
| Czechoslovakia | 565 |
| USA | 509 |
| Hungary | 247 |
| USSR | 182 |
| Japan | 133 |
| Bulgaria | 142 |
| United Kingdom | 53 |
| France | 48 |
| Syria | 17 |
| Sweden | 7 |
| The Netherlands | 6 |
| Other countries | 475 |

**Table 2.** Wild species of the genus *Hordeum* in Bulgaria

| Species | Distribution | Importance, use |
|---|---|---|
| *Hordeum silvaticum* | Spread | Forage / in association |
| *Hordeum crinitum* | Local | Weed |
| *Hordeum asperum* | Spread | Forage / in association |
| *Hordeum bulbosum* | Widespread | Forage / in association |
| *Hordeum secalinium* | Local | Forage / in association |
| *Hordeum murinum* | Widespread | Weed |
| *Hordeum leporinum* (syn. *H. murinum* var. *leporinum*) | Widespread | Weed |
| *Hordeum hystrix* | Widespread | Forage / in association |

**Table 3.** Barley varieties used in Bulgaria (updated in 1996)

| | Varieties | Origin |
|---|---|---|
| **Two-row** | | |
| Obzor | WS | Bulgaria |
| Oglon | W | Bulgaria |
| Korten | W | Bulgaria |
| Perun | WS | Bulgaria |
| Aster | WS | Bulgaria |
| **Six-row and intermediate** | | |
| Hemus | W | Bulgaria |
| Vesletz | WS | Bulgaria |
| Panagon | W | Bulgaria |
| Izgrev | W | Bulgaria |
| Aheloj 2 | W | Bulgaria |
| Zenit | WS | Bulgaria |
| Plaisant | W | France |

## *Workplan*

- To continue collecting, evaluation of the whole collection, regeneration of some accessions and data computerization.
- To find a sponsor for the publication of a catalogue of the first 2000 barley accessions.
- To continue contacts for joint work with the Institute of Barley in Karnobat, the Agricultural Institute in Plovdiv and the Institute of Beer in Sofia.

# The national collection of winter and spring barley in Croatia

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Activities in the field of barley breeding in Croatia date back to the beginning of this century. They began with the collecting of initial breeding material of domestic and foreign origin (Germany, France, Great Britain, the Netherlands, USA, etc.) at the Faculty of Agronomy Zagreb (Academician Aloiz Tavčar), at the Brestovac Plant Breeding Station in the eastern part of Croatia (Baranja), which was located only a few kilometers from Osijek and was established in 1922 (Šeput *et al.* 1995), and at the Osijek Agricultural Institute (Prof. Dr Mato Valenčić).

The important variety of two-row winter barley in Croatia was 'Maksimirski 45' which was created at the Faculty of Agronomy Zagreb by Aloiz Tavčar. Afterwards, the varieties of two-row winter barley 'Satir', 'Mursa' and 'Alkar' (Valenčić 1973a, 1973b; Valenčić and Mađarić 1973), and the varieties of two-row spring barley 'Velebit' and 'Jaran', were created at the Osijek Agricultural Institute and registered in 1970, 1972, 1973, 1977 and 1983, respectively.

The old variety of two-row spring barley 'Belje 607' was selected from the domestic landrace, which was grown at the beginning of this century in the east of Croatia (Baranja) at the Brestovac Plant Breeding Station. This variety of two-row spring barley had an important role in the origin of two-row winter barley varieties ('Mursa' and 'Alkar') and the other newer two-row winter barley varieties ('Pan', 'Sladoran', 'Rodnik', 'Rex',' David', etc.) and six-row winter barley varieties ('Baranjac' and 'Podravac') (Table 1). This old variety also had an important role in the spring barley breeding programme at the Osijek Agricultural Institute.

For the European collection and barley breeding, the Dalmatian barley population (Croatia) had an important role. A variety of two-row spring barley was selected by German breeders in 1929 near the Croatian town of Dubrovnik, on the Adriatic sea, formerly known as Ragusium. The name of this variety is 'Ragusa' (Baumer, pers. comm.).

Now, the Osijek Agricultural Institute has winter and spring barley collections, which contain 266 varieties and lines of winter barley and 451 varieties and lines of spring barley. However, only 38 varieties and lines of winter barley and 65 varieties and lines of spring barley have a Croatian origin (created by the Osijek Agricultural Institute).

We cannot guarantee the genetic purity, especially in the older samples of our barley collection, but we can guarantee it in the younger samples of our barley collection, which are presented in Table 1. Owing to the lack of adequate storage space, this material is being continuously multiplied.

All the new buildings of the Osijek Agricultural Institute were completely destroyed during the war in Croatia and long-term storage of seed samples is impossible. Now, we can expect that the national plant genetic resources could benefit from the FAO Global System, through the strengthening of national capacities for collecting, conservation and utilization of local germplasm (Sikora 1994).

The barley varieties (spring and winter) of Croatian origin are well-known in the region for their high genetic potential for grain yield, short and strong stem, high resistance to lodging and good resistance and tolerance to the most important diseases (Kovačević *et al.* 1995).

**Table 1.** Registered varieties of the Osijek Agricultural Institute

| Variety | Year of registration | Origin |
|---|---|---|
| **Two-row winter barley** | | |
| Satir | 1970 | 71 A 3 × Kruǿevački 1 |
| Alkar | 1973 | (Belje 607 × 73 B.3) × Herta) × Rika |
| Mursa | 1972 | (Belje 607 × 73 B.3) × Herta) × Rika |
| Osječki goli | 1974 | Osk.101/19 × (COAC × Maksimirski) × Herta) |
| Marsonija | 1977 | Satir × Osk. 6. 1/39/66 |
| Slavonac | 1980 | Osk.5.1/155-65 × Hauters |
| Pan | 1983 | Mursa × Maris Otter |
| Dorat | 1983 | Satir × Kearney |
| Sladoran | 1984 | Alpha × Mursa |
| Osječanin | 1984 | Mursa × Alpha |
| Sokol | 1984 | Osječki goli × (Osk.5.2/30-65 × Haganemugi) |
| Baja | 1985 | Alpha × Mursa |
| Rodnik | 1986 | Alpha × Mursa |
| Panonac | 1987 | Alpha × Osk. 3.145-77 |
| Val | 1989 | (Dorat × (Alpha × Mursa) |
| Rex | 1990 | (Dorat × (Alpha × Mursa) × Osk.5.59/6-78 |
| Danko | 1991 | (Dorat × (Alpha × Mursa) × Osk. 5.59/6-78 |
| David | 1993 | Pan × NS 293 |
| Mihael | 1993 | Osk. 5.59/6-78 × Osk.5.96/2-76 |
| Zvonimir | 1995 | Osk. 5.59/6-78 × (Pan × NS 293) |
| Viktor | 1996 | Osk.5.88/2-80 × Osk.5.48/9-82 |
| Olimp | 1997 | Osk.6.59/9-79 × Osk.4.58/2-81 |
| **Six-row winter barley** | | |
| Val-Ma | 1976 | Haunter × Montendin |
| Kornakum | 1977 | Hauters × Osk. 5.1/155-65 |
| Osječki rani | 1983 | Osk. 5.1/155-65 × Hauters |
| Osijek | 1988 | Morgenrote × Osječki rani |
| Posavac | 1993 | Osk.6.59/10-79 × Osk.3.52/2-81 |
| Baranjac | 1993 | Sladoran × Plaisant |
| Podravac | 1996 | Ciklon × Pan |
| **Two-row spring barley** | | |
| Velebit | 1977 | Wisa × Hunter |
| Dilj | 1980 | (Browarny × Volla) × Sultan |
| Kalnik | 1980 | Osk.4.5/4-67 × Ofir |
| Papuk | 1980 | Hassan × Amsel |
| Nehaj | 1981 | Osk.4.5/4-67 × Ofir |
| Jaran | 1983 | (Browarny × Volla) × Sultan |
| Prenj | 1985 | Osk.4.1/1-70 × Hassan |
| Osvit | 1988 | Kr. 72310 × (Osk.4.1/1-70 × Carina) |
| Pivarac | 1990 | Osk.4.1/1-70 × (Carina × Triumph) |
| Orion | 1990 | Menuet × Osk.4.27/6-76 |
| Astor | 1991 | Villa × Nehaj |
| Lux | 1991 | Osk.4.1/1-70 × (Carina × Triumph) |
| Lunar | 1991 | Menuet × Osk.4.27/6-76 |
| Favory | 1993 | (Osk.5.3/4-77 × Cornell) × NS 301 |
| Vitez | 1993 | Osk.6.27-78 × Europa |
| Baltazar | 1993 | Osk.3.74/5-81 × NS 301 |

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# Cyprus barley genetic resources and their use in breeding programmes

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Cyprus with its limited human resources has made considerable progress in collecting germplasm of local landraces of barley, in collecting and evaluating wild barley germplasm, and finally using it in breeding programmes aiming at developing improved barley cultivars for drylands. A brief account of this work is given below, together with available references.

## *Gene Bank collections*

Detailed lists of material stored in the Gene Bank of the Institute have been provided by A. Della to H. Knupffer for presentation at this meeting. In all, the Institute holds 26 accessions of barley collected in 1978 and 3354 inbred lines (progenies of single spikes collected during regeneration of the 26 accessions).

## *Landraces*

Landraces played an important role in Cyprus, as feed and food sources for thousands of years. Our ancestors have selected valuable genetic material which was evaluated during 1989-92 with improved recently selected varieties (Hadjichristodoulou 1993b, 1994a). It was concluded that this material does not have any undesirable traits and can be used in breeding programmes for adaptation to dry and hot Mediterranean climates. The landraces are stored in the ARI Gene Bank of Cyprus.

## *Germplasm of* Hordeum vulgare *subsp.* agriocrithon

The subsp. *agriocrithon* lines originated from natural crosses between subsp. *vulgare* and subsp. *spontaneum* and were subjected only to natural selection. They are six-row, tough rachis genotypes resembling wild barley. Selected genotypes from the natural hybrids gave grain yields approaching those of the best genotypes selected by scientists (Hadjichristodoulou 1994a). These naturally bred genotypes expressed valuable measurable traits, such as 1000-grain weight, crude protein content, volume weight, lodging and disease resistance, which could be used in breeding programmes. Furthermore, non-visible gene complexes for adaptation to moisture, heat and other stresses that are present in natural hybrids could be exploited by breeding. The natural hybrids apparently contributed towards maintaining genes present in landraces that became extinct long time ago.

## *Crosses with wild germplasm*

Selected germplasm of *H. spontaneum* subsp. *spontaneum* and subsp. *agriocrithon,* and also landraces, were used successfully in crosses with improved barley cultivars in Cyprus and the results have been published (Hadjichristodoulou 1993a, 1993b). More recent data of selection from a cross with wild barley (*H. spontaneum* subsp. *spontaneum)* demonstrate the usufulness of such crosses. 'Trachonas', selected from a cross with wild barley, outyielded the improved breeding line 'Lefkonoico' and the improved cultivars 'Athenais' and 'Kantara' (Table 1). Earliness, spike fertility (number of grains per spike) and volume weight were among the traits for which 'Trachonas' was superior to cultivars. The mean grain yield superiority of 'Trachonas' over 'Athenais' was improved by 29% and 1000-grain weight was lower, but in an extremely dry environment, 'Trachonas' outyielded 'Athenais' by almost 100% and the size of its grains was equal to that of 'Athenais'. Thus, this is an indirect indication that hidden non-measurable genes in the wild barley incorporated into improved cultivars could improve their performance, particularly under stress conditions.

**Table 1.** Traits of 'Trachonas' †, a selection from a cross with wild barley, in comparison with improved cultivars

| Cultivar | Grain yield (kg/ha) | Heading date (1=1st March) | Plant height (cm) | Tiller number /m² | Harvest Index (%) | 1000-grain wt. (g) | Volume wt. (kg/hl) | No. grains per spike |
|---|---|---|---|---|---|---|---|---|
| Athenais | 3817 | 29 | 82 | 348 | 45.4 | 40.3 | 57.4 | 32.9 |
| Lefkonoico | 4757 | 30 | 78 | 334 | 53.5 | 41.5 | 59.8 | 40.3 |
| Kantara | 3693 | 33 | 72 | 605 | 44.9 | 45.2 | 61.7 | 17.7 |
| Trachonas | 4914 | 26 | 83 | 318 | 50.3 | 37.3 | 64.1 | 44.9 |

† Trachonas = UNION/CI 3576//COHO/3/H. Spnt. Athal. CYB 84-3861-ID-OA-OD-Sel B.

## Pasture barley

Permanent pastures were successfully established with mixtures of bulks of crosses of *Hordeum vulgare* subsp. *vulgare* with subsp. *agriocrithon* (given the name 'Mia Milia') and with mixtures of natural crosses involving *H. vulgare* subsp. *agrioctithon* (given the name 'Akhera'). These crosses were made to exploit the brittle rachis gene of wild barley in order to develop self-reseeding pasture barley (Hadjichristodoulou 1994b, 1995).

No reseeding of the pasture was necessary but a light cultivation to cover the seed in the first year of sowing improved plant establishment. No cultivation was necessary in the following years. Genotypes with a tough rachis were rapidly eliminated from the 'Milia' pastures ($F_2$ bulks) because of their poor seed dispersal. Nitrogen and phosphorus fertilizer increased dry matter yield. Levels of seed dormancy in the wild barley were adequate to provide a safeguard against extreme dry weather conditions and other natural hazards. Forage quality was very high, with a crude protein content of 18% and digestible organic matter of 80% in harvested dry matter. Permanent barley pastures that exploit the brittle-rachis gene of indigenous genetic material have considerable potential for increasing the animal-carrying capacity of permanent pastures and marginal cropped lands.

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# The Czech barley collection[17]

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## *Characteristics of the Czech cereal collection*

The major objectives of the collection are to obtain new accessions, and study their characteristics, effective utilization and maintenance.

Activities are carried out in the framework of the Czech National Programme for the conservation and utilization of plant genepools.

## *Characteristics of the Czech barley collection*

The collection is maintained at the Agricultural Research Institute Kroměříž, Ltd. It includes 2465 accessions, 69 varieties and 3 botanical species of *Hordeum* from 70 countries.

**Table 1.** Cereal collections in the Czech Republic (1996)

| Institute | Winter barley | Spring barley | Winter wheat | Spring wheat | Rye | Oat |
|---|---|---|---|---|---|---|
| IPP PRAG | 1618 | – | 5683 | 3747 | – | – |
| ARI KROMERIZ | – | 2465 | – | – | 687 | 1903 |

**Table 2.** Comparison of performances of a 6-row and a 2-row winter barley, Czech Republic (1993-95)

| Variety | Wintering (%) | Yield (t/ha) 1993-95 | Height (cm) | Lodging (1-9) | 1000-grain weight (g) | Sieving 2.5 % |
|---|---|---|---|---|---|---|
| 6-row Luxor (CZ) | 94 | 6.82 | 89 | 8.8 | 43.1 | 71.3 |
| 2-row Marna (F) | 95 | 6.45 | 83 | 7.5 | 46.5 | 81.7 |

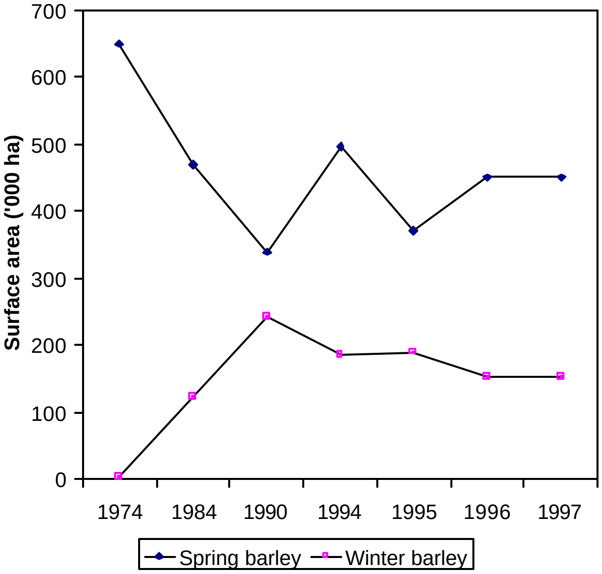

**Fig. 1.** Development of barley cultivation in the Czech Republic, 1974-97.

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[17] Summary of data from slide presentation.

# The French barley national collection: present status and organization

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## *Status, composition, and management rules of the collection*

The composition of the French Barley Collection was established for the first time at the beginning of 1997 as defined in the frame of the Cereal Genetic Resources Programme developed since 1983 in France.

This collection comprises at present 467 entries (i.e. much less than the corresponding bread wheat list of 1968 entries). In the present situation this collection is intended to concern:

1. Old barley land varieties from France (in practice pure lines extracted from the original multiline populations): 78 accessions.
2. Barley cultivars previously marketed and registered on the French Official Catalogue of Cultivated Species which have been bred in France, and which had been struck off this Catalogue: 201 accessions.
3. Breeder's lines from France, with the agreement of their originator, and recognized worth to be included: 171 accessions.
4. Special barley material from scientific programmes in France, e.g. Induced mutants, cytogenetics material, lines derived from interspecific crosses and/or carrying identified alleles (17 accessions only, to date).

The everyday management of this collection is organized by the Cereal Genetic Resources Unit, under the present responsibility of Annick Le Blanc (GEVES-Le Magneraud, France) (also for other cereals).

A scientific steering committee has defined an appropriate series of rules and specifications, which serve as operation guidelines for the management unit; this committee observes in addition the cereal genetic resources actions carried out in France. To exemplify briefly some of these rules:

1. *Composition* (see above).
2. *Conservation standards* (quantity, environmental conditions, germination tests, duplication).
3. *Sharing of responsibilities* for conservation, as much as possible: every originator (in general a breeding company or institution) of a given material is requested to maintain properly the barley genetic resources he created. Otherwise the conservation is ensured at GEVES, INRA or by other organizations. Measures are taken to prevent the loss of entries in case one or other curator can no longer fulfil his task. The aim is to associate concretely every partner or user concerned with barley genetic resources as much as possible. The various curators are encouraged to participate, in particular to make suggestions as to the inclusion of new accessions (including the extended list of the network mentioned below), or potential non-inclusion or even suppression of some lines.
4. *Access* by and *exchanges* with other organizations, in particular foreign genebanks: the principle is free access, on a reciprocity basis.

### Database and catalogue

A National Cereal Genetic Resources database, using ERGE, a Microsoft-Access application written by A. Le Blanc, is managed and regularly updated by the GEVES management unit at Le Magneraud. This database is unified for all small grain species, with a corresponding index code, unique for each cereal entry, irrespective of its species. After checking and approval by the community of organizations and companies interested in barley genetic resources, a Catalogue of the French National Barley Collection is issued. This document should be issued by end July 1997 (Le Blanc 1997); it comprises also the Bread Wheat Collection list. A further issue should include the other species for which work is in progress: durum wheat, oats, rye and triticale.

The organization of this database should be basically the same as for the European Wheat Database (EWDB) (Le Blanc and Faberová 1997), and is the same as the INRA Cereal Genetic Resources Database using the ERGE application, and other barley or cereal curators of the French network are strongly advised to adopt the same system.

The 467 accessions listed in the Catalogue are documented with the main passport data, including the pedigree whenever possible. No agronomic evaluation data, gene information – apart indirectly from winter vs. spring habit, two-row vs. six-row and naked vs. hulled kernel- or principal attributes have been considered for the present issue.

An Internet access will be scheduled as soon as the appropriate support is available. At present, any request may be addressed by email to A. Le Blanc (annick.leblanc@geves.fr).

### Complementary barley genetic resources list

For practical reasons and for internal use within the French genetic resources network only, it has been felt necessary or useful to append a complementary list of genotypes to the Barley collection list – which nevertheless does not form a part of the latter. This complementary set comprises:

- marketed cultivars originating from France, still registered, with the aim to prepare their later fully documented introduction in the national collection, as soon as they will have been crossed off from the Official Catalogue of registered and marketed cultivars
- some foreign entries which either have been registered and widely cultivated in France and then serve as reference for comparisons in networks, or have been widely used as parents in crosses or standard controls for diseases and pests. In the first case their conservation is generally granted abroad, but it is convenient to have information at hand. In the latter case, the accession is not either claimed to belong to the national list, however it may seem safer to ensure its conservation whenever it is not granted that this is done somewhere abroad.
- barley material which has been collected by French expeditions or travellers, in particular from Nepal, Ethiopia and Northern Africa, and conserved in local collections since.

This series is not published with the national collection, but the accessions are present in a local collection or another – especially in INRA collections – where information can be requested.

## *Status of the barley collection within the framework of the Cereal Genetic Resources Network in France*

### The Cereal Genetic Resources Network

The cereal genetic resources programme in France is run as a network associating all potential organizations interested, or users via their representatives. These include in particular:

- the Ministry of Agriculture and Fisheries
- BRG (Bureau des ressources génétiques) – an office depending on the Ministry of Research and Industry, in charge of the policies for genetic resources (wild and domesticated, plant, animal, fungi, etc.) and of genetic diversity conservation
- GEVES (Groupe d'étude et de contrôle des variétés et des semences) – in charge of plant variety testing for registration)

- INRA (Institut national de la recherche agronomique) – state-funded agricultural research institute (Lefort and Doussinault 1994)
- SPSS (Syndicat des producteurs de semences sélectionnées) – union of the French private breeding companies
- CTPS (Comité technique permanent de la sélection des plantes cultivées) – plant registration advising committee
- ONIC (Office national interprofessionnel des céréales) – national office for cereal production
- GNIS (Groupement national interprofessionnel des semences, graines et plants) – seed producers union.

In this way, the programmes carried out meet more easily the requests of the interested groups, including priorities, research actions, support for financing.

This structure appears both decentralized and cooperative. However the tasks usually devoted to a formal genebank are shared in practice between GEVES and INRA (Jestin *et al.* 1994), with some delegation to breeding companies as seen above, under the coordination and attention of the cereal genetic resources management unit.

As well as the coordination of cereal collections and databases, the network is active in two other fields: implementation of multisite cereal resources evaluation networks, and involvement in international cooperation.

### Cooperative genetic resources evaluation nurseries

These nurseries comprise 50-100 entries for each crop, of which 20-35% are reference controls for various traits. They have been sown every year since 1989 for winter barley and winter wheat and despatched by the Cereal Genetic Resources management unit (A. Le Blanc). For spring barley, new sets are distributed every two years only. In 1996-97, for instance, the winter barley series RGOH97[18] comprising 51 genotypes (of which 17 were controls) was hosted by 22 participants – 16 private companies and 6 public institutions; some installed this nursery in two or three sites, in particular with regard to yellow mosaic free conditions, or soil infectious for Y1 or Y2 of this virus disease.

The standard and basic nursery design is a bed, with three consecutive rows per genotype; when feasible, a total of two replications is recommended. For diseases, only degree of apparent resistance vs. susceptibility scorings after natural infection are recorded, although a more accurate evaluation with artificial infections in one site, for major foliar diseases, would be desirable in the future.

The purposes of such multisite nurseries, covering fairly well the French territory (except in the southeast) are:

- To give a rapid access to novel germplasm, potentially useful for research or commercial breeding. These include notably INRA material or from other participants incorporating disease resistance genes or adaptation traits. For instance the German variety 'Borwina' displayed a high resistance level to frost in a well-adapted general background and was incorporated therefore in our frost-resistance scale (controls); for yellow mosaic, a number of resistant Japanese varieties were crossed with European progenies, and some lines associating BaYMV resistance with a better overall adaptation than the original resistance source were circulated and evaluated.
- To carry out agronomic evaluations, serving to document these accessions, in particular in the database. Most participants can contribute every year with at least one or two scorings (trivial observations for highly heritable characters already studied, such as plant height, number of rows, growth habit, earliness, etc. are not requested). Grain yield is not estimated, at this stage, it is considered sufficient to have a visual

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[18] RGOH = Ressources Génétiques Orge d'Hiver (Winter Barley Genetic Resources).

appreciation of the adaptation level, in 3-4 classes, from entries equal or superior to current standards to those visibly not adapted and yielding 50% or less of the controls. No testing for utilization quality is performed on barley on these series, as is the case for bread wheat.

One or two years of pre-evaluation, in an INRA nursery, is carried out before proposing any entry in the multisite evaluation nursery. Fully unadapted genotypes, e.g. very susceptible to lodging, extremely susceptible to a local disease, etc. are discarded from the beginning and may eventually be crossed in a pre-breeding programme before circulating acceptable or near-acceptable recombined progenies incorporating the desired trait.

A brief report summarizing the multisite data recorded is then circulated in autumn among the participants.

Alterations likely to improve the efficiency of such nurseries and the satisfaction of the contributors are regularly discussed by the cereal genetic resources steering committee.

### International cooperation

Cooperation on barley genetic resources concerns at once regular exchanges of evaluation nurseries. These are carried out in the frame of the national programme, where INRA laboratories generally observe nurseries, although not always: CIMMYT or ICARDA nurseries are often studied by several breeders.

For many years, a European Barley Disease Nursery (EBDN), with chiefly spring barley, was organized yearly by the former SVP in Wageningen (The Netherlands) and two or three INRA stations participated in this network. In the last years, the genotypes included did not change much, but this network represented a useful opportunity to test new resistance sources, to be informed quickly and on a broad base of the collapse of such resistance. So this EBDN was missed, although the material included often needed more than one selection cycle to reach commercial material standards. A similar winter European Nursery was run for some years by the Technical University of Munich (Germany) by E. Schwarzbach and collaborators, bringing in particular powdery mildew resistance especially recommended for a coordinated use within European breeding programmes.

At present the INRA Genetics and Breeding Station in Clermont-Ferrand still participates in some evaluation nurseries from abroad:

- CIMMYT International Barley Observation Nursery (IBON) (irregularly)
- MTS (Mehltausortiment) and ZTS (Zwergrostsortiment) spring barley nurseries for powdery mildew and brown rust from IPK Gatersleben/BAZ Aschersleben.

The French RGOH nursery is also being observed in Belgium for the two Y1 and Y2 BaYMV pathotypes. Other cooperation involves tentative European projects on barley genetic resources, and participation to the EBDB (European Barley Database) based in Gatersleben, Germany (Knüpffer 1988).

## *Concluding remarks – future prospects*

The present situation of the French barley collection appears acceptable concerning primary conservation and base passport data stored in an appropriate database. Ensuring safety-duplicates is in progress.

The involvement of users – chiefly breeders – seems to work, and most participate. They declare that they regularly use two to five entries from the evaluation network yearly in their breeding programme, which is considered satisfactory.

However, some gaps remain: a standard agronomic evaluation of all barley resources is far from complete and progresses too slowly. It is hoped that international cooperation on such practical aspects as sharing conservation tasks for some entries, developing common evaluation networks if possible, or exchanging more germplasm will increase, on a pragmatic basis in the future.

