

Enhancing The Practical Value Of Barley Genetic Resources In Europe Through Evaluation And Documentation

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Introduction