A point of concern is that the rule for carrying out work on genetic resources may become more stringent in the future, a tendency which is also observed as far as biotechnology is concerned. This may represent a threat on such genetic resource programmes, as an exchange or compilation of data limited to old germplasm without an acceptable level of adaptation, only, would make little sense. However full attention should be paid to such rules as those proposed by the US National Wheat improvement committee (Sears and Peterson 1994).

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# Status of the barley collection of the Genebank of IPK Gatersleben

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## *Introduction*

The Gatersleben genebank in its 54th year comprises almost 100 000 accessions, including about 20 000 accessions in external branch stations which have belonged to IPK since 1992. Among these, barley is one of the most important crop collections, with over 12 000 accessions. The branch stations do not hold barley material.

Through the history of the Gatersleben institute and its genebank, barley has always been one of the main targets of different kinds of research and evaluation. This can be seen from the large number of publications on barley genetic resources by IPK staff, mainly from the genebank, and by cooperation partners for evaluation (Annex 1, this paper).

The international recognition of Gatersleben as a centre of excellence for barley genetic resources is reflected by the fact that the ECP/GR Barley Working Group designated Gatersleben as the place to hold all five meetings in 1983, 1986, 1989, 1993 and 1997 (IBPGR 1983, 1986b, 1989b; Frison *et al.* 1993) and a Barley Workshop in 1985 (IBPGR 1986a). The IBPGR International Barley Working Session in 1989 (IBPGR 1989a) as well as the meeting of the IBGRN (International Barley Genetic Resources Network) database task force in 1993 also took place at Gatersleben.

## *Composition of the Gatersleben barley collection* [19]

The present species composition of the 12 832 barley accessions is given in Table 1. The 573 accessions referred to as *Hordeum* sp. are recent introductions which will be determined during the next multiplication period. Most of the material belongs to the primary genepool of barley, i.e. *H. vulgare* (11 554 accessions, among them 66% are landraces and 34% cultivars and lines, 22% winter and 78% spring barleys) and the related species *H. agriocrithon*, *H.* × *lagunculiforme* and *H. spontaneum* comprising altogether 507 accessions. The secondary genepool is represented by 67 accessions of *H. bulbosum*. The remaining wild species belong to the tertiary genepool which is represented by 131 accessions.

Table 2 lists the barley accessions according to their countries of origin. Of these, 25% originate from Ethiopia, followed by Turkey (8%), Germany (6%) and the USA (5%).

Additionally, a collection of barley mutants with about 700 accessions was taken over by the genebank from another department of the institute five years ago.

## *Acquisition of material*

The barley collection, like other collections of the genebank, has two main sources:

1. collecting activities, mainly of Gatersleben staff (e.g. Central Europe, Mediterranean, Near East, Caucasus, Central Asia, China, Korea, Ethiopia), but also old collections from the first half of this century (e.g. Turkey, Tibet, Nepal, Hindu-Kush, Ethiopia, Balkan),
2. breeders, botanical gardens, research institutions.

Large parts of the collected material under (1) have to be considered as unique.

In self-pollinating species such as barley, populations of morphologically different types are being split up into lines which are maintained as separate accessions, in order to reduce the danger of genetic changes in accessions during multiplication.

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[19] Figures have been updated as of May 1998.

**Table 1.** Species composition of the Gatersleben barley collection

| ***Hordeum* species** | **Accessions** |
|---|---|
| *H. agriocrithon* Åberg | 40 |
| *H. arizonicum* Covas | 1 |
| *H. bogdanii* Wilensky | 4 |
| *H. brachyantherum* Nevski | 3 |
| *H. brevisubulatum* (Trin.) Link | 12 |
| *H. bulbosum* L. | 67 |
| *H. californicum* Covas & Stebbins | 1 |
| *H. capense* Thunb. | 1 |
| *H. chilense* Roem. et Schult. | 2 |
| *H. comosum* Presl | 2 |
| *H. cordobense* Bothmer *et al.* | 1 |
| *H. depressum* Rydb. | 1 |
| *H. flexuosum* Steud. | 1 |
| *H. fuegianum* Bothmer *et al.* | 1 |
| *H. intercedens* Nevski | 1 |
| *H. jubatum* L. | 21 |
| *H.* × *lagunculiforme* (Bacht.) Bacht. ex Nikif. | 44 |
| *H. lechleri* (Steud.) Schenck | 1 |
| *H. marinum* Huds. | 18 |
| *H. murinum* L. | 33 |
| *H. muticum* Presl | 2 |
| *H. parodii* Covas | 1 |
| *H. patagonicum* (Haumann) Covas | 3 |
| *H. procerum* Nevski | 1 |
| *H. pubiflorum* Hook. f. | 1 |
| *H. pusillum* Nutt. | 1 |
| *H. roshevitzii* Bowden | 3 |
| *H. secalinum* Schreb. | 5 |
| *Hordeum* sp. | 573 |
| *H. spontaneum* Koch | 423 |
| *H. tetraploidum* Covas | 1 |
| *H. turkestanicum* Nevski | 3 |
| *H. violaceum* Boiss. et Huet. | 6 |
| *H. vulgare* L. | 11554 |
| **Total** | **12832** |

### *Reproduction and storage*

The barley accessions are multiplied in the field, about 1000 accessions per year. Seeds are stored in the long-term storage under conditions of 0°C or -16°C, respectively. Germination results covering 20 years of cold storage are shown in Figure 1.

The multiplication of wild species accessions is labour-intensive. However, expertise exists at Gatersleben as could be shown with a selection from the Scandinavian *Hordeum* Collection (Svalöf, Sweden) which was handed over to IPK for that purpose.

### *Characterization and evaluation*

The accessions are characterized routinely in the field during multiplication and rejuvenation. Morphological characterization includes the botanical determination of varieties and convarieties. The following descriptors are observed, among others: phenological data (such as days to flowering), 1000-grain weight, lodging, wintering, mildew and rust field resistance. Every new accession is determined botanically during the first cultivation.

In cooperation with other groups of the Gatersleben institute, and with partners from other institutions, large parts of the collection have been extensively evaluated for resistance

**Table 2.** Composition of the Gatersleben barley collection by countries of origin. Only the countries with the highest numbers of accessions (≥ 40) are listed

| Accessions | Country of origin |
|---:|---|
| 3126 | ETH – Ethiopia |
| 977 | TUR – Turkey |
| 717 | DEU – Germany |
| 637 | USA |
| 474 | JPN – Japan |
| 423 | CHN – China |
| 402 | IND – India |
| 376 | NPL – Nepal |
| 336 | GRC – Greece |
| 289 | ITA – Italy |
| 208 | PAK – Pakistan |
| 191 | FRA – France |
| 185 | KOR – Korea, Republic of |
| 181 | RUS – Russian Federation, cf. also SUN |
| 163 | SVK – Slovakia |
| 160 | AUT – Austria |
| 157 | LBY – Libya |
| 155 | SUN – (former) Soviet Union, cf. also RUS, GEO, TKM, UKR, UZB |
| 152 | AFG – Afghanistan |
| 149 | POL – Poland |
| 144 | IRN – Iran |
| 127 | GBR – Great Britain |
| 126 | GEO – Georgia, cf. also SUN |
| 123 | PRK – Korea (North) |
| 120 | CAN – Canada |
| 116 | TKM – Turkmenistan, cf. also SUN |
| 111 | DNK – Denmark |
| 107 | SWE – Sweden |
| 105 | BGR – Bulgaria |
| 96 | UKR – Ukraine, cf. also SUN |
| 86 | CHE – Switzerland |
| 83 | CSK – (former) Czechoslovakia, cf. also SVK, CZE |
| 83 | ROM – Romania |
| 68 | HUN – Hungary |
| 65 | IRQ – Iraq |
| 65 | NLD – Netherlands |
| 56 | TUN – Tunisia |
| 55 | ESP – Spain |
| 51 | ALB – Albania |
| 49 | ISR – Israel |
| 48 | YUG – (former) Yugoslavia |
| 43 | UZB – Uzbekistan, cf. also SUN |
| 40 | ARG – Argentina |
| 1017 | Unknown |
| 389 | 43 other countries with less than 40 accessions |

to diseases and abiotic stresses (see below, **Review of barley literature**). A protein screening of the cereal collections was carried out in the 1970s and 1980s.

Molecular characterization of the barley collection will be carried out within the recently established large IPK research project "Plant Genome Resource Centre" (PGRC) (see Graner, this volume, p. 87).

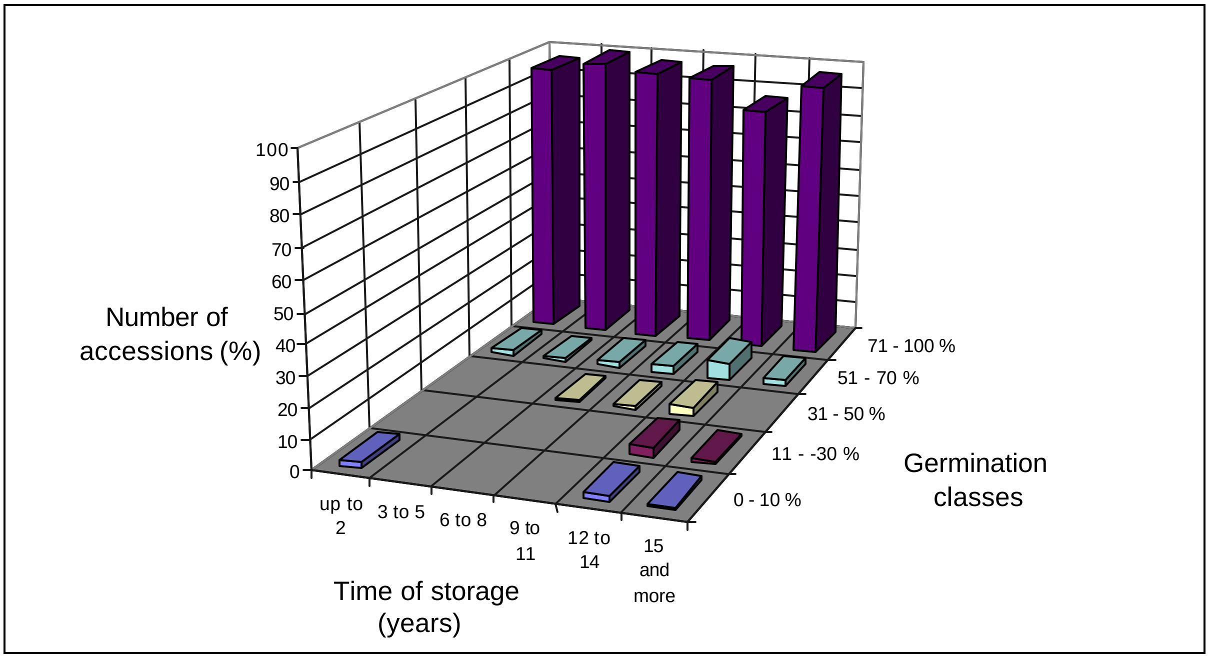

**Fig. 1.** Germination ability of *Hordeum* spp. stored in Gatersleben at 0°C.

### *Documentation*

The traditional manual documentation is carried out with a sophisticated system of card files and books, with cross-references. Passport data and some management and characterization/evaluation data are registered in a database system, using the database software FoxPro in a LAN (local area network) of PCs, which is part of IPK's LAN and thus connected with the Internet. Selected descriptors of the genebank's passport database for all crops (about 80 000 accessions) are searchable on-line on the Internet (see Knüpffer and López, this volume, p. 42). At present, emphasis is given to recording "historical" characterization and evaluation data of the genebank for incorporation into a German "Federal Information System for Evaluation Data of PGR" within the project EVA, focusing mainly on barley (see Harrer, this volume, p. 89).

The Gatersleben genebank also maintains the European Barley Database of the ECP/GR since 1984. It has been updated in 1997 (see Knüpffer and López, *op. cit*.)

The development and the present state of the International Barley Core Collection, in which IPK's genebank took an active part, are described separately (see relevant section in Part I, p. 15).

A herbarium or spike sample and a seed sample are taken from every accession for later reference, e.g. to check the identity after regeneration.

### *Review of literature on the basis of results from Gatersleben*

Various research activities have been carried out on barley genetic resources at Gatersleben. They range from taxonomic research (classification of cultivated barley), to genebank-specific questions of reproduction, pollination ecology, genetics, mutation research or physiology. The literature consists of about 100 papers covering more than 50 years (see Annex 1, this paper). A complete overview of relevant literature about the genebank covering the period from 1943 to 1993 was given in Ref. (92). The following topics have been selected (the numbers of the relevant papers are indicated in parentheses):

- Taxonomy and evolution (1, 52, 73)
- Morphology and anatomy (2, 26, 30, 46)

- Resistance (3, 4, 6, 7, 13, 14, 15, 16, 18, 19, 20, 22, 24, 25, 27, 28, 29, 33, 34, 35, 36, 38, 44, 45, 47, 54, 59, 62, 63, 68, 69, 70, 75, 76, 79, 80, 84, 85a, 95, 96, 98, 99, 101); see also paper by Walther *et al.* (this volume, p. 93)
- Mutations (5, 8, 9, 10, 11, 12)
- Physiology (17, 21, 23)
- Quality characters (26, 30, 42, 43, 58)
- Alternative uses (90a)
- Pollination ecology (31, 32, 37, 39, 40, 41, 49, 51, 88a)
- Collecting missions (50)
- European Barley Database (53, 55, 56, 57, 60, 61, 64, 65, 66, 67, 71, 72, 78, 82, 85, 89, 90, 97, 100, 103)
- Barley Core Collection (74, 77, 81, 83, 86, 88, 91, 94)
- Documentation (87, 93, 97, 100, 103).

### *Availability of material to users*

The available accessions (i.e. those with enough seeds and germinability) are listed in the Index Seminum which appears every two years. Material is freely available on request. Users may also query the on-line database of the genebank via the Internet **<http://fox-serv.ipk-gatersleben.de>**. Queries in the local database, which contains more information, are also carried out on request of interested parties.

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## *Annex 1. Literature related to the Gatersleben barley collection*

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# BAZ Gene Bank: status report on the barley collection

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## *Introduction to the BAZ Gene Bank*

The Braunschweig Genetic Resources Collection (BGRC) was founded at the Federal Agricultural Research Centre Braunschweig-Völkenrode (FAL) in 1970 and was managed by the Institute of Crop Science of the FAL until 1996. Breeding research at FAL ceased shortly after the reunification of Germany. Therefore, the responsibility for the BGRC was assigned to the Federal Centre for Breeding Research on Cultivated Plants (BAZ) in July 1996. The official name of this new BAZ branch office is 'BAZ Gene Bank – Plant Genetic Resources Collection'.

The plant genetic resources collection at Braunschweig was established with the objective to improve access to information and germplasm held in Germany and abroad. To allow for efficient data documentation, retrieval and dissemination, a computerized documentation system was developed between 1972 and 1979 (Seidewitz *et al.* 1993). In parallel a technical seed handling and conservation unit with a capacity of 48 000 accessions stored at –10°C and 12 000 accessions at +3°C was built. In 1972 the Technical Advisory Committee (TAC) of the ICAR recommended to establish a world network consisting of regional genebanks of which the Institute of Crop Science was intended to serve as a subregional centre for northwestern Europe. At that time excellent storage facilities such as those available at Braunschweig were rare in Europe. The genetic resources collection therefore accepted a broader responsibility for germplasm conservation in Europe and offered its seed storage and data documentation capacities to collection-holders in Germany and in Europe. In particular, research institutes without adequate storage facilities requested the Braunschweig genebank to accept collections that they could no longer maintain. A typical case is the durum wheat collection from Switzerland (Zürich-Reckenholz) for which the germplasm material and the responsibility was taken over. Many similar germplasm stocks were accepted, documented, maintained and kept available for international exchange over more than two decades. When more European countries created their own storage facilities, duplicates of their collections were also sent to Braunschweig for security storage.

A multitude of crops and wild species collections were joined at Braunschweig. The incoming data and the material were correctly documented and stored as provided by the germplasm donors; however, a critical review of the information, taxonomy, etc. on the accepted collections could not be performed systematically. Throughout its existence the genebank at Braunschweig had to function with a very limited number of permanent scientific staff. The ratio 'number of accessions/number permanent scientific staff' is still unique in the world. Today, the BAZ Gene Bank team consists of two scientists. Limited manpower capacity was partly buffered by the availability of modern data documentation and seed production equipment during the past two decades. This allowed coping with the workload with respect to seed stock maintenance and national/international seed exchange. Varying from year to year, 6000 to 10 000 accessions were distributed to users between 1986 and 1996. Wheat and barley proved to be the most frequently requested germplasm stocks. Obviously, our fast access to information and germplasm, flexible response with respect to 'urgent requests' and seed sample amounts, the user-tailored advice that can be given by the BAZ Gene Bank documentation group, are attractive to users and constitute our strength. Cost-effective genetic resources management, easy, free access to information and material, and services like mediation to germplasm held at other genebanks are the assets of the BAZ Gene Bank.

In the early years, the genetic resources collection served as a seed storage and documentation unit for collections that had been gathered and further developed in the course of research and breeding programmes. The material has been investigated, characterized and purposefully evaluated by donors. This part of our collection should not only be considered as a seed sample stock but also as the result of expensive investments into crop improvement that are preserved along with the physical sample. From 1980 onwards, several collecting missions have been implemented by the Institute of Crop Science of the FAL in cooperation with partner genebanks. This, as well as other unique material, forms an important fraction of the BAZ Gene Bank holding which deserves highest attention during regeneration and maintenance. Today, the collection comprises about 50 000 accessions of which cereals account for about 56%. The technical management of such a large, diverse collection with limited staff capacity is a problem and currently forces the BAZ Gene Bank to function as a genepool management unit rather than a genebank in the wider scientific sense. Since July 1996, improvement of the data documentation and germplasm stock management are underway, which should enhance the technical efficiency and cost-effectiveness.

During its affiliation with the Institute of Crop Science, much emphasis was given to the maintenance and evaluation of the genetic resources of neglected crops with industrial potential. As a result, the Institute of Crop Science only contributed data to the ECP/GR Barley Working Group in the past and never participated actively in workshops. As a genebank of the Federal Centre for Breeding Research on Cultivated Plants, priorities will automatically shift more towards cereals since these crops determine the research profile of the BAZ to a large extent.

### The BAZ Gene Bank barley collection

The main donors of the collection are presented in Table 1. Currently, the total barley collection amounts to 8892 accessions of which 1294 accessions are temporarily out of the collection. In the early 1980s this material was provided by the Ethiopian genebank with the request to keep safety-duplicates. Since the principles of security storage have been misinterpreted under the former genebank heading, there is a need for clarification of the status of the Ethiopian material. The germplasm could either be stored as security-duplicate samples according to international rules or – as the agreement of the Ethiopian Biodiversity Institute provided – as Plant Introduction Accessions (PIAs). The Ethiopian counterpart has already been approached and their response is awaited. The BAZ Gene Bank has recently identified 173 accessions as duplicated material that has also been maintained by the Dutch counterpart during the past two decades. As the maintenance of the germplasm collected during a Dutch/British expedition in the Hindukush area is the responsibility of CGN (the Netherlands), this material is no longer considered as part of our active collection. The material is kept in our storage but it is no longer accessible to users. Requests will therefore be forwarded to CGN. Our decision contributes to a more rational genetic resources management in Europe.

The largest fractions of the barley holding came from the Max-Planck-Institut für Züchtungsforschung (Köln) with 42%, the Institut für Pflanzenbau und Pflanzenzüchtung (München) with 17%, and Ethiopia (15%) (Table 1). For the time being, the germplasm gathered by donors CHEFAP, DEUBSAH and DEUGTZJEM is considered as unique. It is categorized according to our new system as 'Primary Genetic Resources' material that needs to be maintained at highest technical standards.

*Hordeum vulgare* L. is the prevalent species with 92% of all material. Respectively 52%, 20% and 16% of the collection have been described as landraces, cultivars and breeder's lines.

Ethiopia, Germany, Switzerland, Turkey are the main origins of the BAZ Gene Bank barley collection; these accessions are complemented by a fairly large fraction of very diverse geographic origin.

**Table 1**. Main donors (largest collection portion only)

| Donor_ID | % | Institute | Place | Country |
|---|---|---|---|---|
| DEUMPIZFK | 42 | Max-Planck-Institut für Züchtungs-forschung | Köln | DEU |
| DEUTUMPZFS | 17 | Institut für Pflanzenbau und Pflanzen-züchtung | Freising-Weihenstephan | DEU |
| ETHPGRC/E | 15 | Plant Genetic Resources Center of Ethiopia | Addis Ababa | ETH |
| CHEFAP | 8 | Eidgenössische Landwirtschaftliche Forschungsanstalt | Zürich-Reckenholz | CHE |
| DEUBBAVIBS | 3 | Biologische Bundesanstalt, Institut für Biochemie | Braunschweig | DEU |
| DEUBBAGRUEN | 3 | Bundesanstalt für Züchtungsforschung an Kulturpflanzen | Grünbach | DEU |
| DEUFUBIOB | 2 | Freie Universität Berlin, Angewandte Genetik | Berlin | DEU |
| DEUBSAH | 1 | Bundessortenamt | Hannover | DEU |
| DEUUIAGH | 1 | Institut für Angewandte Genetik der Universität Hannover | Hannover | DEU |
| DEUGTZJEM | 1 | Deutsche Gesellschaft für Technische Zusammenarbeit | Eschborn | DEU |
| GBRUCNW | ] 8 | University College North Wales | Bangor | GBR |
| IRNSPII | ] | Seed and Plant Improvement Institute | Karaj | IRN |
| DEUFHSLWNT | ] | Fachhochschule Nürtingen, Fachbereich Landwirtschaft | Nürtingen | DEU |

## *Characterization and evaluation*

Only parts of the data contained in the BAZ Gene Bank database have been gathered at the site of Braunschweig. Most data were received from many different donors, resulting in an accumulation of heterogeneous data sets in the documentation system. The information can be retrieved without problems and can be traced back to the original data source which sometimes is helpful for clarification reasons. However, the new central database like PGRDEU developed by ZADI/IGR or any other central database requests information in a standardized manner which forces us to harmonize and compile data that were not gathered by us. Most of the information is valid. However, from time to time we are faced with the 'historical load' of the former BGRC database in which the first barley data were entered in 1977 (Seidewitz 1987; Seidewitz *et al.* 1990). Upgrading the passport data with the objective to offer them for on-line data searches in PGRDEU or to contribute them to the European Barley Database is almost completed. This work will meet its limits since for the time being we cannot offer higher-quality information than the data provided by donors allow. Likewise the taxonomic description provided by some donors may require some verifications.

During seed increase a minimal description of the material is performed. Since production of high-quality seeds requires plant protection measures, observations on disease susceptibility are only taken occasionally (mainly *Erysiphe graminis* f.sp. *hordei*). Evaluation has always been implemented in cooperation with private plant breeders and breeding institutes. Where adequate, the collection will of course be integrated into screening projects planned or conducted by BAZ institutes. Recently, parts of the barley collection have been screened in the GFP research project G64/94 AiF for amylose/amylopectin content. The data are currently entered into the database. The revision of the evaluation data will be the next activity. Sixty-two descriptors have more than 100 records; within this subset the number of records per descriptor runs up to 7506 in the case of row number.

## *Regeneration status*

The cereal seed regeneration programme is fully mechanized. Sowing, harvesting and threshing of the plots in the field are done with modern equipment normally used by plant breeding companies. In general, seeds are multiplied on a single 2-m$^2$ plot. If a high request for specific accessions can be anticipated, two plots are sown. Because of the GFP research activities, 684 accessions were sown in 1996 and 389 accessions in 1997 at Braunschweig.

Private plant breeders and breeding institutes have always assisted the BAZ Gene Bank in coping with the workload. In 1996, 79 barley accessions were seed-increased by the company

Ackerman & Co. Irlbach and in 1997 the Pflanzenzucht Dr.h.c. Carstens, Schwartau is assisting in the multiplication of 50 accessions.

The BAZ Gene Bank now discerns between 'accessible' and 'available' fractions of the holding, thus 15% of the barley holding, i.e. the germplasm from Ethiopia is currently not accessible because of the reasons given above, and 29% of the germplasm is currently not available because of limited amounts of rest seeds and/or low germination. The germination of 89% of the barley holding ranges between 40 and 100% (Fig. 1).

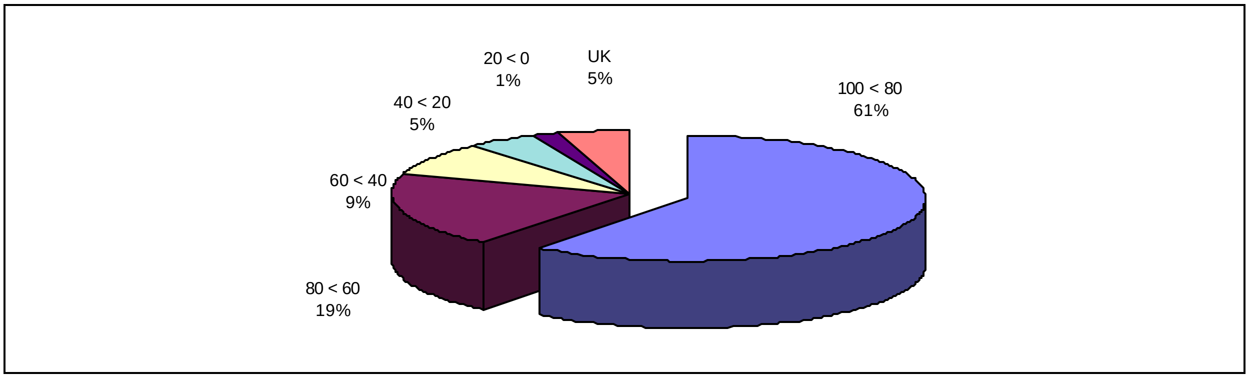

**Fig. 1.** Percentage of accessions by germination class (July1997).

### *National and international cooperation*

At the national level the BAZ Gene Bank made two major contributions. First, passport data records on 7467 accessions were provided to ZADI/IGR to support the establishment of PGRDEU. This set does not include 31 accessions which are probable duplicates received from the IPK, another 100 accessions for which the status/responsibility is not yet clear either, and the set from Ethiopia. This updated barley file was also sent to the European Barley Database.

The BAZ Gene Bank is not an official partner of the EVA project. The BAZ Gene Bank has no backlog in data computerization and hence no support was felt to be necessary. The BAZ Gene Bank provided its characterization and evaluation data to ZADI/IGR in 1996 and the data can be used by the project team for research purposes.

Between 1992 and 1996, 780 accessions were sent to users abroad. Most of the material was requested by research institutes and public organizations. In the same period 3285 accessions were sent to users in Germany. The majority was requested by private plant breeders (Table 2).

**Table 2.** Number of accessions distributed between 1992 and 1996

| User | Number of accessions |
|---|---|
| **Foreign countries** | |
| Research institutes | 399 |
| Genebanks | 40 |
| Public organizations | 229 |
| Private sector | 39 |
| Universities | 73 |
| **Germany** | |
| Schools | 50 |
| Botanic gardens | 57 |
| Research institutes | 69 |
| Genebanks | 1 |
| Public organizations | 115 |
| Private sector | 136 |
| Universities | 61 |
| Breeders | 2796 |

## The future

Next to wheat and sugarbeet, barley belongs to the most frequently requested germplasm held at Braunschweig. Barley is thus an important part of the total holding. A framework concept required for streamlining the collection and the database has been developed and will be implemented stepwise with the aim to (i) focus our capacities on unique samples and (ii) improve the technical quality standards and services.

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# The Irish National Programme for repatriation of cereal accessions*

***Michael Miklis***
*Irish Seed Saver Association, Raheen, Piltown, Co. Kilkenny, Ireland*

At the time of the fifth meeting of the Barley Working Group in July 1997, Ireland did not have a national collection or genebank. Thanks to the information provided during the meeting and the following discussions held afterwards at home, Ireland now has a National Programme for repatriation of cereal accessions.

In situ: ***care of the***
Irish Seed Saver Association
Michael Miklis
Raheen, Piltown
Co. Kilkenny
Ireland
Tel. / Fax: +353 51 643519
Email: miggo@tinet.ie

Ex situ: ***in the National Gene Bank held by the***
Irish Genetic Resource Conservation Trust
Dr Stephen Waldren
Trinity College Dublin Botanic Gardens
Palmerstown Park, Dartry
Dublin 6
Tel.: +353 1 4972070
Email: swaldren@tcd.ie

The first four accessions were grown out in 1997 and harvested; some material is now stored in the Gene Bank and propagated further *in situ*. The *in situ* programme has been awarded a Heritage Grant which will greatly help the harvest, storage and cleaning possibilities.

In the autumn of 1997 the Irish Seed Saver Association sent out over 30 requests for genetic material of Irish origin. We received four replies and only one genebank supplied us with genetic material. Institutes which have not replied yet are reminded to please do so.

The Gene Bank is open to discussions on the "black box system" and as partners for research programmes.

Ireland is now able and willing to participate in conservation and sharing of responsibilities.

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* This update was received after the meeting.

# Barley germplasm collections in Israel

***Abraham Korol***

*Institute of Evolution, Haifa University, Israel*

There are three main barley collections in Israel. They are presented below according to the size of the collections.

## *Lieberman Germplasm Bank, Institute for Cereal Crops Improvement, Tel Aviv University*

This collection includes 8000 *Hordeum spontaneum* lines and 500 *H. vulgare* varieties collected in Israel. Some of the *H. spontaneum* are single lines collected randomly, some are selections for disease resistance made in natural habitats, and most lines belong to transects sampled from different natural populations. The collection was evaluated for leaf rust of barley (*Puccinia hordei)* and for powdery mildew (*Erysiphe graminis hordei).* The *Hordeum vulgare* accessions in the collection are differential varieties and varieties from different international nurseries. The collection is preserved at 5°C at 35% relative humidity.

## *Institute of Evolution, University of Haifa*

The collection of *Hordeum spontaneum* held by this institute consists of 3500 genotypes from various sources:

(a) Macrogeographic studies
- 33 populations from Israel (1300 genotypes)
- 20 populations from Iran (500 genotypes)
- 20 populations from Turkey (450 genotypes)
- 27 populations from Jordan (700 genotypes).

(b) Microgeographic studies (550 genotypes)
- Nahal Oren ("Evolution Canyon")
- Tabigha (Basalt vs. Terra Rossa)
- Neve Yaar (sun vs. shade)

The collection was evaluated for many genetic, physiological and important agronomic traits. Out of the 3500 genotypes, 2200 genotypes were evaluated for all or some of the following traits: genetic diversity analyzed by 50 allozymic loci; genetic diversity analyzed by RAPD; morphology; germination; heat production; milling energy; protein content; resistance to powdery mildew and leaf rust; salt and drought resistance.

Polymorphism of natural populations of *H. spontaneum* is one of the central problems studied on this material. Recently, new aspects have been started including genetic mapping of QTLs for stress tolerance and disease resistance genes.

## *Israeli Gene Bank for Agricultural Crops, Volcani Center (Agricultural Research Organization)*

This collection includes about 700 accessions, of which 150 are landraces *(H. vulgare* convar. *distichon* and *H. vulgare* var. *hexastichon*) and 550 are *H. spontaneum.*

# Spring barley collections in Lithuania

***Algë Leistrumaitë***

*Lithuanian Institute of Agriculture, Dotnuva-Akademija, Këdainiai district, Lithuania*

The National Plant Genetic Resources Programme was started in Lithuania in 1994. It is subsidised by the Lithuanian Research Foundation. The Programme is coordinated by the Lithuanian Institute of Agriculture. The Lithuanian Institute of Agriculture (Dotnuva), Vilnius University (Vilnius) and the Lithuanian Agricultural University (Kaunas) maintain cereals collections. All spring barley accessions are kept in working collections in these three locations. The type of material and the number of accessions are shown in Table 1.

**Table 1.** Lithuanian spring barley collections

| Material held | Number of accessions |
|---|---|
| **Lithuanian Institute of Agriculture** | |
| 490 varieties; 54 lines; (12) [†] | 644 |
| **Vilnius University** | |
| 10 mutant lines Riso as donors of various lys genes; 16 lines and stocks with fungi resistance genes and barley chromosome markers; 200 induced quantitative and morphological mutants; 7 varieties; (3) [†] | 233 |
| **Lithuanian Agricultural University** | |
| 19 varieties and lines (1) [†] | 19 |

[†] = Lithuanian varieties.

The inventory of the collections was completed during the last three years. It was found that they contained 12 spring barley varieties of Lithuanian origin, and that 2 old spring barley varieties of Lithuanian origin had been lost. The Nordic Gene Bank (NGB) now provides facilities for long-term seed storage to the Lithuanian Institute of Agriculture. Spring barley accessions of Lithuanian origin have already been placed in the NGB (seed number per accession = 10 000).

In the Lithuanian Institute of Agriculture the spring barley collection is a working collection, used only for breeding purposes. It is not stored in long-term storage. In the past we used to evaluate collections according to the rules elaborated by the N.I. Vavilov Research Institute of Plant Industry for agronomic evaluation. Accessions with valuable agronomic characteristics were the only ones to be maintained for longer periods. The number of accessions was not constant. Since 1989 we have been collecting and maintaining all the spring barley varieties which come to the Lithuanian Institute of Agriculture, which increased the number of accessions up to 644. Most of the accessions (405) were received from VIR. Every year we plant and evaluate about 300 accessions in the field. In order to maintain high viability of seed the varieties must be regenerated every 3 years.

In the Lithuanian Agricultural University the spring barley collection is used exclusively for educational purposes. It consists mostly of morphologically different lines representing different subtaxa.

In Vilnius University the spring barley collection is used for genetic research. Approximately 100 mutants of this collection will be passed to long-term seed storage.

Documentation and evaluation of the material has not been completed yet either. A catalogue of Lithuanian Plant Genetic Resources, including the spring barley collection with some evaluation data, was published in 1997 by the Lithuanian Institute of Agriculture.

# The present status of the *Hordeum* collections at the Nordic Gene Bank

***Jens Weibull***

*Nordic Gene Bank (NGB), Alnarp, Sweden*

## *General information*

Details about the *Hordeum sensu lato* collection at the Nordic Gene Bank (NGB) have earlier only been provided through the European Barley Database (EBDB) and not as separately published reports. Thus, this is the first of its kind aiming at giving a brief overview of the barley material available. Two special collections are not treated in this report: (1) the barley mutant collection comprising almost 9900 accessions, coordinated by Dr Udda Lundqvist, and (2) the collection of wild *Hordeum* taxa presently maintained by Professor Roland von Bothmer. NGB is only involved in keeping the base collection of the wild material and does not carry out regeneration of these species, some of which are notoriously difficult to multiply.

The number of accessions of cultivated barley, *Hordeum vulgare* subsp. *vulgare* L., amounts to 1634 (Table 1), a figure devoid of duplicated Nordic accessions. Hence, about 60% or 985 accessions are of Nordic origin, 16% (262 accessions) have unknown origin and the remaining 24% (387 accessions) are of foreign origin. As more information is being brought together these figures are continuously subject to change.

Table 2 summarizes the distribution of accessions between status categories accepted for long-term conservation, those pending a decision and those stored temporarily, indicating that a number of accessions are in the process of being reclassified. All wild *Hordeum* spp. were donated 8-10 years ago by the Royal Agricultural College in Copenhagen and no additional material of the Nordic species has been collected since then.

## *Recent evaluations/descriptions of particular interest*

The collection of spring barley accessions has been evaluated three times (1995-97) at Kvithamar Research Station near Trondheim (Norway) for resistance against scald (*Rhynchosporium secalis*). Although infection levels varied between years the results allowed for valuable discrimination between susceptible and resistant genotypes.

Furthermore, during 1997 the spring barley collection was multiplied at Risø National Laboratory (Denmark) to prepare homogenous seed for quality analyses. As a first step the collection will be characterized for a range of malting quality traits. It is anticipated that other characteristics, which are also expensive to analyze, will be studied later.

## *Projects*

A 3-year joint Nordic project on development of molecular markers ended in 1997. Using varieties 'Regatta' and 'Alexis' as crossing parents, maps were constructed to locate identified QTLs (quantitative trait loci) of genes for disease resistance (powdery mildew, leaf rust, scald, cereal cyst nematodes) and malting quality (viscosity, malt colour, protein content). Since it turned out to be rather difficult to find enough polymorphic markers to cover the whole genome, it appears that the two varieties share a high degree of common sequences. Project coordinator has been Henriette Giese at Risø National Laboratory, Denmark (h.giese@riso.dk).

In 1997 the Cereal Working Group at NGB initiated a project to study the processes and problems associated with repatriation of germplasm (e.g. identification and duplication). Barley was selected as a pilot crop and accessions have been searched for and obtained from the NSGC (National Small Grain Collection, Aberdeen, Idaho, USA), VIR (Vavilov Research Institute of Plant Industry, St. Petersburg, Russia), and genebanks in Germany, the Czech Republic, United Kingdom and Japan. Project leader is former NGB associate Birgitte Lund (bli@kvl.dk).

**Table 1.** Current (19/05/1998) composition of *Hordeum vulgare* L. accessions at the NGB when Nordic duplicates have been removed

| **Country of origin**[†] | **Varieties** | **Local varieties/ landraces** | **Wild/ semiwild** | **Breeding material** | **Unknown type** | **Total** |
|---|---|---|---|---|---|---|
| AFG | 0 | 42 | 0 | 0 | 0 | 42 |
| ARG | 0 | 0 | 0 | 0 | 1 | 1 |
| ARM | 0 | 0 | 0 | 0 | 1 | 1 |
| AZE | 0 | 0 | 0 | 0 | 1 | 1 |
| BEL | 0 | 4 | 0 | 0 | 1 | 5 |
| BGR | 0 | 0 | 0 | 3 | 0 | 3 |
| CAN | 0 | 1 | 0 | 0 | 4 | 5 |
| CHN | 0 | 3 | 0 | 0 | 1 | 4 |
| CZE | 0 | 28 | 0 | 0 | 0 | 28 |
| DEU | 6 | 30 | 0 | 1 | 25 | 62 |
| DNK | 91 | 18 | 0 | 275 | 1 | 385 |
| DZA | 0 | 0 | 0 | 0 | 1 | 1 |
| EGY | 0 | 1 | 0 | 0 | 0 | 1 |
| ESP | 0 | 1 | 0 | 0 | 0 | 1 |
| EST | 0 | 2 | 0 | 0 | 1 | 3 |
| ETH | 0 | 0 | 0 | 0 | 3 | 3 |
| FIN | 60 | 43 | 0 | 90 | 0 | 193 |
| FRA | 0 | 35 | 0 | 0 | 7 | 42 |
| FRO | 0 | 3 | 0 | 0 | 0 | 3 |
| GBR | 5 | 0 | 0 | 0 | 15 | 20 |
| GBS | 0 | 0 | 0 | 0 | 4 | 4 |
| GRC | 0 | 1 | 0 | 0 | 0 | 1 |
| HRV | 0 | 7 | 0 | 0 | 0 | 7 |
| HUN | 0 | 2 | 0 | 0 | 1 | 3 |
| IND | 0 | 0 | 0 | 0 | 1 | 1 |
| IRL | 0 | 2 | 0 | 0 | 2 | 4 |
| IRN | 0 | 0 | 0 | 0 | 1 | 1 |
| IRQ | 0 | 1 | 1 | 0 | 0 | 2 |
| ITA | 0 | 10 | 0 | 0 | 0 | 10 |
| KOR | 0 | 0 | 0 | 0 | 1 | 1 |
| LTU | 0 | 10 | 0 | 0 | 0 | 10 |
| NLD | 3 | 27 | 0 | 1 | 10 | 41 |
| NOR | 44 | 14 | 0 | 25 | 0 | 83 |
| NPL | 0 | 1 | 0 | 0 | 0 | 1 |
| PER | 0 | 1 | 0 | 0 | 0 | 1 |
| POL | 0 | 1 | 0 | 0 | 0 | 1 |
| PRT | 0 | 1 | 0 | 0 | 0 | 1 |
| ROM | 0 | 21 | 0 | 0 | 0 | 21 |
| RUS | 0 | 5 | 0 | 2 | 4 | 11 |
| SWE | 147 | 11 | 0 | 165 | 1 | 324 |
| USA | 0 | 1 | 0 | 27 | 12 | 40 |
| Unknown | 0 | 70 | 0 | 12 | 180 | 262 |
| **TOTAL** | **356** | **397** | **1** | **601** | **279** | **1634** |

[†] ISO Country codes (according to Appendix III *in* Lipman *et al.* 1997).

**Table 2.** Distribution of *Hordeum s.l.* accessions between different status categories.

| **Species** | **Accession status** | | | **Total** |
|---|---|---|---|---|
| | **Accepted** | **Pending** | **Temporary** | |
| *Hordeum bulbosum* L. | – | – | 2 | **2** |
| *Hordeum jubatum* L. | – | – | 2 | **2** |
| *Hordeum marinum* Huds. | – | – | 2 | **2** |
| *Hordeum murinum* subsp. *murinum* L. | – | – | 2 | **2** |
| *Hordeum nodosum* L. non auct. | – | – | 3 | **3** |
| *Hordeum vulgare* subsp. *spontaneum* (C. Koch) Thell. | – | 3 | 13 | **16** |
| *Hordeum vulgare* subsp. *vulgare* L. | 597 | 104 | 906 | **1607** |
| **TOTAL** | **597** | **107** | **930** | **1634** |

## *Utilization*

During the last few years the NGB has noted a growing interest in *Hordeum* landraces or local cultivars. Several local farmers' groups and/or non-governmental organizations showing particular interest in the history of cultivation or of rural life, such as open-air museums, now grow this redundant material for demonstration. This has opened a possibility for new conservation regimes (e.g. on-farm conservation) for this kind of heterogeneous germplasm.

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# Collection and evaluation of barley varieties in Poland

***Małgorzata Małysa***

*Plant Breeding Station, Bąków, Poland*

The Genebank of the Plant Breeding and Acclimatization Institute in Radzików (IHAR) holds many barley varieties from different geographic origins. They are differentiated in respect to ecological, morphological and biochemical characters. They represent rich genetic resources to improve useful characteristics such as quantity, quality and fidelity of yield.

All work related to plant material collection is conducted in the Centre for Plant Genetic Resources, IHAR Radzików. The tasks related to the regeneration and evaluation of winter barley (since 1987) and spring barley (since 1993) are conducted in the Plant Breeding Station in Bąków. Regeneration concerns varieties kept in long-term storage. The purpose of regeneration is the rejuvenation of seeds and the improvement of their germinative ability. The evaluation data allow identification of the morphological attributes which are important for breeding purposes. The evaluation of genetic resources is necessary to increase their use and benefits to breeders.

The value of particular forms for different characters, and the interdependence of these characters, must be known before they are introduced into breeding programmes. Winter barley varieties are evaluated over 3-year or 1-year periods. Studies of two- and six-row winter barley varieties were carried out in 3-year periods.

In 1990-93, 69 two-row and 47 six-row winter barley varieties were evaluated. The following characters were analyzed: number of days from sowing to heading; winterhardiness; lodging (twice: since heading to harvest); resistance to powdery mildew and brown rust; plant height; ear length; number of grains per ear, and 1000-grain weight.

The analysis of variance showed significant differences between varieties with regard to vegetation period from sowing to heading, resistance to powdery mildew, lodging and grain yield per ear, resistance to brown rust, number of grains per ear and 1000-grain weight in the group of two-row varieties. The influence of environment was high for winterhardiness and plant height in both groups and yield structure traits in the group of six-row varieties.

The heritability expressed by the degree of genotypic variability was high for resistance to lodging, resistance to powdery mildew after plant heading, vegetation period from sowing to heading and grain yield in the group of six-row varieties and also for resistance to lodging, resistance to brown rust, 1000-grain yield per ear in the group of two-row varieties. The heritability of plant height was low in both groups.

Useful correlations between the traits important from particular points of view were determined. The yield of six-row varieties was most significantly influenced by the number of grains per ear and 1000-grain weight; the influence of winterhardiness was lower. The yield of two-row varieties was mainly determined by 1000-grain weight, followed by length. The influence of the number of grains per ear and number of days to heading was lower.

Based on statistical analysis, some varieties were selected as potential sources for winter barley breeding.

Since 1993 regeneration and multiplication of spring barley varieties from the Genebank have been carried out (Table 1). Spring barley samples are investigated in 1-year periods.

**Table 1.** Regeneration and multiplication of spring barley

| Year | Number of accessions | Activity |
|---|---|---|
| 1993 | 187 | regeneration |
| 1994 | 414 | regeneration |
| 1995 | 691 | regeneration |
| 1996 | 691 | multiplication |

## *Annex 1.* ***Varieties of winter barley with good resistance to powdery mildew and winterhardiness (chosen for crossing programmes)***

- **Six-row varieties**

Athene
Luther CI 13340
Albert
Mobsy
Berit
Marcone
Balkan Hor 991
Narcis
Clayton
Ny 516 B-3B-1
Catskill CI 10 889
No 16
Cenad 1
Nogradyest
Cenad 399
Ola
Cluj 156
Oma CI 9565
Decatur
Pennnrad
Herefordia
Pallidum
Horpasci
Parallelum 402
HVW 810/75
Rapidan
HVW 819/75
Rachel
HVW 858/76
Rebekka
HVW 527/72
158-70 A
Immerdorfer
52 M 1
James
44 M !O
Judith
Lilli
Logic

- **Two-row varieties**

Alpha
Barlena
Camaro
Chestnut
CB 272/2
Firefly
F 117
H-477-53
Hannna
Pamir
Paris
Pepita
Panda
29h-339
105h-143

# The Romanian barley collection at the Genebank Suceava

***Ilie Gaspar and Claudia Ciotir***

*Genebank Suceava, Suceava, Romania*

Recent data indicate that in Romania the barley crop represents about 23.3% of the cereals cultivated, on an area of about 3 million ha.

In Romania, there are 14 registered advanced cultivars, seven of *Hordeum vulgare* (winter barley) and seven of *Hordeum distichum;* the latter includes three winter advanced cultivars and four spring advanced cultivars.

The institutes involved in the cultivation and breeding of barley are:

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

The national programme coordinator is ICCPT Fundulea.

All three institutions have breeding collections that are renewed every year. Their holdings are listed in Table 1, together with those of the Suceava Genebank.

**Table 1.** Barley collections in Romania

| | Number of accessions in holding institute | | | | |
|---|---|---|---|---|---|
| **Type of material** | **Turda** | **Fundulea** | **Suceava** | **Suceava Gene Bank** | **Total** |
| **Indigenous origin** | | | | | |
| Wild | – | – | – | – | 0 |
| Landraces | – | – | – | 43 | 43 |
| Advanced cultivars | 6 | 17 | 3 | 19 | 45 |
| Breeders lines | 74 | – | 58 | 107 | 165 |
| Mutants | 6 | – | 4 | – | 4 |
| Other | – | – | – | 11 | 11 |
| **Total** | **86** | **17** | **65** | **180** | **348** |
| **Foreign origin** | | | | | |
| Wild | 1 | – | – | – | 1 |
| Old cultivars | 125 | 18 | 29 | 441 | 613 |
| Advanced cultivars | 128 | 2342 | 123 | 6 | 2599 |
| Breeders lines | 28 | 53 | 136 | 387 | 604 |
| Mutants | 9 | 5 | 7 | – | 21 |
| Other | – | 40 | – | – | 40 |
| **Total** | **165** | **2529** | **335** | **834** | **3863** |

## *Geographical distribution*

The three institutions are situated in three distinct regions. Therefore the advanced cultivars are distinct from one region to another because of the specific climatic conditions (temperature and humidity) which are different for the Transylvania plateau, the Baragan and Dobrogea fields, the Moldavians hills and the Subcarpathian hills.

It can be noted that winter barley has almost replaced the spring barley cultivated for fodder.

The maximum productivity of these crops is about 6.5-12 t/ha, varying with climatic factors.

The Suceava Gene Bank collaborates with the other three institutes. All the above-mentioned advanced cultivars and other foreign advanced cultivars are present in the collection. This collection is relatively new since the first barley accessions were received in 1989, when the genebank was founded.

### *The Suceava Gene Bank barley collection*

The Suceava Gene Bank has a permanent collection and a working collection.

As indicated above, the total number of accessions is 1014, of which 180 are indigenous and 834 foreign (from the USA, UK, Canada, Russia, etc.)

The seeds are preserved in sealed glass containers at 4ºC and 7-8% humidity. Freon is used for cooling. The cooling machines are made in Romania.

Provided some financial help is received, the genebank is willing to receive any European collection, guaranteeing its proper conservation.

### *Evaluation*

Since 1997, barley was given greater attention. There are 118 landraces in the experimental field, including 30 for study and research purposes, and 88 for multiplication. IPGRI descriptors are used for evaluation.

Diseases recorded were *Erysiphe graminis*, *Pyrenophora graminea* (conidian form *Helminthosporium graminea)*, *Pyrenophora teres* (conidian form *Helminthosporium teres)*.

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# The VIR barley collection

***Olga Kovaleva***

*N.I. Vavilov Research Institute of Plant Industry (VIR), St. Petersburg, Russia*

Our Institute originated and developed from the Bureau of Applied Botany established in 1894 under the Ministry of Agriculture and State Property of Russia. In 1917, the Bureau was transformed into the Department of Applied Botany and Plant Breeding. At present, the Institute bears the name of the N.I. Vavilov All-Russian Research Institute of Plant Industry. It is the only research institution in Russia involved in collecting, studying and preserving in live conditions the genetic resources of cultivated plants and their wild relatives.

Initiation of the VIR barley collection dates back to the days of the Bureau of Applied Botany. Before 1917, the collection included 3000 accessions. During that period, landraces and bred varieties from West European countries came to Russia. The collection mainly contained local barley accessions from different climatic zones and areas of Russia, while foreign samples from Western Europe accounted for 20%. That collection kept expanding, for instance, thanks to samples received from seed companies, private breeders and also during the participation in various agricultural exhibitions.

The first botanical investigation of the barley diversity was carried out by Prof. R. Regel, a famous Russian botanist, first director of the Bureau who described new barley varieties. His research was of great value for the systematics and classification of barley.

When Vavilov was director of the institute, he organized collecting missions for cultivated plant genetic resources all over the world. Vavilov himself and his successors explored almost all continents for plants. As a result, VIR's barley collection was composed to represent the ecological, genetic and botanical diversity of barley worldwide. In 1947 the number of accessions in the collection amounted to 9000, representing 38 countries besides Western Europe.

Practically all activities of the Institute have been closely associated with Vavilov's theories on plant genetic resources and the global genetic diversity of cultivated plants. As of 1952 the study of the centres of diversity of cultivated plants began. Botanical diversity of local barleys showing different biological characters was collected in China, Mongolia, Ethiopia and Japan.

In 1960-70 the countries of the Mediterranean region were investigated carefully. This allowed VIR to enrich the collection with drought-resistant accessions from Syria, Tunisia, Morocco and other countries from the region. Other missions were organized for collecting barley from the New World – Canada, USA and Latin American countries.

The fundamental objectives of our scientific activities are as follows:

- to collect plant genetic resources both within and outside the country
- to preserve accessions of the world collection in viable conditions
- to study the global plant genetic diversity with the goal of identifying promising materials for breeding and donors of most important traits required for breeding
- to supply the breeding centres with initial genetic material for practical breeding.

The VIR barley collection now consists of more than 17 000 accessions. The composition of the collection is as follows: wild species (1%), Russian local and old varieties (11%), foreign local and old varieties (8%), foreign breeding lines (12%), Russian varieties (42%) and foreign varieties (26%).

Thus, VIR's collection includes landraces, bred varieties, breeding lines combining a complex of valuable characters, mutants, sources and donors of valuable characters, and almost all botanical forms.

# The Slovak barley collection

***S. Žák, O. Horňáková, F. Debre and J. Kraič***

*Research Institute of Plant Production (RIPP), Piešťany, Slovakia*

The total surface area of Slovakia is 4 904 000 ha and it is highly diverse. Agricultural land covers 2 446 000 ha, of which 1 483 000 ha are arable land. In 1997, cereals are grown on 843 000 ha, with barley on 230 000 ha of this area. The average barley yield in the last years in Slovakia was about 3.5 t/ha and the annual barley production is about 800 000 t.

The expected home consumption in 1997 is 901 000 t, of which 300 000 t is for food, 45 000 t for seed production, 470 000 t for forage production, and 86 000 t for other uses.

In the Slovak National List of Released Varieties, there are 27 registered spring barley varieties for 1996, 14 local and 13 foreign varieties, and 8 winter barley varieties, all foreign. Two varieties of winter barley, 'Marinka' and 'Monaco', are two-row varieties.

The first information on barley breeding in Slovakia dates back to 1899. Fr. Dezasse in Bohunice selected Slovak barley landraces. In Sládkovičovo, barley breeding started in 1909 and is still ongoing. It is the most successful barley breeding centre in Slovakia (Klinovský *et al.* 1970).

Barley breeders were the first collectors and maintainers of barley genetic resources collections. The Research Institute of Plant Production (RIPP) in Piešťany was the first organization in Slovakia to start systematic work on cereal genetic resources in 1955. In the beginning, the work related to plant genetic resources (PGR) was part of the Czecho-Slovak programme. In November 1991, the National Programme for Plant Genetic Resources of the Slovak Republic was approved. At present, RIPP Piešťany coordinates the National Programme for the Conservation of Cultivated Plant Genetic Resources. Collection of barley genetic resources is an integral part of this Programme.

Besides the barley collection, RIPP Piešťany also works on 27 other collections.

RIPP Piešťany cooperates with 20 specialized institutions in Slovakia, situated in localities suitable for the genetic resources on which they focus.

In November 1996, a new Gene Bank was opened in RIPP. It has a storage capacity of 50 000 accessions of cultivated plant seeds, with the possibility of seed storage at –18°C for 50 years (2 boxes), storage at +2°C for 10 years (boxes), storage of dry parts of the plants at 10°C. The preparation and implementation of the PGR programme is financed and supported by the Ministry of Agriculture of the Slovak Republic.

The barley genepool is very narrow. However, essential structural reconstruction of the original genepool of spring malting barley has been realized through breeding activities. The stem length has been shortened and lodging resistance increased. Varieties produce higher number of productive spikes and grains per $m^2$. In addition to significant yield improvement, health conditions also have been improved, especially resistance to powdery mildew.

When collecting genetic resources, attention is focused especially on local varieties, germplasm as the product of breeding, landraces, special genetic resources with expression of certain characters and characteristics, as well as foreign varieties most frequently grown. We are also preparing to collect wild forms of barley (e.g. *Hordeum spontaneum*, *H. bulbosum*, etc.) in the near future.

In evaluation, we concentrate on the description of phenotypic variability, which will be registered within a common information system. We will also direct our attention to the detection of those barley genetic resources which are directly usable in breeding programmes, thanks to a higher potential. At present the barley genetic resources collection comprises 1470 accessions of spring and winter barley with passport data; 733 accessions are described and duplicated, of which 677 accessions are stored in the active collection (see Table 1).

**Table 1.** Barley accessions in the active collection

| **Country of origin** | **Winter barley** | **Spring barley** | **Total** | **Country of origin** | **Winter barley** | **Spring barley** | **Total** |
|---|---|---|---|---|---|---|---|
| AFG | – | 7 | 7 | IND | – | 1 | 1 |
| ASA | – | 2 | 2 | IRN | – | 1 | 1 |
| AUS | – | 1 | 1 | ITA | 1 | 1 | 2 |
| AUT | 6 | 13 | 19 | JPN | – | 1 | 1 |
| BEL | 6 | – | 6 | MNG | – | 4 | 4 |
| BGR | 3 | 4 | 7 | NLD | 4 | 17 | 21 |
| BOL | – | 1 | 1 | POL | – | 8 | 8 |
| CAN | – | 13 | 13 | PRT | – | 1 | 1 |
| CHE | – | 2 | 2 | ROM | 2 | 1 | 3 |
| CHN | – | 2 | 2 | SUN | – | 13 | 13 |
| CSK | 54 | 63 | 117 | SVK | 32 | 80 | 112 |
| DEM | 85 | 46 | 131 | SWE | – | 15 | 15 |
| DNK | – | 10 | 10 | SYR | – | 2 | 2 |
| ESP | 1 | 1 | 2 | TUR | 1 | – | 1 |
| ETH | – | 3 | 3 | UKR | – | 1 | 1 |
| FIN | – | 1 | 1 | USA | 3 | 6 | 9 |
| FRA | 25 | 29 | 54 | YUG | – | 1 | 1 |
| GBR | 6 | 19 | 25 | Unknown | 15 | 60 | 75 |
| HUN | 2 | 1 | 3 | **Total** | **246** | **431** | **677** |

Morphological characteristics were described according to a Descriptor List which was developed on the basis of UPOV, EVIGEZ and IPGRI Descriptor Lists, by using a more precise description and completing the range of characters studied. In the Description Part, 43 characters are currently studied for winter barley and 42 for spring barley (Annex 1). Seven quantitative and two qualitative characters, determined by weight, measurements or in percentage, are treated by the programme so that it is possible to use their point values (after transformation) or directly those obtained originally.

Besides morphological and agronomic traits, we use different types of molecular markers (protein and DNA) for the evaluation of genetic diversity in the barley collection. For identification, verification and distinction of genotypes we use analyses of hordeins in acid-PAGE and DNA-based techniques. A set of barleys can be differentiated by hordein analyses into several subsets followed by complete differentiation into individuals by DNA-based techniques. Polymorphic SSR (simple sequence repeats) markers are very effective in revealing DNA polymorphism between barley accessions. SSR markers produced by five SSR primers also clearly separate spring genotypes from winter genotypes (genotypes no. 32-40 in Fig. 1) and differentiate 40 genotypes evaluated into 35 groups (Fig. 1).

Researchers from breeding stations (Sládkovičovo, Trebišov, Radošina) and breeding and research institutes (SELEKT Bučany) were informed of the results every year. In 1994-97, genetic resources were distributed to be used mainly in breeding and research programmes as well as for education purposes (Table 2).

**Table 2.** Barley accessions distributed, 1994-97

| **Crop** | **1994** | **1995** | **1996** | **1997** | **Total** |
|---|---|---|---|---|---|
| Spring barley | 42 | 20 | 82 | 67 | 211 |
| Winter barley | - | 67 | 49 | – | 116 |

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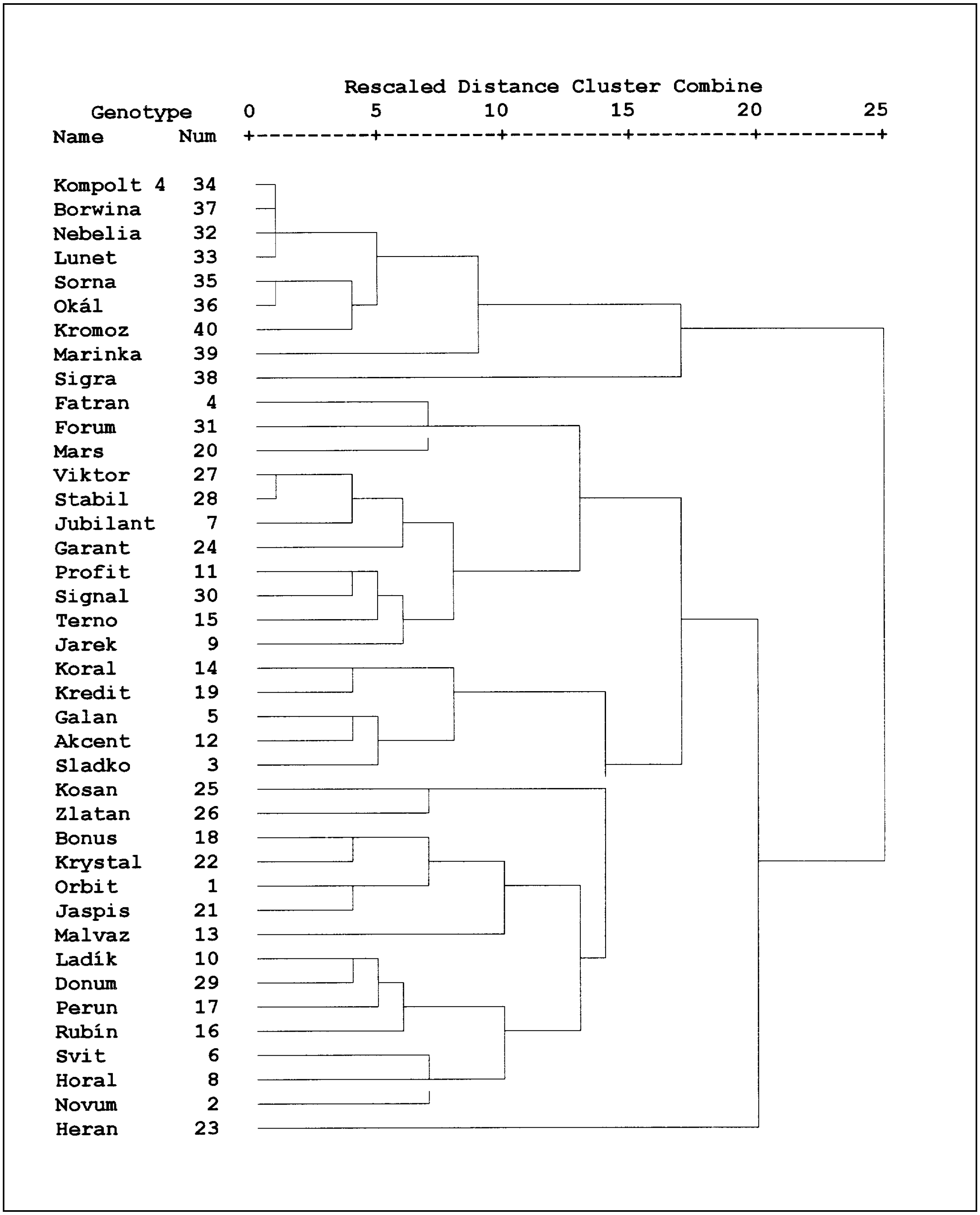

**Fig. 1.** The dendrogram based on polymorphism detection of simple sequence repeats (SSR).

## *Annex 1.* **List of barley traits evaluated**

Growth habit
Plant height
Length of the upper internode
Stem – brittleness
Leaf – flag – position
Leaf second upper – length
Leaf second upper – width
Leaf – colour
Leaf – ligule presence
Leaf – anthocyanin colour of auricules
Leaf – indumentum of sheath
Spike – colour
Spike – position
Spike – type
Spike – shape
Spike – length
Spike – density
Awn: length compared to ear
Lemma awn / hood
Caryopsis (grain) – huskiness
Caryopsis (grain) – shape
Caryopsis (grain) – colour
Grain: hairiness of ventral furrow
Caryopsis – basal seta
Tip awn – colour of anthocyanin
Intensity of colour tip awn
Vegetation – character
Winter – hardiness
Lodging – resistance
*Puccinia hordei* Otth.
*Erysiphe graminis* DC. Marsch
*Ustilago*
*Rhynchosporium secalis* Oud.
*Pyrenophora teres* Died. Drechs.
Caryopsis – 1000-kernel weight
Grain – uniformity
Crude protein content
Malt – extract content
Germinating seed – store
Sowing date
Emergence date
Heading date
Harvest date

# The Spanish Barley Core Collection

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The National Germplasm Bank (BNG) at the Centro de Recursos Fitogenéticos (CRF-INIA) in Alcalá de Henares holds a collection of 2000+ barley accessions, mostly landraces collected in Spain. The study of the genetic diversity present in this (or any) collection, and its use by barley breeders would be facilitated by the assembly of a core collection of a manageable size (Frankel 1984). The process of making this collection followed a series of necessary steps, which are described below.

## *Steps for entry selection*

These steps essentially follow the recommendations made by van Hintum (1996).

### Domain and size of the core collection

The domain of the core collection is the *Hordeum vulgare* types grown in Spain prior to the introduction of modern varieties. A set of about 160 entries was considered likely to be sufficiently representative.

### Making of groups based on knowledge of germplasm

It was decided to include several groups of entries, according to different selection criteria. The groups were:

A. Cultivars or landraces extensively grown in Spain.
B. Entries in common with the European Barley Core Collection.
C. Entries in common with the USDA Barley Collection.
D. Two-row entries from the BNG collection. These entries are a small part of the collection, as most of the barley traditionally grown in Spain was six-row.
E. Six-row entries from the BNG collection, other than in group A.

The inclusion of entries in group A ensures that materials presenting best adaptation to Spanish conditions are included in the core collection. Entries also present in other collections (groups B and C) were included to become reference points for comparison across collections. Groups D and E were the only genetically distinct types which could be identified from passport data, and their size was proportional to their representation in the BNG collection.

### Allocation of entries over the groups

For this purpose, we proceeded in a subjective manner, based on the relative importance and diversity of the groups. The final allocation of entries is summarized in Table 1.

### Choice of entries

Selection in groups A through D was agreed among the authors, taking account of diversity and completeness of passport data, and of previous knowledge on the past importance and denominations of some entries. For group D, for instance, care was taken to include entries representing the *ladillas* and *pámulas*, two of the main traditional two-row types grown in Spain.

Selection in group E was more elaborate, owing to the abundance of entries present in the BNG collection. The procedure used was as follows.

According to the literature (Brown 1989; van Hintum 1996), it is advisable to make a stratified sampling, based on an agro-ecological classification of the origins of the entries. Usually, the actual geographic origins of entries in the collection are used as the basis for classification. This approach assumes that the BNG germplasm collection is an undistorted representation of barley germplasm grown in Spain.

In our case, however, we used historical data on barley cultivation to determine agro-ecological regions in Spain. We extracted data on barley yields per province (Spain has 50 provinces) from the Yearbooks of Agricultural Statistics. We assembled a database with six-row barley provincial yield estimates for 47 contiguous years from 1948 till 1994. Provinces where either barley cultivation was negligible, or the six-row barley acreage decreased until almost disappearing, were not taken into account.

For most of the 34 remaining provinces, there was a significant increase in yield over time (but differing in magnitude across provinces). Thus, to remove confounding effects of improved crop management or introduction of better varieties, the yield time-series for each province were detrended as follows: first, a linear regression of year on yield was fitted for each province. Then, the residuals from the regression were added to the mean average yield across years for each province. This new set of data actually has the same average provincial yields as the original one, but without time trends.

We did a cluster analysis (Ward method) on the new dataset, using years as variables, to produce groups of provinces with both similar average yield, and consistency in the fluctuation of yield across years. The analysis produced four clearly distinct groups, presented in Table 2.

The first three clusters include contiguous provinces, whereas the fourth includes the four provinces from Cataluña and another three geographically scattered high-yielding provinces. Another group was made with six provinces in which six-row barley cultivation was important in the past, but not recently.

A stratified logarithmic sampling on the regions so determined would increase the probability of capturing allelic variation conferring both wide and local adaptation (Brown 1989). We sampled according to logarithmic proportion of the area devoted to barley in each agro-ecological region. Within each region, the allocation of number of entries per province was done according to strict proportionality to barley hectarage.

Barley hectarage means were not derived from the same dataset as the agro-ecological regions for yield. The distribution of barley hectarage in Spain has changed markedly for the last 30 years. Thus, the dataset including the last 47 years would not be representative of barley cultivation during the period prior to the introduction of modern varieties, which we propose as the domain of the core collection. For that reason, we gathered barley hectarage data available for the period prior to 1960, when it can be assumed that most varieties grown were primitive cultivars and local landraces. Data from only 15 years were found, which were enough for an assessment of area devoted to barley per province and agro-ecological region (hectarage did not vary much among years during that period). These areas are summarized in Table 2.

The choice of entries within each province was made among those accessions presenting complete passport data. The criteria for selection aimed at maximizing the inclusion of potential genetic diversity. For this purpose, we paid special attention to the altitude of the collecting site, one of the main factors influencing crop adaptation in Spain, and also to agronomic data from the evaluation of about 900 BNG accessions carried out by the authors in previous years.

**Table 1.** Groups of entries for the Spanish barley core collection

| Group | No. accessions |
|---|---|
| Successful old varieties | 15 |
| European Core Collection | 2 |
| USDA collection | 15 |
| Two-row accessions from BNG | 10 |
| Six-row accessions from BNG | 120 |

**Table 2.** Agro-ecological regions for barley production in Spain

| Agro-ecological group | No. of provinces | Historical (1930-60) barley area (%) | Mean yield 1948-94 (kg/ha) | No. of entries for the core |
|---|---|---|---|---|
| South | 10 | 42.4 | 1086 | 32 |
| Ebro-Castilla La Mancha | 9 | 22.5 | 1576 | 27 |
| Castilla-León | 8 | 14.9 | 1876 | 23 |
| High yield | 7 | 9.3 | 2056 | 19 |
| Disappeared | 6 | 9.9 | – | 19 |

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# Activities in barley genetic resources in Turkey

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Among the cereal crops grown in Turkey, barley ranks second after wheat in growing area and production. In 1994 the average cultivated area was 3 440 000 ha and average annual production was 6 900 000 tonnes.

The genebank contains about 700 barley accessions and is responsible for providing the germplasm material needed by scientists to develop improved varieties.

The barley material stored in the AARI genebank was collected in different parts of Turkey in the last two decades. National surveys were carried out systematically. For the majority of barley and its wild relatives, seeds were maintained in the AARI genebank. Barley germplasm is stored in a base collection at –18ºC and in an active collection at 0ºC. The active collection is used for regeneration, multiplication, distribution, characterization and evaluation. All accessions are well documented in the genebank (passport data, storage data, etc.). Herbarium specimens are also kept in the AARI Herbarium. They are used for further identification and reference of the samples maintained.

The barley programme includes a project of characterization of the accessions collected all over Turkey. The project started last year [1996] and will end in 1999. The majority of the accessions used in this project are landraces. The results of the first year of the project are as follows: 116 accessions collected from the southeast Anatolian Region were analyzed by principal component analysis for 11 characters. The main characters were number of kernels per ear, 1000-kernel weight, and lodging for PRIN1; number of tillers for PRIN2; 1000-kernel weight and plumpness for PRIN3. There was a wide variation among accessions collected from the region for all characters.

Another project deals with preliminary evaluation of some barley landraces for malting quality. Further evaluation has been carried out in our barley programme since 1996. The purpose of this evaluation is to provide information on the variation in the available indigenous landraces used as sources of breeding material.

# Promoting the use of barley genetic resources

## The breeder's perspective on barley genetic resources

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### *An American survey*

In 1984 Don Duvick, a maize breeder at Pioneer Hi-Bred, wrote an article entitled 'Genetic diversity in major farm crops on the farm and in reserve' (Duvick 1984). His aim was to get an estimate about the genetic vulnerability of North American plant breeding. In 1981 he therefore distributed a questionnaire to a large number of leaders of breeding programmes in the five 'big' crops: maize, wheat, sorghum, soyabean and cotton. Altogether he received 101 answers from both the private and the public sector, equalling a response frequency of slightly more than 80%.

One has to keep in mind that his paper describes a situation 15 years ago and only American plant breeding, but nevertheless one can learn a lot from the highly informative paper he wrote and many connections can be made to the situation in Europe.

Of all the tables Duvick presented in the paper, a few were selected for the present article, the first one relating to how breeders choose to broaden the diversity of their breeding material (Fig. 1). If one considers all five crops it is obvious that old landraces and local or primitive varieties played a very important role in broadening germplasm diversity. But differences occur, as can be seen from the data on wheat where breeders seem to have relied more heavily on elite material (Fig. 1b). The wild relatives constituted only a minor proportion of the germplasm used, which may perhaps be explained by the fact that crossing barriers or incompatibility effects limited their usefulness – at least then.

Where did the North American breeder turn to in his, or her, quest for new resistance genes? Well, according to Duvick's paper elite breeding material was the first option, comprising almost two-thirds (Fig. 1c). Again the wild relatives seemed to be utilized only to a limited extent and, in fact, even much less when it came to breeding for resistance to stress tolerance (Fig. 1d) where elite material was by far the most preferred source.

### *The value of genebank collections*

Duvick followed this up by asking a number of questions relating to the role of genebanks and genebank collections in providing additional genetic variation. Asking 'Do you use genebank collections?' (Fig. 1e) he found that approximately two-thirds regularly received germplasm from genebanks to be introduced into the breeding programmes. Less encouraging was the response he obtained on the subsequent question, namely 'Are the collections satisfactory?', where only about 40% of those responding seemed to be happy with what they could get (Fig. 1f).

Overall, the American breeders did not appear to be particularly concerned about the risk of decreasing diversity in their breeding programmes, although wheat breeders tended to be slightly more worried perhaps because of the regular epidemics of new stem and leaf rust races on the North American continent.

Duvick concluded by discussing a number of ominous tendencies in American breeding programmes and crop cultivation, trends that may apply equally well in a European situation:

- the diversity of varieties is decreasing as they become phenotypically more uniform
- they are also to a large extent genotypically related
- farmers tend to favour the same varieties.

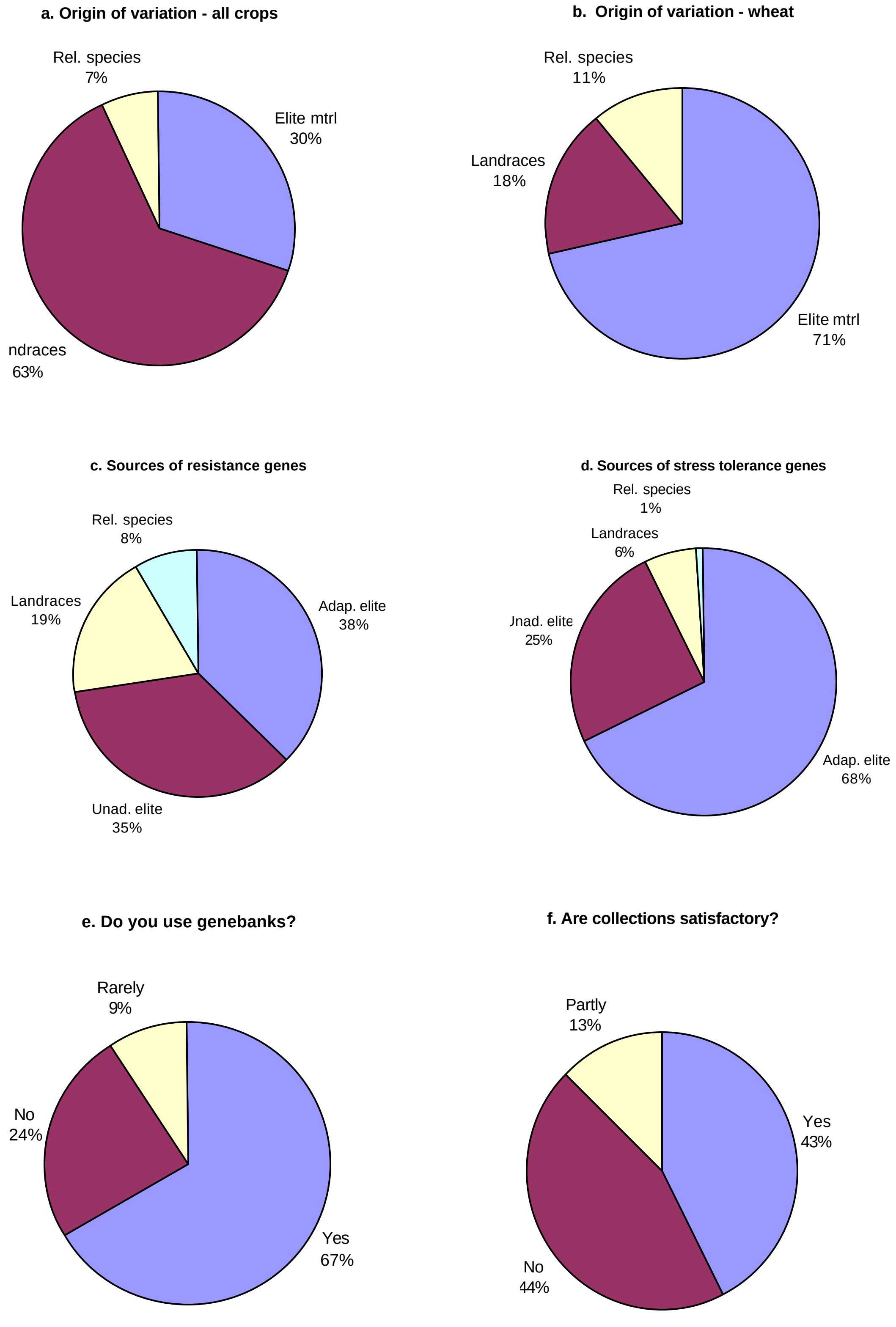

**Fig. 1, a-f.** Graphical presentations of some selected tables from Duvick (1984).

But he also foresaw some other trends which could counteract a worsening scenario with respect to crop diversity:

- there is diversity in **time** as varieties are being replaced rapidly
- there is diversity in **reserves** as hitherto unexploited genetic resources
- there is diversity in **anticipation** because, thanks to modern information networks, we can foresee epidemics and other problems much earlier than before.

What he could **not** foresee, however, was the Convention on Biodiversity and all that has followed in its aftermath such as restrictions on germplasm exchange, extended discussions on the establishment of a multilateral agreement, etc.

### *Priorities of European breeders*

In a slightly similar study the ECP/GR Barley Working Group, in the mid-1980s, actually sent out a questionnaire to 150 European breeders to assist in developing a strategy for the European Barley Database. In doing so the Working Group also indirectly took a bearing of the breeders' preferences, priorities and general position regarding barley genetic resources and how they should be best utilized.

From this survey (UNDP/IBPGR 1986) one can conclude that European breeders behave remarkably like their North American colleagues in the search for novel disease resistance genes. They seemed, however, to be more critical about the status of germplasm collections held at genebanks – whether they meant European or international is not quite clear – with regard to both the quality and the quantity of information. The survey did not reveal if breeders also were dissatisfied with the nature of samples kept in the collections.

A ranked list of the 10 most important traits demonstrates the reality in which our European breeders try to survive, where they put their breeding emphasis and what priorities they make. There are really no distinct differences between the national and the international set of priorities. The main diseases are being repeated as well as some basic agronomic features as a testimony of the information wanted by the breeding community.

### *Lack of information*

Two years ago, when the author came to the Nordic Gene Bank (NGB), he made a survey of the degree of completeness of the barley database concerning evaluation data on pest and disease resistance. The result was rather disappointing (Table 1). Although the situation for some diseases, such as leaf rust (*Puccinia hordei*) and scald (*Rhynchosporium secalis*), has improved lately, there still remains a huge number of empty spaces to fill in. Some diseases, such as spot blotch (*Drechslera teres*) or barley yellow mosaic virus, or pests such as cereal aphids or wheat gall midges, have not even been considered. This is not because the NGB Cereal Working Group is lazy or ignorant or unconscious of the problems, but simply because lack of funding and this is a fact causing permanent dissatisfaction.

**Table 1.** Available information about some resistance traits of the NGB barley collection (end of 1995)

| Pest or disease | % of records with data |
|---|---|
| Powdery mildew | 87 |
| Leaf rust | 61 |
| Yellow or stripe rust | 60 |
| Smut (*incl. pseudoresistance*) | 38 (*11*) |
| Cereal cyst nematode, pathotype 11 & 12 | 37.19 |
| Net blotch | 20 |
| Scald | 17 |
| Leaf stripe | 6 |
| Saddle gall midge | 56 |
| Barley Yellow Dwarf Virus (BYDV) | - |

### *Wanted: financial support for basic research*

One final example will be provided (Weibull 1993). During the author's time as a resistance breeder at the former Weibullsholm Plant Breeding Institute (Sweden), the rule was to regularly screen for disease resistance all breeding material entering preliminary yield trials. One programme concerned resistance against barley yellow dwarf virus (BYDV) and aimed at identifying genotypes with promising background which would complement the known dominant or semi-dominant *Yd2* resistance gene. Unfortunately most material was fully susceptible but one day an erectoid breeding line, W8172, was found to show highly interesting levels of tolerance. Crosses with lines carrying the known *Yd2* gene gave exciting results and we believed we had found something new.

Considering the pedigree of W8172 one can highlight a few things (Fig. 2). As one parent we find the old Norwegian variety 'Domen' which itself has a very interesting background, and while moving further back in its ancestry one rapidly ends up in local Nordic varieties and landraces. Barley yellow dwarf is a viral disease with a long history in the Nordic countries and it seems probable that unconscious selection over the decades may have resulted in the accumulation of minor genes, the effect of which suddenly is expressed in a single breeding line.

The author was approached by Professor Helms Jørgensen at Risø National Laboratory (Denmark) who wondered whether it would be possible to screen the whole barley collection of NGB, which certainly would have been an exciting exercise. However, applications for funding from Swedish research funds were turned down with the argument that this type of research was not 'innovative' enough to justify support.

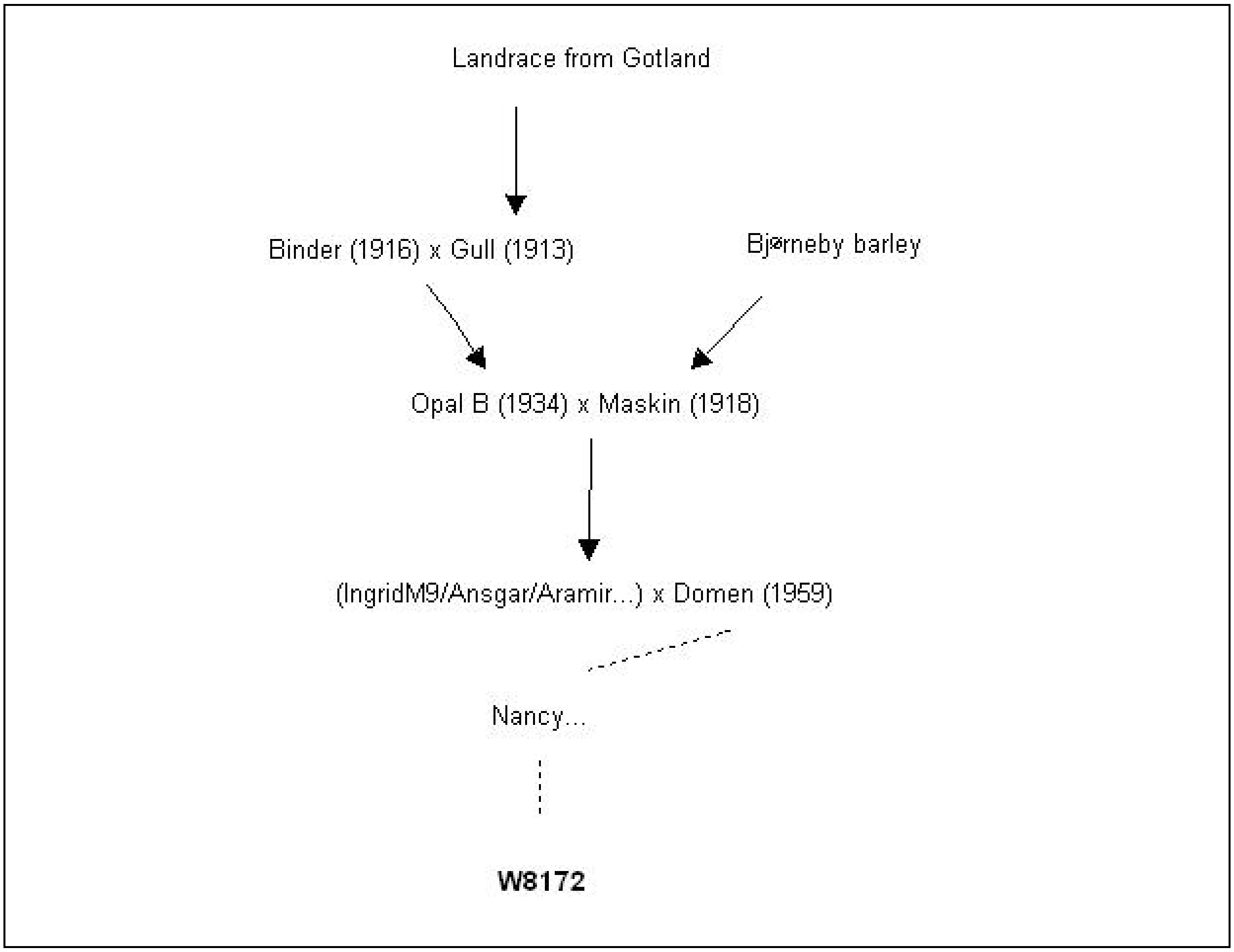

**Fig. 2.** Summarized pedigree of breeding line W8172 demonstrating interesting tolerance levels against barley yellow dwarf virus (BYDV).

### Conclusion

To conclude, therefore, a few things that may have been said before should be emphasized:

1. Breeders and genebank curators live mutualistic lives and should, to obtain synergistic effects, work even closer.
2. This interdependence may possibly increase as a result of implementing the CBD and a possible future multilateral agreement on access.
3. **But**, to make this happen we need to complement our databases and fill all the blank spaces with useful and valuable information, otherwise the breeding community will ignore the collections.
4. We need to cooperate when evaluating germplasm, in pre-breeding programmes which a private breeder otherwise never could afford to pursue, and in relevant research.
5. Breeders could take active part in maintaining collections, for instance by creating adapted male-sterile populations aimed for specific purposes, such as virus resistance, resistance against necrotrophic fungi, malting quality, winter hardiness, etc. which would be a cheaper way of preserving and accumulating minor genes.
6. And, finally, genebanks should take more advantage of the vast knowledge breeders have about varieties and plant characters and make use of them in training programmes. Although some breeders are 'lone wolves' many are also willing to share their competence with others.

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# Spring barley breeding in Lithuania

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## *Introduction*

Spring barley is the most widely grown cereal in Lithuania. It occupies about 500 000 hectares every year. Most of the barley grain is used for feed and about 6% for the beer industry. Among all cereals cultivated in Lithuania, barley ranks second after winter wheat in terms of yield. Varieties play an important role in increasing the yield capacity. The primary objective of spring barley breeding in Lithuania is to develop high-yielding varieties for malt and feed, with good straw strength and resistance to diseases such as mildew, spot blotch, scald and loose smut.

Barley breeding started in Lithuania in 1924, two years after the Dotnuva Plant Breeding Station was founded (Mackevichius 1939). Initially the barley collection maintained was that which had been brought by Prof. D. Rudzinskas from the Moscow Plant Breeding Station. Real spring barley breeding started in 1924 with the work of the agronomist J. Bulavas (Rudzinskas 1977). Up to 1928 barley breeding in Dotnuva was carried out by means of individual selection and in 1927 multiplication of the two spring barley varieties 'Auksiniai' and Nr. 12 ('Plikieji') was started. Since 1928 intervarietal hybridization also has been used. Breeding activities expanded every year. Thus, 167 different varieties and lines were grown in 1924, while in 1933 this number amounted to 949. During the Second World War the volume of the varieties and lines decreased to 495 in 1943. During the post-war period barley breeding expanded again. In 1953, 879 varieties and lines were investigated (Leistrumas 1968). Now every year we evaluate 6000 to 8000 varieties and lines and perform 110-150 crosses.

Success in breeding is very much dependent on the abundance and value of the initial material. At Dotnuva Plant Breeding Station much attention was paid to the initial material for barley breeding (Bulavas 1953). From 1924 to 1934 356 specimens were collected under the guidance of the plant breeder J. Bulavas. So far 401 local specimens have been collected and studied (Leistrumas 1992). Much consideration is also given to the material obtained from other breeding institutions and from abroad; 2848 spring barley varieties and lines were obtained from almost the whole world. Most of them were obtained from the N.I.Vavilov All-Russian Institute (1947). The lines obtained in the breeding process have been registered in Dotnuva since 1934, and 3240 of such lines have already been registered in the catalogue.

Since the beginning of spring barley breeding in Dotnuva in 1924 14 varieties of spring barley have been developed, 2 of which have been lost – Nr. 12 ('Plikieji') and 'Lietuvos 799' – and 7 which were or still are registered. One of them entered the Official Trials in 1997 as variety 'Aura'. Three spring barley varieties have been registered since 1994: 'Aidas' (1994) 'Ûla' (1995) and 'Alsa' (1996).

A further barley breeding objective is to develop new spring barley varieties with a yielding capacity of 6.5-7.5 t/ha, with good resistance to lodging and diseases and suitable for on-farm cultivation with different levels of farming.

## *Materials and methods*

Barley breeding activities are carried out at the Cereal Breeding Department of the Lithuanian Institute of Agriculture. The soil of the experimental site is soddy-gleyic light loam. The preceding crop was seed clover, and fertilizer application was N60-P60-K60.

The main method used for spring barley breeding at the Lithuanian Institute of Agriculture is intervarietal hybridization, with subsequent individual selection. Spring barley breeding is carried out according to the following design: (1) collection; (2) initial material nursery ($F_1$, $F_2$); (3) first year selection nursery; (4) second year selection nursery; (5) check (control) nursery; (6) preliminary trials, and (7) competitive trials (Leistrumas 1992). The spring barley variety collection is grown for the maintenance of Lithuanian varieties and for the evaluation of new varieties obtained from other institutions and countries. In this nursery we evaluate period of maturity, plant height, resistance to lodging and resistance to diseases. After harvesting, grain yield is measured and grain quality is evaluated: 1000-kernel weight, hectoliter weight, content of crude protein and starch in the grain.

After field and laboratory investigations we select varieties for crosses. Crosses are performed according to the "twirl method" (Guliajev and Guzhov 1978). For one crossing combination we emasculate 5-6 spikes in each 10-12 flowers. The obtained hybrid kernels are sown in a greenhouse or field ($F_1$). The $F_1$ kernels are sown in a $F_2$ nursery, where individual selection of elite plants or spikes is done. When selecting the plants the following characters are taken into consideration: tillering, resistance to lodging and diseases, thickness and shape of spike. These characters positively correlate with grain productivity (Nettevich 1981; Gluchovcev 1982; Gorshkova and Gorodov 1986).

The best lines selected are sown in selection and check nurseries and evaluated for 1 year. After selection, the best lines are tested for another 1-2 years in preliminary trials. The most promising lines are tested for another 3-4 years in competitive trials. The best new varieties are evaluated in ecological trials in foreign breeding institutions. The best-performing varieties in all the breeding stages are entered into Official Trials.

In all nurseries the same observations are made as in the collection nursery. New varieties from the competitive trials and collection are evaluated for disease resistance in an infected background.

Sizes of field plots are:

| | |
|---|---|
| in collection nursery | 1-2 m$^2$ |
| $F_1$, $F_{2,}$ nurseries | 0.4-25 m$^2$ |
| first year selection nursery | 0.2-0.4 m$^2$ |
| second year selection nursery | 2 m$^2$ |
| check nursery | 2 × 5 m$^{2,}$ |
| preliminary trials | 4 × 10 m$^2$ |
| competitive trials | 4 × 20 m$^2$ |

## *Results and discusions*

Since the beginning of spring barley breeding at the Dotnuva Plant Breeding Station the main breeding method was individual selection. The first crosses were made in 1928. Since 1931, with the exception of 1944, intervarietal hybridization was carried out every year. Intervarietal hybridization with subsequent individual selection now represents and will remain the principal method of barley breeding in Dotnuva. By 1997, 3209 crosses have been performed.

Fourteen varieties of spring barley have been bred in Dotnuva up to 1997 (Table 1). The List of the Recommended (Registered) Varieties of Lithuania includes four Lithuanian spring barley varieties: 'Auksiniai 3' (1987), 'Aidas' (1994), 'Ûla' (1995) and 'Alsa' (1996). A new variety has entered the Official Trials in 1997.

### 'Auksiniai 3'

This variety was developed by intervarietal crossing of the 'Carina' (Germany, France) and 'Tarra 26' (Japan) varieties in 1973. In 1974-81 the selected line 2257-10 was studied in the initial breeding nurseries and in the competitive variety trials. In 1983 the line entered the Official Trials as the variety 'Auksiniai 3'.

Every year the variety shows a high yield capacity of 4.6-6.1 t/ha (Table 2). It is a semi-intensive type. 'Auksiniai 3' is good at tillering and gives a good 'crowding-out' effect of weeds. 'Auksiniai 3' matures in 83 days and is a mid-season variety. 'Auksiniai 3' is medium resistant to lodging and diseases such as loose smut and foliar diseases. Plant height is 80-86 cm. The grains are large (1000-kernel weight = 45-50 g). 'Auksiniai 3' is distinguished for its high hectoliter weight (713-740 g/L). The variety contains 11.5-11.7% of crude protein, and 60.1-63.0% of starch. 'Auksiniai 3' has the best malting quality of the registered Lithuanian barley varieties – extract yield 80.7%. 'Auksiniai 3' belongs to the *nutans* variety. Spikes are two-row, 7.5-9.5 cm long. Awns are 13-15 cm long. 'Auksiniai 3' has been registered in Lithuania since 1987.

**Table 1.** Spring barley varieties developed at the Lithuanian Institute of Agriculture

| Variety | Released | Registered |
|---|---|---|
| Auksiniai † | 1927 | |
| Nr. 12 (Plikieji) † | 1927 | |
| Dotnuvos 4-eiliai † | 1930 | |
| Auksiniai II | 1947 | 1950-90 |
| Dziugiai | 1947 | 1950-75 |
| Lietuvos 799 | 1950 | |
| Gausiai | 1961 | |
| Gintariniai | 1973 | 1979-86 |
| Dainiai | 1981 | |
| Auksiniai 3 | 1983 | 1987- |
| Aidas | 1990 | 1994- |
| Ûla | 1992 | 1994- |
| Alsa | 1993 | 1995- |
| Aura | 1997 | |

† Individual selection method.

**Table 2.** Grain yield of new spring barley varieties in the Official Trials (1994-96)

| Variety testing station | Variety | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Ûla(control) | | Auksiniai 3 | | Aidas | | Alsa | |
| | Mean | Relative value | Mean | Relative value | Mean | Relative value | Mean | Relative value |
| Silutë | 4.99 | 100 | 4.48 | 89.8 | 5.38 | 107.8 | 5.39 | 108.0 |
| Plungë | 5.65 | 100 | 5.20 | 92.0 | 5.54 | 98.0 | 5.77 | 102.1 |
| Kaunas | 5.92 | 100 | 5.65 | 95.4 | 6.62 | 111.8 | 6.23 | 105.2 |
| Pasvalys | 6.83 | 100 | 6.13 | 89.8 | 6.52 | 95.5 | 6.60 | 96.6 |
| Utena | 3.63 | 100 | 3.54 | 97.5 | 3.98 | 109.6 | 3.78 | 104.1 |
| Vilnius | 2.96 | 100 | 2.43 | 82.1 | 2.77 | 93.6 | 2.83 | 95.6 |
| **Mean** | **5.00** | **100** | **4.57** | **91.4** | **5.14** | **102.8** | **5.10** | **102.0** |

**'Aidas'**

This variety has been developed by intervarietal crossing and individual selection. In 1982 the native selected barley line 27781-7 ('KM 1192' × 'Ofir') was crossed with a Dutch variety 'Effendi'. The selected line 4988-3, which was good at the initial stages of selection work, was studied in competitive variety trials. According to the average 3 years' data the new variety had a higher-yielding ability than the check variety by 9.7%. The yielding capacity of 'Aidas' barley is 7.0-7.5 t/ha. 'Aidas' plant height is about 70-72 cm and resistance to lodging is 9 (on a 1-9 scale). The new variety is less attacked in natural and infectious background by loose smut, powdery mildew and by root rot. The grains are large – 1000-kernel weight is 48-52 g, hectoliter weight 660 g/L. The grains contain 11.5-13.0% of crude protein, 58.2% of starch. The grains are fit for food and fodder. Barley 'Aidas' matures in 86 days. It is 6-8 days later than the standard variety. Barley 'Aidas' belongs to the *nutans* variety. Its spikes are two-row, yellow, 7.2-9.2 cm long, thin. Awns are 12-14 cm long, not opened. In 1990 the new barley cultivar 'Aidas' was passed on to the Official Trials and this variety has been registered in Lithuania since 1994. The yield of this variety in the Official Trials for 1994-96 is given in Table 2.

### 'Ûla'

This variety has been developed by intervarietal crossing and individual selection. In 1984 the Swedish variety 'Roland' was crossed with the Danish number 'Ca 33787'. In 1985-91 the selected line 5775-64 was tested in the initial breeding nurseries and in the competitive trials. In 1992 the line entered the Official Trials as the variety 'Ûla'.

The average 3 year's yield of the new variety in competitive trials was 6.1 t/ha. It outyielded the check variety by 0.77 t/ha (14.4%). The variety is high-yielding. In 1996 in the Pasvalys Plant Variety Testing Station 'Ûla' produced 8.69 t/ha. The study in plant breeding stations in Latvia and Estonia shows a large potential ecological plasticity of the new variety. 'Ûla' is resistant to lodging (score 9), plant height is 79 cm. The variety is also resistant to foliar diseases. 'Ûla' barley matured 1-2 days earlier than the standard variety and can be grown as a continuous crop. The grains are large – 1000-kernel weight is 49-54 g, hectoliter weight – 688 g/L, they contain 11.6-12.6% of crude protein, 57.3% of starch. 'Ûla' belongs to the *nutans* variety. Spikes are two-row, yellow, 7.2-8.8 cm long. The seeds are of straw-yellow colour with grown-in glumes. Awns are 13-16 cm long. 'Ûla' has been registered in Lithuania since 1995. Since 1996 'Ûla' has been a check variety in the Official Trials (Table 2).

### 'Alsa'

The new barley variety 'Alsa' has been developed by complex intervarietal crossing and individual selection. In 1985 our line 3762-37 ('Mirena' × mutant derived from 'Gintariniai') was crossed with the breeding line ('Abava' × 'Emir') from the Stende Plant Breeding Station. In 1986-91 the selected line 5995-49 was studied in the initial breeding nurseries and in the competitive variety trials. The 'Alsa' variety entered the Official Trials in 1993.

This variety is high-yielding (yielding capacity 8.05 t/ha) and with good resistance to lodging (score 9) and foliar diseases, especially powdery mildew. Plant height is 70-80 cm. 'Alsa' matures in 77-99 days and the variety is rather late. The grains are large – 1000-kernel weight is 46-48 g, hectoliter weight 665 g/L. They contain 11.8-12.3% of crude protein, 59.0 % of starch. The variety was studied in Svalof Weibull AB in Sweden and shows a very good malting quality – extract yield 81.1%.

'Alsa' belongs to the *erectum* variety. Its spikes are two-row, dense, 7.5-8.5 cm long. Awns are 12-14 cm long. The seeds are of straw-yellow colour with grown-in glumes. 'Alsa' has been registered in Lithuania since 1996. This variety has almost the highest yield among Lithuanian varieties (Table 2).

Quite a large number of good breeding lines have been selected. Some promising lines with high yield capacity and good malting qualities are now being investigated in competitive trials. One of them has entered the Official Trials in 1997 as the variety 'Aura'.

## Conclusions

In total 14 barley varieties have been developed in Dotnuva, 4 of which – 'Auksiniai 3', 'Aidas', 'Ûla' and 'Alsa' – are registered. The main task of spring barley breeding in Lithuania is to reach high yield levels in combination with a good grain quality, disease resistance, lodging endurance and suitability for cultivation on the farms with different levels of farming practices. Future plant breeding must be planned so that agriculture can be supplied with the varieties bred in Lithuania. It is necessary to conduct research into the development of a technical basis for breeding in order to maintain a good productivity.

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# Barley genome research at the IPK – the Plant Genome Resources Centre

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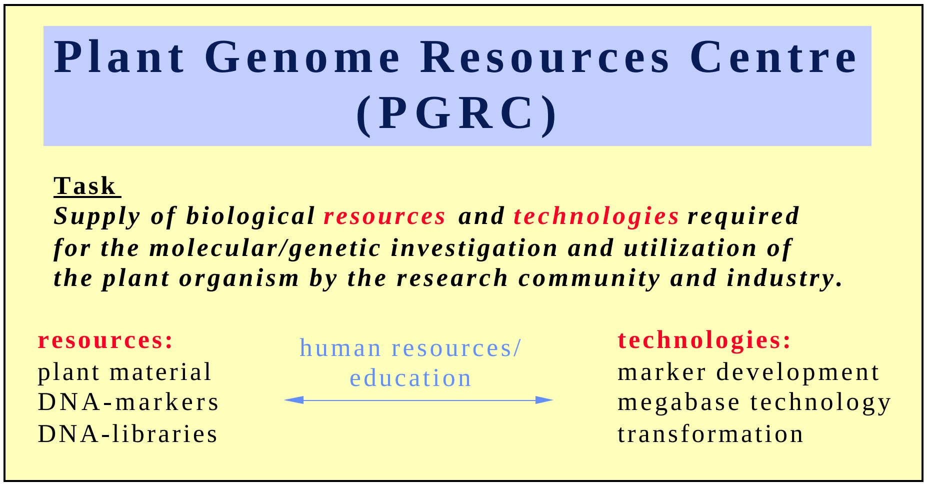
In addition to its major feature, the Gene Bank, the IPK comprises four departments (Taxonomy, Cytogenetics, Molecular Genetics and Molecular Cell Biology), which are methodologically and thematically linked at the junction of molecular biology and genome analysis. This unique association, now known as **genomics**, is already undergoing changes during which we will apply knowledge gained from the analysis of model genomes, such as yeast and *Arabidopsis*, to enable us to understand and manipulate the complex genomes of agriculturally important crop species.

Genomics extends from simple DNA-fingerprinting through phenotypic analysis and genetic mapping to gene isolation and transformation. To account for this increasing complexity and to efficiently support future research activities in this field, the IPK Plant-Genome-Resources-Centre was established in 1997 (Box 1). Its major goal is to maintain and to provide biological resources such as probe repositories, DNA libraries and mapping populations together with the appropriate technology including the development of molecular markers, the refinement and application of megabase technologies for map-based cloning, and the production of transgenic plants. In this way, the PGRC forms a base from which to initiate and implement interactive research activities both within individual groups of the IPK and with collaborators from academic and industrial sectors. Individual research projects are attached to a central service unit providing the above-mentioned biological tools combined with technical facilities and computer support needed to undertake, for example, DNA-fragment or DNA-sequence analyses. This service core is linked to seven satellites termed **modules**, each contributing scientific expertise in a specific field related to genomics (Box 2).

To provide a scientific focus, research activities at the PGRC mainly concentrate on cereals, particularly barley, mainly because its cultivated form (*Hordeum vulgare* L.) and its wild ancestor (*Hordeum spontaneum*) represent one of the major collections of the Gene Bank, comprising more than 10 000 accessions. In addition, genetic research on this crop has a long-standing tradition at the IPK. The seven chromosomes of the barley genome represent the basic complement of the Triticeae species including all major cereals. Hence, genetic data obtained from other cereal species can often be directly transferred to barley or, conversely, from barley to other cereals and even more distantly related grasses. As a basis for the application of molecular marker techniques, well-developed molecular marker maps are available for genetically mapping nearly any trait that is inherited in a Mendelian way. Moreover, a correlation of the genetic and physical maps has been achieved by PCR analysis of microisolated chromosomes, a feat that has not been realized for more complex genomes. Finally, as a prerequisite for map-based isolation of individual genes, a comprehensive YAC library is available and attempts are being made to improve further the transformation efficiency.

With the establishment of PGRC, the IPK has performed a major step towards satisfying the future demands of plant genomics. Its integrated structure will facilitate genetic research extending from the analysis of a phenotypic trait to the isolation of the corresponding gene. The close interaction with plant breeders will facilitate a rapid transfer of know-how and technology and provide new avenues to access barley germplasm maintained at the Gene Bank for genetic studies and breeding purposes.



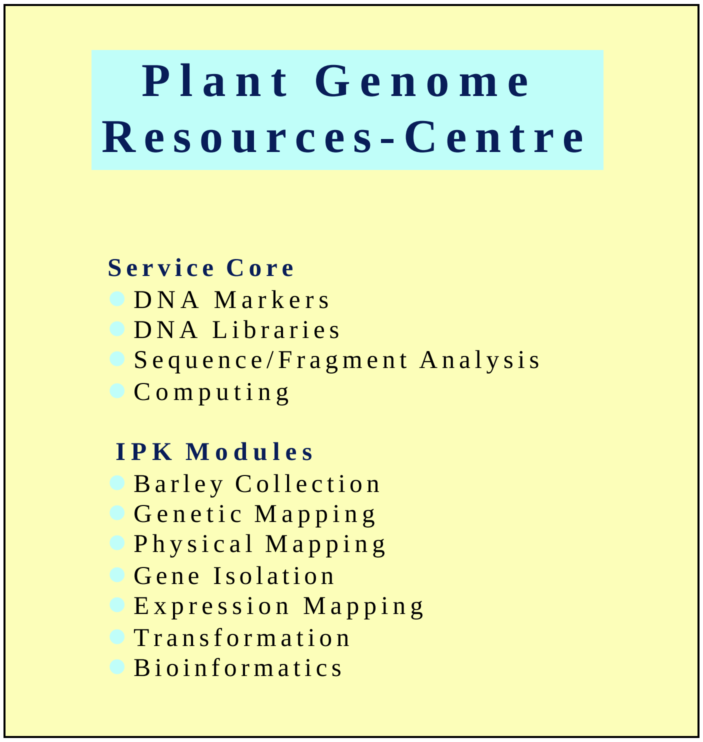
# Plant Genome Resources Centre (PGRC)

**Task**

***Supply of biological resources and technologies required for the molecular/genetic investigation and utilization of the plant organism by the research community and industry.***

| **resources:** | human resources/<br>education | **technologies:** |
|---|---|---|
| plant material<br>DNA-markers<br>DNA-libraries | ⟷ | marker development<br>megabase technology<br>transformation |

**Box 1.** The IPK Plant Genome Resources Centre represents a platform for the generation of biological resources and the development and application of DNA technology.



# Plant Genome Resources-Centre

**Service Core**

- DNA Markers
- DNA Libraries
- Sequence/Fragment Analysis
- Computing

**IPK Modules**

- Barley Collection
- Genetic Mapping
- Physical Mapping
- Gene Isolation
- Expression Mapping
- Transformation
- Bioinformatics

**Box 2.** Structure of the PGRC comprising a service core and modules targeted to specific subareas of barley genomics.

# EVA: Information system for evaluation data of barley genetic resources

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## Introduction

The use of barley genetic resources in practical breeding as well as in breeding research programmes becomes more and more necessary. New breeding aims such as industrial use, resistance against viruses, insects or fungi or even improvement of adaptation to abiotic stress (e.g. drought, salinity, acidity, etc.) require a steady enlargement of the genetic variability in such programmes. To meet this demand, barley breeders and researchers are highly dependent on the availability of information on barley genetic resources, because it is necessary to preselect the material according to this information before evaluating it in their own nurseries. Therefore, the availability of reliable information about the traits relevant for breeding is essential. For breeders, data of evaluation traits such as yield, agronomic performance, resistance and quality are the most relevant.

## Information sources

In Germany different data sources are available for the kind of information mentioned above: first of all, genebank documentation, but also research institutes and, for example, the data of the performance trials system conducted by German official authorities for variety certification and recommendation.

At the moment, the use of all this information is difficult because of the multiplicity of data sources and structure, and of the different ways of accessing data (information available on hard copy, diskettes, off-line or on-line databases).

Another major problem consists in the lack of a common analysis of all data available for each genotype. A possible solution could be an information system combining all available and relevant data in one database with free access from everywhere at any time.

According to the way of accessing the information, databases show different features (Jiménez Krause and Lipman 1997). Regarding the present developments in information technology, on-line systems on the Internet offer optimal access and searchability, even if the availability of such systems, at least up to now, might be limited because of some technical constraints.

Other advantages of on-line systems on Internet are worldwide access, easy updating and the possibililty of linking to other relevant information on Internet.

## The EVA information system

The aim of the EVA project therefore is the development of an information system for evaluation data as an on-line database with worldwide access via the Internet. Different data sources have to be combined in the system. Therefore, a standard data structure has to be developed, data have to be checked and their structure has to be reorganized and, finally, methods for a combined statistical analysis must be developed. Data will also be linked to other relevant data (e.g. literature, research projects, etc.).

The system will combine the information of relevant local information systems (some of them are even on Internet now, but only with a part of their information) under a common shell (see Fig. 1). Additional information will be available by statistical analysis of all data and by linking to other national and international information sources. There will be no further need to get used to different data structures of different information systems. The common data structure will make it easy for the users to request information.

The project is a case study, where at the beginning mainly data of barley and to some smaller extent also data of potato and fruit trees will be considered. Most of the evaluation data available for the project are not stored electronically yet. Therefore, data entry is also one of the tasks in the project. The project started in May 1996 and is funded by the German Ministry of Food, Agriculture and Forestry.

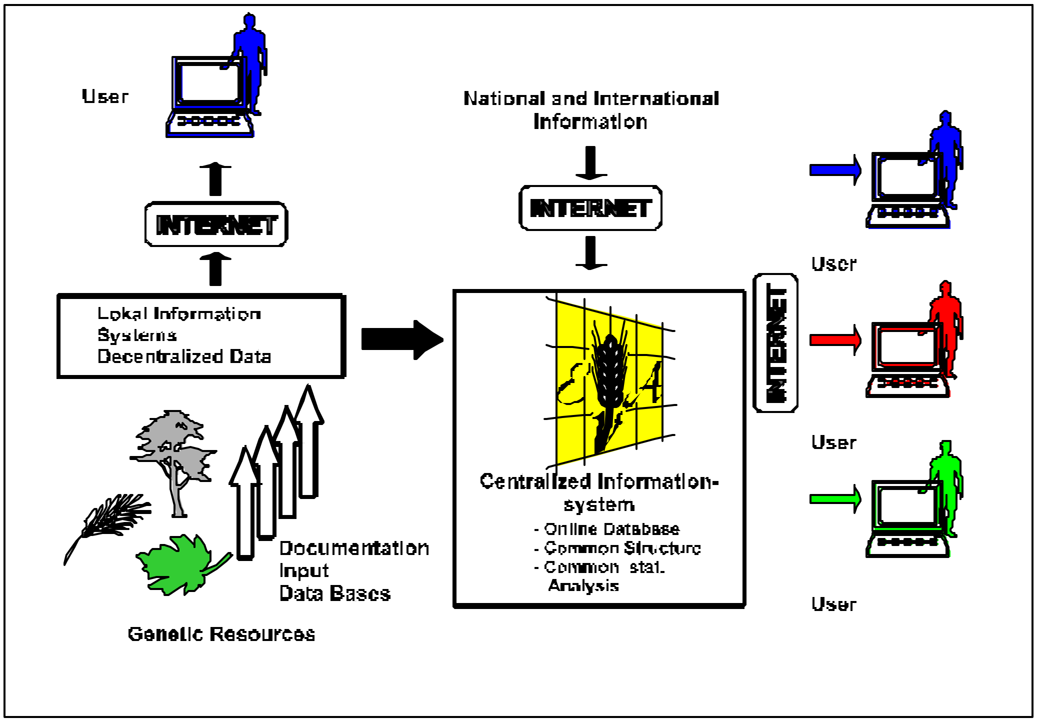

**Fig. 1.** Aims of the EVA system.

## *Project partners*

The genebank of the Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) in Gatersleben contributes with observation, characterization and evaluation data of more than 12 000 accessions of barley. IPK genebank's branch stations in Dresden-Pillnitz and Groß Lüsewitz will register their data of 2500 accessions of fruit trees and 2000 accessions of potato, respectively, to the project. The Institute for Epidemiology and Resistance (IfE/R) of the Federal Centre for Breeding Research on Cultivated Plants (BAZ) in Aschersleben is responsible for entering resistance data of IPK's barley accessions. The genebank of the BAZ in Braunschweig contributes with data of about 7500 accessions of barley. Data of official barley performance trials are being made available by the "AG Datenspeicher", Institute of Crop Science of the University of Halle-Wittenberg in Bad Lauchstädt. The re-analysis of the performance trials and the development of statistical procedures for combining and evaluating all data will also be done there.

Finally, the coordination of the project, the development of the database structure and the establishment of EVA as an on-line database linked to the Information System for Genetic Resources (GENRES)[20] within the German Agricultural Information Network (DAINet)[21] and to other relevant databases will be carried out by the Information Centre for Genetic Resources (IGR) at the Centre for Agricultural Documentation and Information (ZADI) in Bonn.

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[20] **<http://www.dainet.de/genres/genres-e.htm>.**

[21] **<http://www.dainet.de/dain/dain-e.htm>.**

### Database structure

The information will be offered by the system at different information levels. At first level, the user can query the database on the most important passport, characterization and evaluation traits (Table 1). For each trait there is only one value representing all available information (condensation of information will be done by means of statistical methods or expert knowledge). The value itself is linked to the next information level containing more detailed information, e.g. average values over years, location, etc. In cases when raw data are available, the values of the second information level will be linked to the experimental data (third information level: experiment description, raw data, etc.).

**Table 1.** Traits in the first information level

| Passport | Characterization | Evaluation |
|---|---|---|
| Institute code | Seasonality | Yield |
| Accession number | Plant height | Protein content |
| Accession name | Row number | Lodging |
| Other number(s) associated with the accession | Days to flowering/harvest | Winterkill |
| | Spike density | Sprouting |
| Scientific name | 1000-kernel weight | Shattering prior to harvest |
| Status of sample | | Susceptibility to aphids |
| Country of origin | | Susceptibility to mildew |
| Donor institute code | | Susceptibility to yellow rust |
| Donor number | | Susceptibility to brown rust |
| Breeder's name | | Susceptibility to scald |
| Year of first registration | | Susceptibility to net blotch |
| Pedigree | | Susceptibility to BYDV |
| Collecting institute | | Susceptibility to BaYMV |
| Collecting date | | Susceptibility to BaYMMV |
| Country of collection | | |

Most of the descriptors correspond to the FAO/IPGRI Multicrop Passport Descriptor List and the IPGRI Descriptors for Barley. Additional information about breeder, registration and pedigree (only if information is available) is added.

### Examples for the statistical analysis

For the performance trials data (replicated trials; quantitative and qualitative traits) it is planned to do the statistical calculations only for the mean values of the extensive treatment level (less fertilizer, no fungicides). Each year will be calculated separately over all locations. The basis for all calculations is the mean of all orthogonal varieties (BB). Up to now it is planned to calculate parameters such as the arithmetic mean value, minimum, maximum, standard deviation and deviation from BB in percent. For important quantitative traits, e.g. for yield, a regression analysis will be carried out.

Concerning genebank data (not replicated trials) it is planned to calculate the value of the accession, the mean value of all accessions and the relative rank of the accession.

### Next steps

A first prototype of the EVA information system will be established on the Internet at the end of 1997 with a small part of the information available. The information system and the database structure can then be tested by breeders to gain information for the further development of the system.

This prototype will also be compared to existing information systems like the GRIN system in the USA, where it is already possible to query for evaluation traits.[22] Compared

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[22] **<http://www.ars-grin.gov>.**

with GRIN, EVA should be able to provide more detailed information, therefore the development of the 'second' and 'third' information level is another major task of the future work.

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# Evaluation of IPK's barley germplasm for disease resistance

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The experience of the past three decades shows that genetic diversity is the basis of the balance between the development of pathogens and that of agricultural crops. It is the prerequisite of an efficient, ecologically minded agriculture with a low input of pesticides. The period of effectiveness of resistance genes was short, because only one or two genes conditioned the resistance in all registered barley cultivars. For instance the 'Trumpf' resistance to mildew and leaf rust was effective for 4 and 2 years only, respectively. In this time the number of available resistance genes decreased and the amount of fungicides applied and hence the environmental pollution increased.

The knowledge of the coevolution of pathogens and host plants in natural plant populations led to new strategies in plant breeding and agricultural farming. Such strategies are: the use of different genes in winter and spring cultivars, growing of cultivars with different genes in one region, or use of different mechanisms of resistance, e.g. quantitative resistance. However, the implementation of these strategies requires a sufficient number of genes. Therefore, one of the most important tasks of the Federal Centre for Breeding Research on Cultivated Plants (BAZ) is to identify and characterize new sources of resistance, using the diversity available in genebank accessions. Wild relatives and landraces are screened. The genetic basis and the type of resistance are determined by means of classical, biochemical and molecular genetic methods. Pre-breeding programmes are developed to transfer new genes for resistance in cultivars.

This evaluation work of BAZ is the continuation of a long and fruitful tradition of cooperation between the genebank and phytopathologists. In 1955, Nover and Mansfeld started the first screening for resistance of barley to mildew (Nover and Mansfeld 1955). The work was continued and extended for leaf and stripe rust by Nover and Lehmann. For a full list of references about this evaluation programme, see Hammer *et al.* (1994). In the early 1970s, the Institute of Cereal Research Bernburg-Hadmersleben and the Institute of Phytopathology in Aschersleben carried out this work (Walther and Lehmann 1980; Walther 1982, 1990; Hartleb and Walther 1983; Proeseler and Lehmann 1986, 1987; Geißler *et al.* 1989; Proeseler *et al.* 1989; Habekuß and Lehmann 1991). The results of this screening to the end of 1991 are summarized in Table 1.

**Table 1.** Overview of screenings of the Gatersleben barley germplasm for resistance to the economically relevant barley diseases to 1991 in research institutes of the former Academy of Agriculture of GDR

| | | **Seedling reaction** | | | |
|---|---|---|---|---|---|
| **Pathogen** | **No. of samples** | **Susceptible** | **Moderately resistant** | **Resistant** | **Samples with field resistance** |
| mildew [†] | 7488 | 3882 | 2065 | 222 | 522 |
| leaf rust [†] | 6632 | 6366 | 253 | 13<br>(Rph7) | 132 |
| stripe rust [†] | 1501 | 1103 | 342 | 56 | 196 |
| net blotch | 137 | 97 | 27 | 13 | – |
| barley yellow mosaic viruses | 750 | 598 | 66 | 86 | – |
| | | **Susceptible** | | **Tolerant** | **Field tolerant** |
| BYDV | 1300 | 1289 | | 11 | 12 |

[†] Entries tested by Nover *et al.* (not included in the references) were also tested with actual isolates.

Since the foundation of BAZ, the investigations of barley germplasm for resistance to aphids, viruses such as BYDV, BaMMV, BaYMV-1 and BaYMV-2, and fungal diseases such as leaf rust (*Puccinia hordei*) and net blotch (*Pyrenophora teres*) have been continued (Table 2).

In addition, the resistant samples found are tested for resistance to mildew *(Erysiphe graminis)* and stripe rust (*Puccinia striiformis*). The tests are carried out in different ways:

- in field trials with artificial inoculation, normally with one high virulent isolate (leaf rust) or a mixture of relevant isolates
- as a seedling test with defined single isolates of the different pathogens in greenhouses or climatic chambers
- by means of special methods in laboratories, such as leaf segment tests, measurement of enzyme activities or ELISA.

The first step is the selection of barley samples with resistance to one pathogen. In the next step, the material resistant to one of the important diseases is tested for resistance to all other important diseases. The aim is to identify genotypes with a complex resistance to most of the pathogens. The results show that genotypes combining resistance to several diseases are very rare. Therefore, pre-breeding programmes were developed to combine resistance from different sources in one genotype.

### *Aphids*

The aphids are important in a twofold sense, first as a sucking pest and second as vectors of plant-pathogenic viruses. Up to now the number of tested barley accessions is relatively low because the effort in the work with aphids is very high. The results in Table 3 (Schliephake and Geißler 1975) show significant differences in comparison to the susceptible control 'Erfa'. The multiplication rate of the aphids is a good indicator for the host resistance.

Resistance mechanisms of plants to virus-transmitting aphids include the inability of the aphids to transmit the virus and the inability of the virus to multiply in the plant. Important for the infection of plants by viruses is the number of aphids settled on a single plant, and the penetration of the aphid stylets in the plant tissue (Fig. 1). Comparisons of the stylet penetrations with the 'electrical penetration graph' (EPG) on different *Hordeum* genotypes show that especially the salivation time in the phloem is very short in the resistant clone of *Hordeum bulbosum*. The saliva is the means of transport for the virus particles.

### *BYDV*

In Germany the barley yellow dwarf viruses are the most important viruses transmitted by aphids. In contrast to the other barley diseases, there is no resistance to BYDV, only tolerance. In all selected BYDV-tolerant genotypes the presence of virus was detected by means of ELISA, but yield losses were lower than in susceptible cultivars. The tests were carried out under field conditions. The infection success was guaranteed by early planting of infection stripes in the middle of August and of the accessions to be studied in the first decade of September. The activity of aphids and, therefore, the infection pressure is high at this time. In addition the barley samples were tested in climatic chambers by means of aphids infected with defined viruses. Since 1992 two genotypes with tolerance to BYDV were found in 856 accessions tested.

**Table 2.** Current evaluation work of barley germplasm for resistance to diseases and pests of economic relevance in Germany

| Diseases and pests | Pathogen |
|---|---|
| viruses | BYDV, BaMMV, BaYMV-1, BaYMV-2 |
| fungi | *Puccinia hordei, Pyrenophora teres, Puccinia striiformis*[†], *Erysiphe graminis*[†] |
| aphids | *Rhopalosiphum padi, Sitobion avenae, Metopolophium dirhodum, Rhopalosiphum maidis* |

[†] Tested only for samples resistant to at least one of the other pathogens

**Table 3.** Results of the screening of barley to cereal aphids in climatic chamber. Multiplication of *Sitobion avenae, Rhopalosiphum padi* and *Metopolophium dirhodum* in relation to the susceptible standard variety 'Erfa' (=1)

| **Accession** | **Taxonomic group** | ***S. avenae*** | ***R. padi*** | ***M. dirhodum*** |
|---|---|---|---|---|
| GRA 1000 | *H. chilense* Roem. *et* Schult. | – | – | 0.18 |
| GRA 605 | *H. bulbosum* L. subsp*. bulbosum* | – | – | 0.47 |
| GRA 615 | *H. violaceum* Boiss*.* et Huet. | – | – | 0.37 |
| GRA 644 | *H. jubatum* L. | 0.09 | 0.27 | 0.17 |
| GRA 647 | *H. bogdanii* Wilensky | 0.01 | – | 0.16 |
| GRA 876 | *H. turkestanicum* Nevsky | – | – | 0.24 |
| HHOR 3097 | *H. vulgare.* L. var. *hybernum* Vib. | – | – | 0.56 |
| HHOR 4127 | *H. vulgare.* L. var. *hybernum* Vib. | – | – | 0.57 |
| HHOR 4157 | *H. vulgare.* L. var. *hybernum* Vib. | – | – | 0.51 |
| HHOR 4159 | *H. vulgare.* L. var. *hybernum* Vib. | – | – | 0.52 |
| HHOR 991 | *H. vulgare.* L. var. *hybernum* Vib. | – | – | 0.66 |

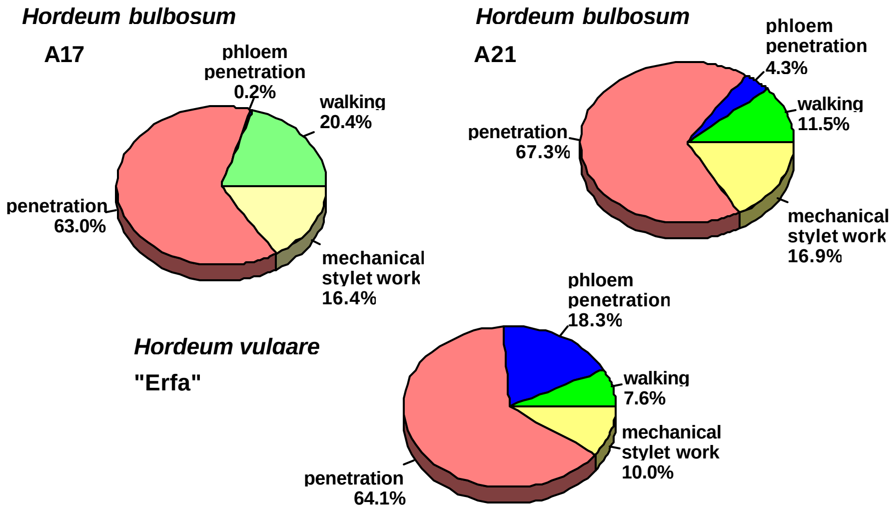

**Fig. 1.** Penetration behaviour of *R. padi* on *H. bulbosum* and *H. vulgare*.

## *BaMMV/BaYMV-1 and BaYMV-2*

Equally as important as the BYDV are the soilborne barley mosaic viruses, transmitted by the soil fungus *Polymyxa graminis*. Evaluation started at the beginning of the 1980s when the first symptoms were found in contaminated areas. The barley entries were tested in trials on contaminated fields and in climatic chambers by inoculation with defined virus strains (Habekuß and Proeseler 1995). The results are presented in Table 4. In contrast to BYDV, real resistance was found, and the plants are virus-free. The reaction of barley genotypes to BaMMV and the two strains of BaYMV was different. Four reaction types were observed. For 46 barleys the investigations were finished and the reaction patterns were classified. Nine genotypes are resistant to all three viruses.

The accessions with BYDV tolerance were tested to the barley mosaic viruses, *Pyrenophora teres* and *Puccinia hordei* (Table 5). Only three barleys were tolerant or resistant to all viruses, one of them was additionally resistant to net blotch. In summary, six out of ten genotypes possess – besides the resistance to one or two barley mosaic viruses – resistance to net blotch, but none was resistant to leaf rust.

**Table 4.** Results of evaluation for resistance to BaMMV, BaYMV-1 and BaYMV-2

| Reaction pattern | Viruses<br>BaMMV | <br>BaYMV-1 | <br>BaYMV-2 | Number of samples per pattern |
|---|---|---|---|---|
| 1 | s | s | s | 1700 |
| 2 | r | s | s | 7 |
| 3 | r | r | s | 30 |
| 4 | r | r | r | 9 |
| generally resistant to one or some virus isolates | | | | 300 [†] |

[†] Investigations not yet finished.

**Table 5.** Resistance reaction[†] of BYDV-tolerant winter barleys to artificial inoculation with BaMMV, BaYMV-1, BaYMV-2, *Pyrenophora teres* and *Puccinia hordei*

| Accession | BaMMV | BaYMV-1 | BaYMV-2 | *P. teres* | *P. hordei* |
|---|---|---|---|---|---|
| HHOR 2297 | (R) | S | S | R | S |
| HHOR 2310 | R | S | S | R | S |
| HHOR 3073 | R | S | S | R | S |
| HHOR 3097 | R | R | R | S | n.t. |
| HHOR 3151 | R | R | R | R | S |
| HHOR 3488 | R | S | S | (r) | S |
| HHOR 4196 | R | S | S | (r) | S |
| HHOR 4224 | R | R | R | S | S |
| HHOR 8273 | R | S | S | R | S |
| HHOR 8274 | R | S | S | (r) | S |

[†] R = resistant, S = susceptible, n.t. – not tested.

### *Fungal diseases*

The fungal diseases of barley are very important and, in contrast to BYDV, the protection of plants by means of agronomic measures such as optimal time of planting is not possible. Therefore the search for new genes for resistance has the longest tradition. In the 1960s, mildew was the most important disease. With the creation of mildew-resistant cultivars, the importance of leaf rust increased. At the beginning of the 1980s, leaf rust and mildew resistant cultivars were grown and the importance of net blotch increased. Assisted by weather conditions this disease gained more and more importance because the actual cultivars have no resistance. An overview of the most important evaluation methods is given in Box 1.

The seedling test for determination of vertical resistance genes and the field tests have a long tradition. Especially the latter have a central importance. Because of weather conditions, artificial infection in field trials is not successful in every year. Therefore, in order to shorten the selection time, different methods – such as leaf segment tests with leaves of different stages of plants and enzyme tests – were developed or modified (Kopahnke and Nachtigall 1995; Müller *et al.* 1996b). In general, the correlation of results of field trials and these methods ranged between 0.7 and 0.9.

### *Net blotch*

In the last six years, 496 accessions of *Hordeum spontaneum* and 400 accessions of *H. vulgare* were tested for resistance to net blotch. The resistance to net blotch is a quantitative resistance, and differences between the entries are gradual. Since the field trials depend on the environmental conditions, laboratory methods are very helpful. The results of the leaf segment tests show highly significant genotype × isolate interactions (Fig. 2).

The number of samples resistant to the low aggressive isolate 'Amelung' is significantly higher than to the more aggressive isolate Re Bu. Therefore, the resistant samples were tested with isolates possessing different degrees of aggressiveness. The determination of enzyme activity as a measure for the resistance level is shown in Figure 3. In most cases the results are in accordance with those from the leaf segment tests.

**Box 1. Overview of methods of evaluation to fungal diseases.**

Field trials: Four replications, artificial infection with a highly virulent isolate (leaf rust) or a mixture of different isolates (net blotch)

- accounting of the Area Under the Disease Progress Curve by 4-6 measurements [assessment of percentage of attacked leaf area (upper 3 leaves) and of a relatively latent period – number of days later than a susceptible control]
- selection of accessions without symptoms (vertical resistance)

Tests in climatic chambers and greenhouse

- investigation with defined isolates (determination of resistance genes, of resistance type, i.e. vertical, partial or moderate resistance)
- genetic analyses of $F_2$ populations in the seedling stage

Laboratory methods

- determination of the level of quantitative resistance (leaf segment test on the second leaf, measurement of enzyme activity in healthy and infected plants)
- investigations of the infection structure by means of fluorescence and electron microscopy
- genetic analyses by use of molecular markers (QTL, RFLP)

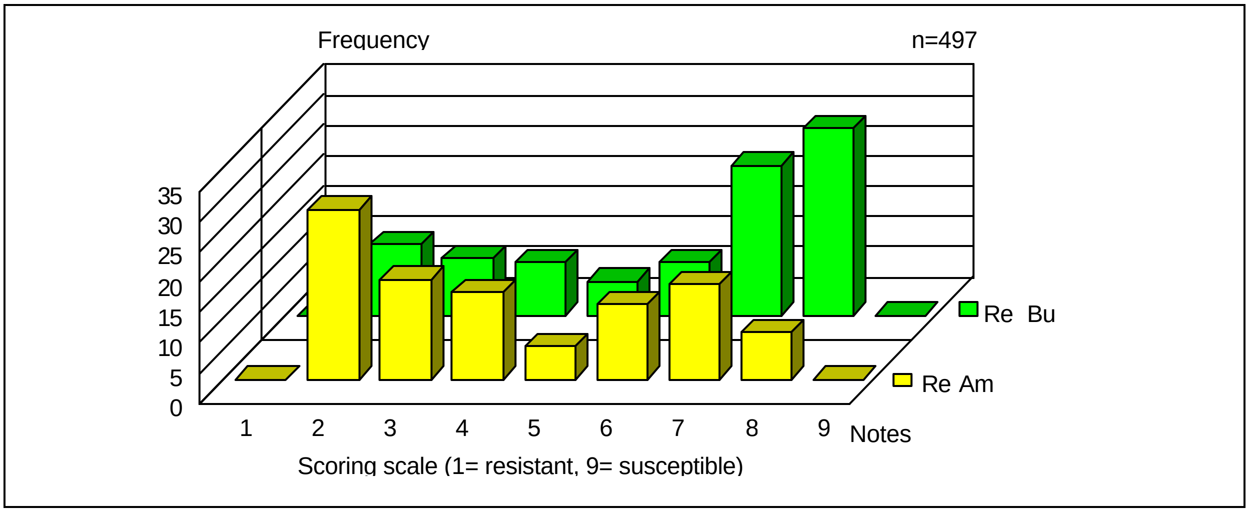

**Fig. 2.** Evaluation of 497 *Hordeum spontaneum* accessions for resistance to two isolates of *Pyrenophora teres* with different levels of aggressiveness (leaf segment tests).

### *Leaf rust*

The evaluation work for resistance of barley to leaf rust started in the 1970s. In the past 6 years, more than 1000 accessions were tested. The results are shown in Table 6. The very intensive breeding and the ability of leaf rust to overcome new resistance genes led to a quick breakdown of efficiency of genes (Prochnow and Walther 1996). This was followed by an intensive search for new sources of resistance.

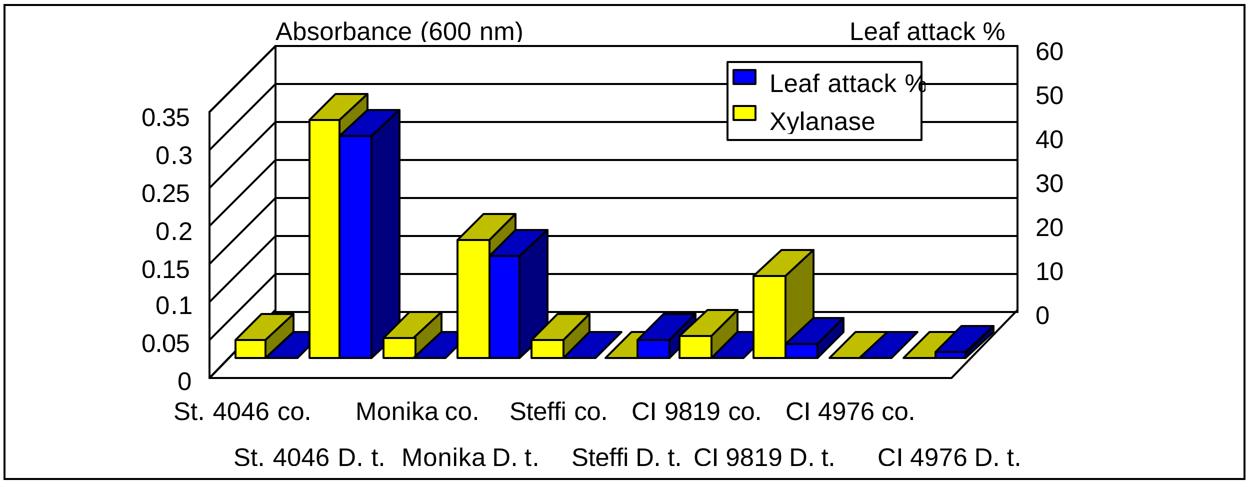

**Fig. 3.** Xylanase activity of different barley genotypes 7 days after inoculation with *Pyrenophora teres* in detached leaf test.

**Table 6.** Evaluation results of 500 accessions of *Hordeum vulgare* and 496 accessions of *H. spontaneum* for resistance to leaf rust (*Puccinia hordei* Otth.) tested since 1992

| | **Vertically resistant** | | **Partially resistant** |
|---|---|---|---|
| **Species** | **Resistant** | **Resistance is overcome** | **(level similar to 'Vada')** |
| *H. vulgare* | 0 | tests not finished | 65 |
| *H. spontaneum* | 41[†] | 126 (Rph1,2,3,4,8,9,Trumpf) | 242 |

[†] Resistance genes different from Rph7.

The results show that new sources of effective vertical resistance were not found in *Hordeum vulgare*. Therefore, it is necessary to work with other, not so closely related barley species. Partial resistance was found in *H. vulgare* and *H. spontaneum*. The accessions of *H. spontaneum* with leaf rust resistance were tested also to mildew, net blotch and stripe rust (Table 7). Barleys with a complex resistance to some diseases were found more frequently in *H. spontaneum* than in *H. vulgare*. Most of the 41 resistant entries were also resistant to at least one of the other diseases, and one genotype was resistant to all four diseases.

It is not only important to find new genes for resistance. The value of such work is determined by the characterization and localization of these new genes (Walther 1983, 1990). In Table 8, the genetic hypothesis for one part of the leaf rust resistant *Hordeum spontaneum* accessions is demonstrated. At least four new genes (two dominant and two recessive ones) were found.

Two research projects deal with the development of RFLP markers for this material.

The use of new vertical genes is one possible strategy. In the future, emphasis will be given to increasing the durability of efficiency of these genes. Breeding for partial or quantitative resistance seems to be the best way in this direction.

In summary, 442 barley accessions with different levels of partial resistance were selected in the past 20 years. As a rule not so many genes are responsible (Walther 1991a; Müller *et al.* 1996). For instance, four genes were determined in the cultivar 'Emir' (Walther 1991b). It is important to combine genes complementing each other. Therefore, it is necessary to

**Table 7.** Results of evaluation of 500 accessions of *Hordeum spontaneum* for complex resistance to leaf rust (*Puccinia hordei*), mildew (*Erysiphe graminis*), net blotch (*Pyrenophora teres*) and stripe rust (*P. striiformis*)

| | **Resistance reaction[†] to the diseases** | | | |
|---|---|---|---|---|
| **No. of genotypes** | **leaf rust (7 isolates)** | **mildew (8 isolates)** | **net blotch (2 isolates)** | **stripe rust (isolate 24)** |
| 1 | R | VR | MR | R |
| 2 | R | R | R | S |
| 1 | R | R | MR | S |
| 10 | R | VR | MR | MR |
| 1 | R | R | S | R |
| 10 | R | VR | R-MR | S |
| 2 | R | VR | S | R |
| 8 | R | VR | S | S |
| 3 | R | S | MR | MR |

[†] R = resistant, MR = moderately resistant to all used isolates, S = susceptible, VR = vertically resistant to some of the races tested only.

**Table 8.** Results of genetic analyses of the heredity of leaf rust resistance investigated in the seedling stage on $F_2$ populations of the crosses *Hordeum spontaneum* × L94 (susceptible parent)

| **Observed segregation** | | | |
|---|---|---|---|
| **Resistant** | **Susceptible** | **Genetic hypothesis** | **No. of accessions** |
| 3 | 1 | 1 dominant gene | 1 |
| 1 | 3 | 1 recessive gene | 12 |
| 7 | 9 | 2 recessive genes (independent) | 8 |
| 9 | 7 | 2 dominant genes (complementary) | 2 |
| 1 | 15 | 2 recessive genes | 2 |

characterize the genes by molecular markers. In the last 3 years, QTLs were determined for the cross 'Krona' × HOR 1063 (partially resistant), cf. Fig. 4 (Kicherer *et al.* 1996).

The combination of resistance caused by several minor genes is difficult. A breeding programme was developed, using double haploid technique (Fig. 5) (Wächter *et al.* 1991). In the last years this programme was completed and the timespan between the first crosses and the establishment of basic material with a high resistance level was drastically shortened.

By means of this method it is possible to select homozygous quantitatively resistant material for breeding programmes. In the past 12 years, pre-breeding programmes started with the aim to transfer partial resistance from wild relatives into barley cultivars. The progress of this work is demonstrated in Table 9. The resistance level of lines ($F_5$) was on the average 2.5 scores better than the parent cultivar. Some lines were approximately fully resistant (score 1.1, which means 1-3 % attacked leaf area).

In the last 20 years, quantitative resistance was used in breeding. The progress in the level of new bred lines shows the success. In 1993 the average resistance level of 34 lines was significantly lower than the partially resistant standard 'Vada'. In 1995 there were no differences (Fig. 6).

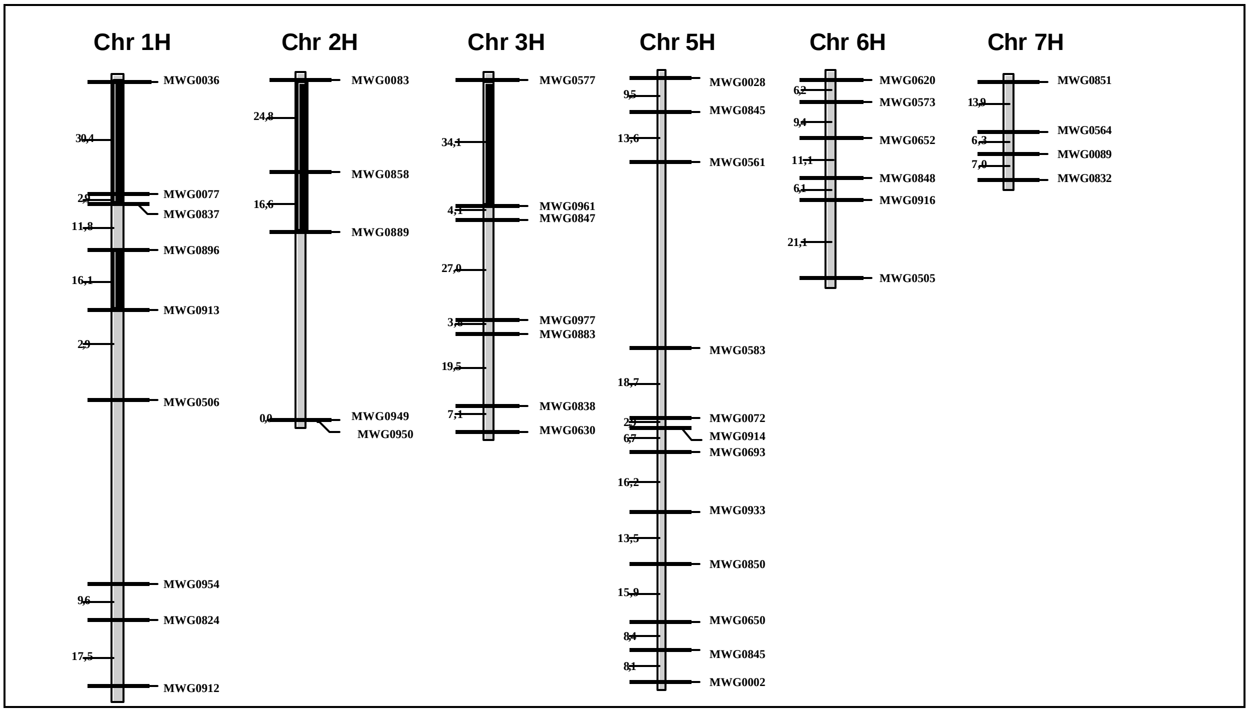

**Fig. 4.** Linkage map of partial leaf rust resistance in the cross 'Krona' × HOR 1063.

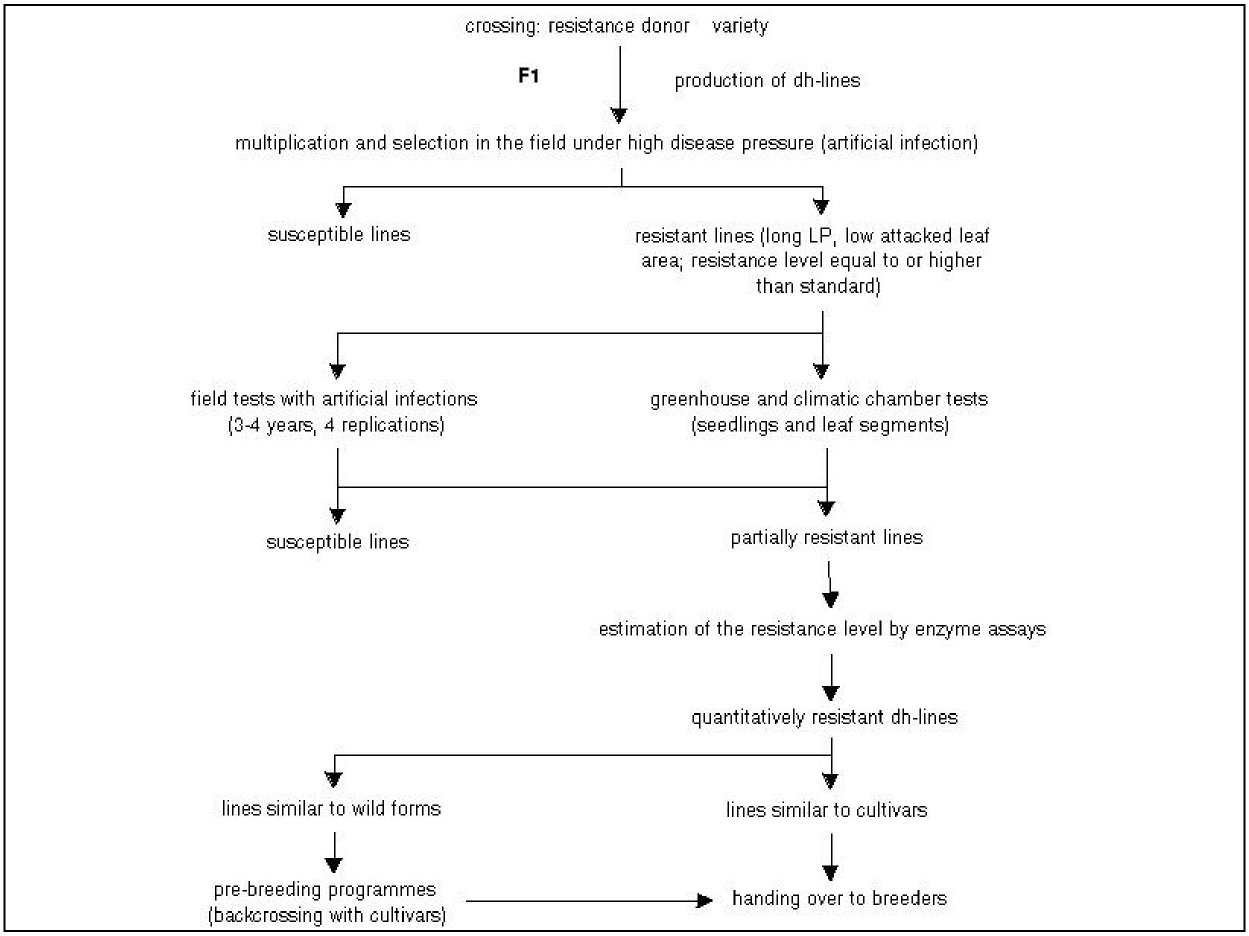

**Fig. 5.** Pre-breeding programme to transfer quantitative resistance to leaf rust

**Table 9.** Results of transfer of barley leaf rust resistance from 31 combinations of wild forms into the variety 'Salome'

| | **Resistance level**[†] | **Range** |
|---|---|---|
| 341 lines | 2.7 | 4.4 – 1.1 |
| standard 'Salome' | 5.2 | – |

[†] 1 = resistant, 9 = susceptible.

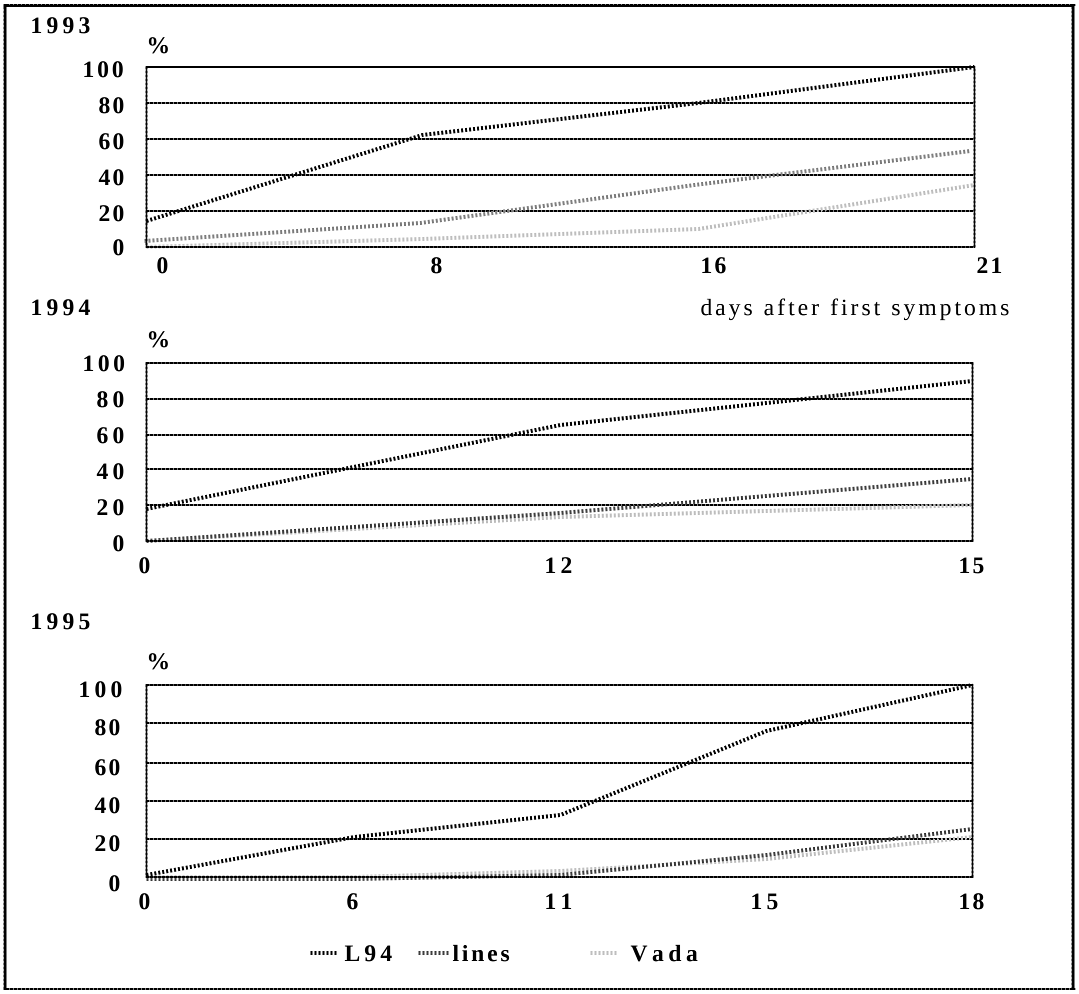

**Fig. 6.** Improvement of the level of partial resistance to leaf rust of new breeding lines compared with the highly susceptible L94 and the partially resistant 'Vada'.

## *Conclusion*

Table 10 gives a short overview of results obtained since 1992 and the practical use of the selected resistant material.

In a project with the German Society of Breeding the lines handed over were tested in the breeding stations. The best lines were included in crossing programmes. On the other side, results from many locations and conclusions about the stability of resistance under different environmental conditions were thus received. The use of this material in breeding increases the diversity in breeding material and last but not least in agriculture.

At present the evaluation results on disease resistance found in the barley collection of the genebank of IPK Gatersleben are being registered for inclusion in a national information system for evaluation data within a cooperative project "EVA" financed by the German

Ministry of Agriculture, in cooperation with IPK Gatersleben and the Central Agency for Agricultural Documentation and Information (ZADI) in Bonn, among others (see Harrer, this volume, p. 89).

In the future it is necessary to develop and finance projects for conservation of genetic resources in close connection with their evaluation and exploitation. High yields achieved by an efficient agriculture in a healthy environment are the basis for the nutrition of humanity. The use of the diversity of genetic resources is the best way to obtain this aim.

**Table 13.** Summary of the tested barley accessions and of samples or lines with a high level of resistance, handed over to breeders

| Resistance /tolerance to | No. of tested genotypes | No. of resistant genotypes | Lines/accessions handed over |
|---|---|---|---|
| BYDV | 857 | 2 (t) [†] | 11 |
| barley mosaic viruses | 1700 | 46 | – |
| net blotch | 496 | 37 | – |
| leaf rust | | | |
| (vertically resistant) | 946 | 41 | 20 |
| (partially resistant) | | 307 | 876 (B)[‡] |

[†] t = tolerance.

[‡] B = basis material from crosses of the mlo-resistant cultivars 'Salome' or 'Krona' with different partially resistant wild barleys.

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# Appendix I. Barley Passport Descriptors, including barley-specific attributes

Based on the FAO/IPGRI Multicrop Passport Descriptors, the main descriptors in the European Barley Database and the IPGRI Descriptors for barley.[23] Passport descriptors which were agreed upon at the meeting and do not belong to the Multicrop Passport Descriptors are numbered A, B, C, D.

## BARLEY PASSPORT DESCRIPTORS

**1. Institute code (INSTCODE)**

Code of the institute where the accession is maintained. The codes consist of the 3-letter ISO 3166 country code of the country where the institute is located plus number or an acronym as specified in the Institute database that will be made available by FAO. Preliminary codes (i.e. codes not yet incorporated in the FAO Institute database) start with an asterisk followed by a 3-letter ISO 3166 country code and an acronym.

**2. Accession number (ACCENUMB)**

This number serves as a unique identifier for accessions and is assigned when an accession is entered into the collection. Once assigned this number should never be reassigned to another accession in the collection. Even if an accession is lost, its assigned number should never be reused. Letters should be used before the number to identify the genebank or national system (e.g. IDG indicates an accession that comes from the genebank at Bari, Italy; CGN indicates an accession from the genebank at Wageningen, The Netherlands; PI indicates an accession within the USA system).

**3. Collecting number (COLLNUMB)**

Original number assigned by the collector(s) of the sample, normally composed of the name or initials of the collector(s) followed by a number. This item is essential for identifying duplicates held in different collections. It should be unique and always accompany subsamples wherever they are sent.

**4. Genus (GENUS)**

Genus name for taxon. Initial uppercase letter required.

**5. Species (SPECIES)**

Specific epithet portion of the scientific name in lowercase letters plus authority[24]. Following abbreviation is allowed: “sp.”

**6. Subtaxa (SUBTAXA)**

Subtaxa can be used to store any additional taxonomic identifier plus authority[24]. Following abbreviations are allowed: “ssp.” (for subspecies); “var.” (for variety); “convar.” (for convariety); “f.” (for form).

**7. Accession name (ACCNAME)**

Either a registered or other formal designation given to the accession. First letter uppercase. Multiple names separated with semicolon.

**8. Country of origin (ORIGCTY)**

Name of the country in which the sample was originally collected or derived. Use the ISO 3166 extended codes, (i.e. current and old 3-letter ISO 3166 country codes)

**9. Location of collecting site (COLLSITE)**

Location information below the country level that describes where the accession was collected starting with the most detailed information. Might include the distance in kilometers and direction from the nearest town, village or map grid reference point, (e.g. CURITIBA 7S, PARANA means 7 km south of Curitiba in the state of Parana)

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[23] IPGRI. 1994. Descriptors for barley (*Hordeum vulgare* L.). International Plant Genetic Resources Institute, Rome, Italy.

[24] Authority is only provided at the most detailed taxonomic level.

**10. Latitude of collecting site** **(LATITUDE)**

Degrees and minutes followed by N (North) or S (South) (e.g. 1030S). Missing data (minutes) should be indicated with hyphen (e.g. 10—S).

**11. Longitude of collecting site** **(LONGITUDE)**

Degrees and minutes followed by E (East) or W (West) (e.g. 07625W). Missing data (minutes) should be indicated with hyphen (e.g. 076—W).

**12. Elevation of collecting site** [m asl] **(ELEVATION)**

Elevation of collecting site expressed in meters above sea level. Negative values allowed.

**13. Collecting date of original sample** [YYYYMMDD] **(COLLDATE)**

Collecting date of the original sample where YYYY is the year, MM is the month and DD is the day[25].

**14. Status of sample** **(SAMPSTAT)**

| | | | |
|---|---|---|---|
| 1 | Wild | 6 | Genetic stock |
| 2 | Weedy | | |
| 3 | Traditional cultivar / Landrace | 99 | Other (elaborate in REMARKS field) |
| 4 | Breeder's line | | |
| 5 | Advanced cultivar | | |

**15. Collecting source** **(COLLSRC)**

The coding scheme proposed can be used at 2 different levels of detail: Either by using the global codes such as 1, 2, 3, 4 or by using the more detailed coding such as 1.1, 1.2, 1.3 etc.

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1 | Wild habitat | 2 | Farm | 3 | Market | 4 | Institute / Research organization |
| 1.1 | Forest / woodland | 2.1 | Field | 3.1 | Town | | |
| | | 2.2 | Orchard | 3.2 | Village | | |
| 1.2 | Shrubland | 2.3 | Garden | 3.3 | Urban | | |
| 1.3 | Grassland | 2.4 | Fallow | 3.4 | Other exchange system | 99 | Other (elaborate in REMARKS field) |
| 1.4 | Desert / tundra | 2.5 | Pasture | | | | |
| | | 2.6 | Store | | | | |

**16. Donor institute code** **(DONORCODE)**

Code for the donor institute. The codes consist of the 3-letter ISO 3166 country code of the country where the institute is located plus number or an acronym as specified in the Institute database that will be made available by FAO. Preliminary codes (i.e. codes not yet incorporated in the FAO Institute database) start with an asterisk followed by a 3-letter ISO 3166 country code and an acronym.

**17. Donor number** **(DONORNUMB)**

Number assigned to an accession by the donor. Letters should be used before the number to identify the genebank or national system (e.g. IDG indicates an accession that comes from the genebank at Bari, Italy; CGN indicates an accession from the genebank at Wageningen, The Netherlands; PI indicates an accession within the USA system)

**18. Other number(s) associated with the accession** **(OTHERNUMB)**

Any other identification number known to exist in other collections for this accession. Letters should be used before the number to identify the genebank or national system (e.g. IDG indicates an accession that comes from the genebank at Bari, Italy; CGN indicates an accession from the genebank at Wageningen, The Netherlands; PI indicates an accession within the USA system). Multiple numbers can be added and should be separated with a semicolon

**19. Remarks** **(REMARKS)**

The remarks field is used to add notes or to elaborate on descriptors with value "99" (=Other). Prefix remarks with the field name they refer to and a colon (e.g. COLLSRC: roadside). Separate remarks referring to different fields are separated by semicolons.

**A. Breeding institute** **(BREEDINST)**

Code for the breeding institute. The codes consist of the 3-letter ISO 3166 country code of the country where the institute is located plus number or an acronym as specified in the Institute database that will be made available by FAO. Preliminary codes (i.e., codes not yet incorporated in the FAO Institute database) start with an asterisk followed by a 3-letter ISO 3166 country code and an acronym.

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[25] Missing data should be omitted, e.g., 197703 or 1953.

**B. Pedigree** **(PEDIGREE)**

Parentage or nomenclature, and designations assigned to breeders' material.[26]

**C. Principal attribute** **(PRINCATTR)**

The most useful characteristics of the accession, justifying its inclusion in the germplasm collection.

1 Translocation 6-7
2 Mildew-resistant
3 Drought-tolerant
4 Mutant brachytic

99 Other (elaborate in REMARKS field)

## BARLEY-SPECIFIC CHARACTERIZATION DESCRIPTORS

**1. Row number** **(ROWNUMB)**

Number of kernel rows of the spike.[27]

1 Two-row, large or small sterile lateral florets (convar. *distichon*)
2 Two-row, deficient (convar. *deficiens*)
3 Irregular, variable lateral florets development (convar. *labile*)
4 Six-row, awnless or awnleted lateral florets (convar. *intermedium* and partly convar. *vulgare*)
5 Six-row, long awns on lateral florets (partly convar. vu*lgare)*

99 Other (specify in REMARKS descriptor)

**2. Growth class (seasonality)** **(SEASONAL)**

1 Winter
2 Intermediate
3 Spring
4 Perennial (in wild species)

99 Other (specify in REMARKS field)

**3. Kernel covering[28]** **(KERNELCOV)**

Whether or not the lemma and palea adhere to the caryopsis.

1. Naked grain
2. Semi-covered grain
3. Covered (hulled) grain

## FAO WIEWS DESCRIPTORS[29]

**1. Location of safety duplicates** **(DUPLSITE)**

Code of the institute where a safety duplicate of the accession is maintained. The codes consist of 3-letter ISO 3166 country code of the country where the institute is located plus number or an acronym as specified in the Institute database that will be made available by FAO. Preliminary codes (i.e. codes not yet incorporated in the FAO Institute database) start with an asterisk followed by a 3-letter ISO 3166 country code and an acronym. Multiple numbers can be added and should be separated with a semicolon.

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[26] A standard notation for pedigrees was not agreed upon for the Barley Working Group, therefore, different notation schemes occur in records of the European Barley Database.

[27] Usually provided by donors of data to the European Barley Database as codes for 2 vs. 6 rows. The more detailed codes proposed in the IPGRI Descriptors for barley correspond to the convarieties used in the classification systems by several genebanks. This correspondence has been added here. For the data from the genebanks using this infraspecific classification system, the information on row number can be derived from the convariety name.

[28] This, and several other morphological characterization descriptors form the basis for classifying cultivated barleys into botanical varieties in the classification systems used by several genebanks. For the data from the genebanks using this infraspecific classification system, the information on these morphological descriptors can be derived from the varietas name.

[29] FAO WIEWS Descriptors are used in the FAO World Inventory and Early Warning System. They are optional descriptors for the EBDB.

**D. Date of safety-duplication** [YYYYMMDD] **(DUPDATE)**

Date of safety-duplication, where YYYY is the year, MM is the month and DD is the day. Multiple dates can be added and should be separated with a semicolon.

**2. Availability of passport data (PASSAVAIL)**

(i.e. in addition to what has been provided)

0 Not available
1 Available

**3. Availability of characterization data (CHARAVAIL)**

0 Not available
1 Available

**4. Availability of evaluation data (EVALAVAIL)**

0 Not available
1 Available

**5. Acquisition type of the accession (ACQTYPE)**

1 Collected / bred originally by the institute
2 Collected / bred originally by joint mission / institution
3 Received as a secondary repository

**6. Type of storage (STORTYPE)**

Maintenance type of germplasm. If germplasm is maintained under different types of storage, multiple choices are allowed, separated by a semicolon (e.g. 2;3). (Refer to FAO / IPGRI Genebank Standards 1994 for details on storage type)

1 Short term
2 Medium term
3 Long term
4 *In vitro* collection
5 Field genebank collection
6 Cryopreserved
99 Other (elaborate in REMARKS field)

**Additional descriptors for EBDB.** Before publication of this meeting report, the EBDB Manager (H. Knüpffer) suggested the use of additional descriptors for inclusion of data in the EBDB. Data submitted to the EBDB Manager in this format will be accepted for inclusion in the EBDB.

## OPTIONAL BARLEY PASSPORT DESCRIPTORS

**E. Introduction number (INTRONUMB)**

Preliminary accession number used by some genebanks for new accessions.

**F. Collector's name or expedition acronym (COLLNAME)**

The name of the collector(s), or acronym of the collecting expedition (with reference to a table of such acronyms used). For example, expedition acronyms used by IPK Gatersleben consist of the 3-letter ISO 3166 country code of the country where the collection was carried out plus a unique acronym containing at least the year of collecting. Codes for expeditions covering several countries start with an asterisk, followed by a three-letter acronym of the continent.

**G. Breeding method (BREEDMET)**

If more than one breeding method, enter in the order of the breeding development and separate with a semicolon.

1 Intrapopulation selection
2 Mass selection (interpopulation selection)
3 Pair cross
4 Polycross
5 Backcross
6 Polyploidization
7 Mutation
99 Other (specify in REMARKS field)

**H. Year of release** [YYYY] **(YEAR_RELE)**

Year of release of the cultivar, or year of registration.

### I. Holder of primary collection (PRIMCOLL)

Code for the institution holding the primary collection of the accession. The codes consist of the 3-letter ISO 3166 country code of the country where the institute is located plus number or an acronym as specified in the Institute database that will be made available by FAO. Preliminary codes (i.e., codes not yet incorporated in the FAO Institute database) start with an asterisk followed by a 3-letter ISO 3166 country code and an acronym.[30]

### J. Plant use (PLANTUSE)

Combined from 'Primary Grain Usage' and 'Primary Fodder Usage' (IPGRI Descriptors for barley). Multiple codes are allowed, separated by a semicolon (e.g. 2;3).

| | | | |
|---|---|---|---|
| 1 | Human food | 6 | Straw for bedding |
| 2 | Livestock feed | 7 | Fuel |
| 3 | Alcoholic beverages | 8 | Green manure or conservation |
| 4 | Grazing | | |
| 5 | Dried hay | 99 | Other (specify in REMARKS field) |

The following additional characterization descriptors are regarded as highly discriminating and, therefore, included in the 'minimum descriptors' (IPGRI barley descriptor list). Field names have not been proposed for these descriptors.

## OPTIONAL BARLEY-SPECIFIC CHARACTERIZATION DESCRIPTORS

### 4. Plant height

At maturity, measured from the ground level to the top of spike excluding awns [cm]

### 5. Stem pigmentation (immature)

| | | | |
|---|---|---|---|
| 1 | Green | 99 | Other (specify in REMARKS field) |
| 2 | Purple (basal only) | | |
| 3 | Purple (half or more) | | |

### 6. Spike density

A subjective observation (see Fig. 4 in IPGRI Descriptors for barley)

| | |
|---|---|
| 3 | Lax |
| 5 | Intermediate |
| 7 | Dense |

### 7. Lemma awn/hood

(see Fig. 5 in IPGRI Descriptors for barley)

| | | | |
|---|---|---|---|
| 1 | Awnless | 4 | Sessile hoods |
| 2 | Awnleted | 5 | Elevated hoods |
| 3 | Awned | | |

### 8. Lemma awn barbs

(see Fig. 6 in IPGRI Descriptors for barley)

| | |
|---|---|
| 3 | Smooth (few barbs at tip) |
| 5 | Intermediate (small barbs on upper half) |
| 7 | Rough |

### 9. Glume colour

| | | | |
|---|---|---|---|
| 1 | White | 4 | Black |
| 2 | Yellow | | |
| 3 | Brown | 99 | Other (specify in REMARKS field) |

### 10. Length of rachilla hair

(see Fig. 9 in IPGRI Descriptors for barley)

| | |
|---|---|
| 1 | Short |
| 2 | Long |

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[30] See Annex 1 of Appendix II in this volume.

**11. Lemma colour**

1 Amber (= normal)
2 Tan / red
3 Purple
4 Black / grey
99 Other (specify in REMARKS field)

**12. Aleurone colour**

(although this trait is difficult to observe, it is used for market type classification in several countries)

1 White
2 Blue

**13. Thousand-kernel weight** [g]

(even though this trait is environment dependent, most growouts will occur in favourable environments). Converted from weighing a lot of 250 kernels or more.

# Appendix II. Sharing of responsibilities for the conservation and use of European barley genetic resources

*A discussion document prepared by the Task Force composed of Jens Weibull, coordinator, František Debre, Olga Kovaleva and Michael Miklis according to the recommendations of the Working Group.*

### *Background*

The objectives of the European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR) include ensuring safe long-term conservation and promoting exchange and utilization. At the establishment of the ECP/GR in 1980, it was recommended that barley genetic resources be given high priority by the Programme, which in turn led to the creation of the Barley Working Group. The Group has proven to be a valuable forum for discussions on the constraints associated with each national or regional collection of barley, the exchange of germplasm, the development of joint research projects, the sharing of research results and other relevant information, and the organization of scientific exchange and training activities. Status reports of conservation activities in the Member countries are regularly being presented to the Group and workplans established to address identified problems. The European Barley Database (EBDB), compiled by joint national efforts and maintained by the Genebank in Gatersleben (Germany) as input in kind, provides the regional overview of the barley genetic resources of the member countries. Besides the reports of the Working Group meetings, this database represents the interface between the Group and potential users of the germplasm, such as breeders and researchers. Once fully developed, it will allow the rapid location of germplasm which can be selected on the basis of passport and characterization data. Finally, the ECP/GR Barley Working Group has been highly proactive in the creation of the Barley Core Collection, representing a tool to facilitate and make more effective a rational conservation and use of barley genetic resources.

Today, genebanks throughout the 33 ECP/GR member countries conserve approximately 125 000 barley samples *ex situ*, excluding the nine associated which hold another 40 000 accessions. About 84% of the accessions belong to the cultivated species, *Hordeum vulgare*, whereas the closest wild relative, *H. spontaneum*, is represented by 22% of the accessions, and the remaining more than 30 wild species are represented by 2% of the accessions.

Despite the large regional differences among European countries they all share a common interest in barley genetic resources, supporting the long history and tradition of collaboration and germplasm exchange. Because of the varying quality of National Programmes in the region – both with respect to structure, mode of operation and level of development – several threats presently act upon the collections:

- general reductions in funding of agricultural research frequently affects genetic resources programmes
- a strained economic situation is further aggravated by the duplication of both efforts and germplasm
- the rapid transition of plant breeding from the public to the private sector, and thus more addressing of short-term goals, may lead to the negligence of genetic resources conservation
- restrictions on the exchange of germplasm and collaboration of breeders may result in a narrowing of the genetic base of commercial varieties and ultimately an increased vulnerability of the barley crop.

Recognizing …

-that the long-term responsibility of conserving genetic resources, and making them available to the users, is primarily a public sector responsibility;

-that a restriction of access to genetic resources conserved in genebanks throughout Europe would seriously impede the efforts of breeders;

-that the economic constraints facing national programmes call for prioritization of genebank activities and the sharing of responsibilities;

-that no single country in Europe can, on its own, conserve all barley genetic resources, and

-that ECP/GR is the platform to facilitate the implementation of the Global Plan of Action on PGRFA (TCC in Nitra, 1995; GPA in Leipzig, 1996)

the ECP/GR Barley Working Group recommends the establishment of a decentralized European Barley Collection comprising the barley accessions that European genebanks would agree to maintain on behalf of all member countries of ECP/GR. The establishment of such a collection would need to give appropriate consideration to aspects such as the scope of the collections (species coverage, type and status of accessions), thereby guiding each country to work towards identifying accessions of national origin and for becoming primary holdings for which the country would accept responsibility. Parties adherent to this agreement would need to define clearly the role of the collection-holders, the hosts of safety-duplicates, the management of the EBDB and other relevant issues.

### *Objectives*

The objectives of establishing this collection would be:

- to formalize the sharing of responsibilities for the conservation of European barley genetic resources
- to ensure the safe conservation of these accessions
- to ensure the continued access of these accessions to all ECP/GR member countries
- to make information about barley genetic resources available to the users through adequate forms of documentation (e.g. the EBDB, the European Internet Platform on crop genetic resources, published reports of Working Group meetings, etc.)
- to promote an intensive exchange of germplasm
- to enhance the use of barley genetic resources
- to reduce the workload for each country and allow a more effective conservation
- to facilitate the establishment of a multilateral system of benefit sharing mechanism
- to comply with countries' obligation under the CBD to conserve genetic resources (Article 9).

### *Scope of the European Barley Collection*

The European Barley Collection would include wild and cultivated species

- of the following taxa:
  *Hordeum brevisubulatum* subsp. *violaceum*
  *Hordeum bulbosum*
  *Hordeum marinum*
  *Hordeum murinum*
  *Hordeum secalinum*
  *Hordeum vulgare* subsp. *vulgare*
  *Hordeum vulgare* subsp. *spontaneum*

- of the following types:
  -cultivated varieties currently in use and newly developed varieties;
  -obsolete varieties;
  -primitive varieties or landraces;
  -wild populations;
  -breeding material (if well documented and at the discretion of the breeder);
  -genetic stocks.

- of the following status:
  -material for which distribution is not restricted;
  -material of indigenous origin (bred or collected);
  -material collected or obtained from other countries, if the safe conservation of or access to this material is unsure.

The inclusion in the collection of registered varieties is useful as these provide valuable traits for breeding. In many countries, however, access to this material requires prior informed consent (PIC) from breeders.

### *Workplan for the establishment of the European Barley Collection*

1. The database Manager for the EBDB would suggest a genebank as the 'primary collection (see Annex 1) for each original accession, which would be the first step of a close interaction between the database Manager, the genebank and the respective national PGR programme to determine the 'home' of the accession. In general, this would be the country in which the accession was collected or bred.
2. National commitment would be sought for long-term conservation and access to the accessions. **It is understood that this responsibility would imply a custody only, and would not be meant to have any implication of 'ownership'.**
3. National programmes would be requested to provide the database Manager a list of accessions for which the country would agree to take long-term conservation responsibility on behalf of the ECP/GR member countries. A copy of this list would be deposited with the ECP/GR Coordinator.
4. The database Manager would record the institute that holds the primary collection in the EBDB for that accession under the descriptor 'Holder of primary collection'.

### *Responsibilities*

The primary collection would:
1. Ensure that the material is maintained under medium- to long-term conservation conditions in compliance with international standards (FAO/IPGRI Genebank Standards);
2. Ensure that an appropriate safety-duplicate is deposited in a genebank, preferably within another ECP/GR member country, and that relevant information about this safety-duplication is provided to the EBDB Manager.
3. Respond in reasonable time to germplasm requests. In the case of shortage of seeds the requesting party may exceptionally be asked to assist in the multiplication of the accession. Requests which are clearly counter to the present initiative (e.g. Requests for most accessions in a collection) may be referred to the Barley Working Group for settlement.
4. Provide unrestricted access to the declared accessions to *bona fide* users from ECP/GR member countries (exemption is made for registered varieties, see above) and ensure through the use of Material Transfer Agreements that receiving parties do the same.

5. Endeavour to give high priority to the adequate characterization, evaluation and documentation of accessions which are part of the European Barley Collection.
6. In the case of an impossibility to honour the commitment for long-term conservation, inform the EBDB Manager and actively seek a new 'primary collection', willing to maintain the material.
7. If no new host genebank may be found, maintain the material under long-term conditions for at least another 2 years.

The EBDB Manager would:

1. Facilitate the repatriation of germplasm by distributing relevant information about accessions conserved in countries other than the country of origin;
2. Update the database every 1-2 years and make it available to the collection-holders;
3. Effect changes to the database when informed by the collection-holders;
4. Rapidly forward to the 'primary collection' any requests for seeds;
5. Provide the collection-holders and the working group with information about the degree of safety-duplication of the collections.

The genebank hosting safety-duplicates should:

1. Maintain a sufficient quantity of the safety-duplicated germplasm in long-term storage conditions in compliance with international standards and under a 'black box' arrangement;
2. Not distribute the germplasm;
3. Not distribute information about the germplasm;
4. Clearly designate as safety-duplicates the accessions provided for this purpose and not include them on *index seminae* / distribution lists;
5. Immediately notify the 'primary collection' in case of any problems with the safety-duplicate;
6. Not carry out viability tests;
7. Not regenerate the safety-duplicated germplasm.

The ECP/GR Barley Working Group:

1. Is composed of representatives of each member country being nominated by the respective National Coordinators and participating in the Group either as Attending or Corresponding Member. Institutions which participate as observers to ECP/GR are also invited to nominate representatives to the Working Group (eg. ASSINSEL, FAO, etc.);
2. Would have the technical oversight over the European Barley Collection. It would address issues such as quality standards and, if necessary, control their implementation;
3. Would endeavour to establish the necessary links with potential users of genetic resources through mechanisms such as core collections, evaluation networks, etc.;
4. Would, through its Chair and in collaboration with the ECP/GR Coordinator, report on an annual basis to the ECP/GR Steering Committee on the status of the European Barley Collection, the EBDB and the progress in implementing the Working Group's workplan.

## *Annex I. Towards a protocol for designating primary holders of accessions*

*(based on draft by R. Sackville-Hamilton*[31]*, member of the ECP/GR Forages Working Group, with comments by J. Weibull (JW) in italics and bracketed)*

### Principles

According to the CBD, each country owns and is responsible for the management of its own biodiversity. Following this principle, the primary holder of each collected accession should normally be a genebank in the country of origin of the accession, provided that the genebank has the facilities and capacity to meet the terms of the European Barley Collection. Notwithstanding this, and recognizing that (a) designating a genebank as primary holder of an accession only concerns curatorship and implies nothing about ownership, and (b) maintenance of genetic integrity is of paramount importance, the choice of primary holder should not be constrained by questions of ownership. **The primary holder must be able to guarantee storage and regeneration conditions that optimize maintenance of genetic integrity regardless of the origin of the accession**. As such, repatriation of a seed sample will always be recommended if it has been lost from all genebanks or collections in the country of origin, but this will not necessarily be associated with repatriation of responsibility.

A genebank will in most cases be designated primary holder of accessions it has collected but not of accessions donated to it. Exceptions include:

- it will **not** be primary holder if repatriation of seed with associated repatriation of responsibility is recommended
- it will **not** be primary holder if another genebank that collaborated in the same collecting expedition is to be sole primary holder
- it will be primary holder of seed that were donated to it with explicit or implicit transfer of responsibility for maintenance.

### Method

The EBDB Manager must first distinguish between accessions collected by a genebank and accessions donated to a genebank. This is done using a SOURCE passport descriptor.[32] An accession with no value in this field will not be assigned a primary holder.

#### Collected accessions[33]

It is assumed that all collecting expeditions conform with the CBD and the International Undertaking. In particular, all collecting expeditions include at least one participant from the country in which the expedition is undertaken, and that visiting collectors agree to repatriate samples of seed on request. A collecting expedition undertaken without collaboration may only take place in the collector's own country.

For all accessions where SOURCE = Collected by holding genebank (i.e. 1), the EBDB Manager should seek duplicated data in the COLLECTING NUMBER field.[34] The search for

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[31] Published as: Sackville Hamilton, N.R. 1998. Appendix II. Towards a protocol for designating primary holders of accessions. Pp. 162-166 *in* Report of a Working Group on Forages. Sixth meeting, 6-8 March 1997, Beitostølen, Norway (L. Maggioni, P. Marum, R. Sackville Hamilton, I. Thomas, T. Gass and E. Lipman, compilers). International Plant Genetic Resources Institute, Rome, Italy.

[32] Field values: 1 = Collected by holding genebank; 2 = Donated with transfer of responsibility; 3 = Donated without transfer of responsibility; 4 = Donated with unknown transfer of responsibility. *[JW: The Barley Working Group did not consider including this descriptor among the Multicrop Passport Descriptors; however, it should be reconsidered.]*

[33] *[JW: Perhaps of higher relevance for the Forages Working Group; however, since the Barley Working Group also has a mandate for some wild species, these and landraces are the focus for this category.]*

duplicates should be based on the parsed components of the data, i.e. separated into groups of letters and numbers with the punctuation marks (space, colon, full stop, etc.) eliminated. This improves detection of accessions with duplicate collecting number even when entered with inconsistent data formats (e.g. with or without a space, colon, full stop, etc. between collector's initials and number, with or without full stops after each initial, upper or lower case letters, etc.).[35]

In all cases, the EBDB Manager should determine whether there is a need to consider repatriation, which occurs in the following situation:

- none of the genebanks holding accessions with duplicate COLLECTING NUMBER is in the country of origin of the accession (e.g. first three letters of INSTITUTE CODE do not correspond to COUNTRY OF ORIGIN for all accessions sharing the same COLLECTING NUMBER) (**N.B.!** Include check for data validity; all accessions sharing the same COLLECTING NUMBER should also share the same COUNTRY OF ORIGIN and identical other passport data on the original collection), **and**
- the country of origin is an ECP/GR member.

In this situation, the EBDB Manager will contact the genebank in the country of origin with a view to recommending repatriation of the accession. By mutual agreement with the holding genebanks it may also be recommended that, following repatriation, the genebank in the country of origin be designated primary holder of the accession.

If repatriation of both seed and responsibility is not appropriate and duplicate collecting numbers are not found, the genebank holding the accession is designated primary holder. This will occur under the following conditions:

- the original collecting expedition was undertaken by the genebank without collaboration
- the original collecting expedition was undertaken in collaboration with at least one other organization, **but**
    - through failure to enter relevant passport data, or through errors in data entry, or through entering data in incompatible formats, or through following different standards for translation or transliteration, or through failure to provide the EBDB Manager with all relevant data, the search for duplicate collecting numbers fails to detect historically duplicate collections;
    - none of the other collaborators is a genebank participating in the ECP/GR, **or**
    - all collaborating genebanks that do participate in the ECP/GR have lost their sample of the accession from their collection.

If accessions with duplicate collecting numbers are found, the EBDB Manager must determine which, if any, are the original duplicates collected by other genebanks collaborating in a joint collecting expedition. This is the case where accessions with duplicate collecting numbers also has SOURCE = 1 (i.e. Collected by holding genebank). If there are no such collaborating genebanks, the sole genebank holding the accession with SOURCE = 1 is designated primary holder, unless repatriation is to be recommended.

If two or more genebanks do hold original samples of accessions with duplicate COLLECTION NUMBER and SOURCE = 1 (i.e. Collected by holding genebank), the EBDB Manager may provisionally recommend one of them to be designated primary holder (unless repatriation is recommended). Recommending all original collecting genebanks

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[34] *[JW: This is yet another descriptor which was not included by the Barley Working Group.]*

[35] *[JW: However, one should note that in general, estimation of similarity between seed samples based on common donor numbers or other common character strings alone can be misleading. After all, evolutionary forces are still working during storage and regeneration. Valuable information could therefore also include the number of rejuvenation cycles during storage and the rejuvenation sites. It should be emphasized that this identification work should not carried out to the extreme, unless for particular research purposes.]*

jointly as primary holders may also be considered an option. Final designation is subject to mutual agreement between the collaborators and the EBDB Manager.

Accessions that have duplicate COLLECTION NUMBERS, but SOURCE ≠ 'Collected by holding genebank', are accepted as having been derived from the original accession. The agreed primary holder of the original collection will be entered as the primary holder of all such donated accessions with duplicate COLLECTION NUMBERS.

### Donated accessions

All accessions where SOURCE ≠ 'Collected by holding genebank' are considered to have been donated. The previous section deals with donated accessions that share a duplicate COLLECTION NUMBER with original collections, and therefore have been assigned a primary holder. This section deals with donated accessions that have not been assigned to an original collection. For these accessions, the EBDB Manager must distinguish between varieties (both primitive and advanced) and other accessions.

For varieties, the EBDB Manager should conduct a simple search for historical duplicates using only the ACCESSION NAME passport data field. The search should not involve detailed inspection and correction of similar names, where differences have arisen through errors of transcription, transliteration, translation, etc. Accessions should be regarded as duplicate varieties if parsed components of the accession name are identical. For each distinct name, the EBDB Manager should inspect the origin(s) of accessions with that name. If there appears to be a single origin for accessions sharing the same name, the EBDB Manager should suggest a primary holder based on that origin. If there appears to be more than one distinct origin for accessions sharing the same name, the EBDN Manager should suggest a primary holder for each group.

- For all types of accession, the EBDB Manager must distinguish between donations made with or without associated transfer of responsibility. This is achieved by reference to the SOURCE passport descriptor described earlier.
- For accessions where SOURCE = donated with responsibility, the genebank will be the designated primary holder.
- For accessions where SOURCE = donated without responsibility, the genebank will not be designated primary holder. No attempt will be made to search for duplicates, so the accession will not be linked to any primary holder.
- For accessions where SOURCE = donated with unknown responsibility, transfer of responsibility is assumed in the following situations:
  -The donor is a breeder or other scientist, as identified by (a) a non-missing entry for the BREEDING INSTITUTE passport data field, or (b) a DONOR INSTITUTE CODE that refers to an institute that has no genebank. It is assumed that the donation was made by a breeder or other scientist specifically because the genebank provides facilities for guaranteed long-term preservation.
  -The DONOR INSTITUTE CODE refers to an institute that (a) does not participate in the ECP/GR, or (b) that no longer exists. IPGRI will provide a list of recognised current genebanks participating in the ECO/GR.
- For all accessions not meeting the above conditions, the genebank is not designated primary holder.

### Discussion and implications

The above protocol will leave many accession having no primary holder. Their historical uniqueness will remain unknown. The EBDB Manager may conduct a more elaborate search for potential historical duplicates, but this is not recommended as a priority activity.

Moreover, one should keep in mind that each sample of a wild population or primitive variety is likely to be biologically unique because of genetic changes associated with each regeneration and each donation. This applies both to accessions with no designated primary holder, and to accessions where the holder is not the primary holder. It will be particularly true for genebanks that do not follow highest possible regeneration standards. As such, **extreme caution** is urged in relation to rationalizing collections based on primary holdings. In particular, no attempt should be made to eliminated an accession from a collection on the basis that is has not been assigned a primary holder.

Rather, the identification of a primary holder should be used as a means of prioritizing characterization, evaluation, regeneration and distribution. A genebank should assign **top priority** to its accession for which it has been designated primary holder. It should assign **lowest priority** to those for which another genebank has been designated primary holder, and will normally refer requests for seed of such accessions to the primary holder unless there is a particular need for seed from its own sample. It should assign **intermediate priority** to those with unassigned primary holder. It is envisaged that the primary holder will be the normal supplier for most external users (breeders and other scientists), whilst usage of other seed samples will be restricted mainly to genebank research.

*[JW: An alternative approach to the concept of a primary holder and the transfer of conservation responsibility, as suggested by my colleagues M. Veteläinen and M. Huldén of the Forages Working Group, could be the use of a 'pointer system'. A 'pointer' would represent an institute holding the accession closest ('of most true origin') to the original seed sample. This system could perhaps be easier to accomplish since it would not involve the concept of 'transfer of responsibility', which often involves a political and economic dimension. According to the CBD it would always be the responsibility of national or regional genebanks to preserve germplasm from their own areas. This responsibility could also include repatriating material from other genebanks using a 'pointer to primary holder', which would be recommended by ECP/GR, but should not require any agreements between donors and receivers concerning responsibility transfer.]*

# Appendix III. Acronyms and abbreviations

| | |
|---|---|
| AARI | Aegean Agricultural Research Institute, Menemen, Turkey |
| ARI | Agricultural Research Institute, Nicosia, Cyprus |
| ARO | Agricultural Research Organization, Israel |
| ASSINSEL | Association internationale des sélectionneurs, Switzerland |
| BAZ | Federal Centre for Breeding Research on Cultivated Plants, Germany |
| BGRC | Braunschweig Genetic Resources Collection, Germany |
| BRG | Bureau des ressources génétiques, Paris, France |
| CCDB | Central Crop Databases |
| CGIAR | Consultative Group on International Agricultural Research |
| CGN | Centre for Genetic Resources, Wageningen, the Netherlands |
| CTPS | Comité technique permanent de la sélection des plantes cultivées, Ministère de l'Agriculture, France |
| CIMMYT | Centro Internacional de Mejoramiento de Maiz y Trigo, Mexico |
| EBDB | European Barley Database |
| ECP/GR | European Cooperative Programme for Crop Genetic Resources Networks |
| EU | European Union |
| FAL | Federal Agricultural Research Centre Braunschweig-Völkenrode, Germany |
| GEVES | Groupe d'étude et de contrôle des variétés et des semences, France |
| GNIS | Groupement national interprofessionnel des semences, graines et plants (Seed producers union), France |
| GPA | Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture |
| ICARDA | International Center for Agricultural Research in the Dry Areas, Aleppo, Syria |
| ICCPT | Research Institute for Cereal and Industrial crops, Fundulea, Romania |
| IfE/R | Institute for Epidemiology and Resistance of the BAZ, Aschersleben, Germany |
| INCO | Cooperation with third countries and international organizations (EU programme) |
| INRA | Institut National de la Recherche Agronomique, France |
| INTAS | International association for the promotion of cooperation with scientists from the independent states of the former Soviet Union, Brussels, Belgium |
| IPK | Institut für Pflanzengenetik und Kulturpflanzenforschung, Gatersleben, Germany |
| NGB | Nordic Gene Bank |
| ONIC | Office national interprofessionnel des céréales, France |
| QTL | quantitative traits loci |
| RIPP | Research Institute of Plant Production, Piešťany, Slovakia |
| SINGER | System-wide Information Network for Genetic Resources (CGIAR) |
| SPSS | Syndicat des producteurs de semences sélectionnées, France |
| VIR | N.I. Vavilov Research Institute of Plant Industry, St. Petersburg, Russia |
| WWW | Word Wide Web |
| ZADI/IGR | Zentralsstelle für Agrardokumentation und -information /Informationszenttrum für Genetische Ressourcen (Centre for Agricultural Documentation and Information/Information Centre for Genetic Resources), Bonn, Germany |

# Appendix IV. List of participants

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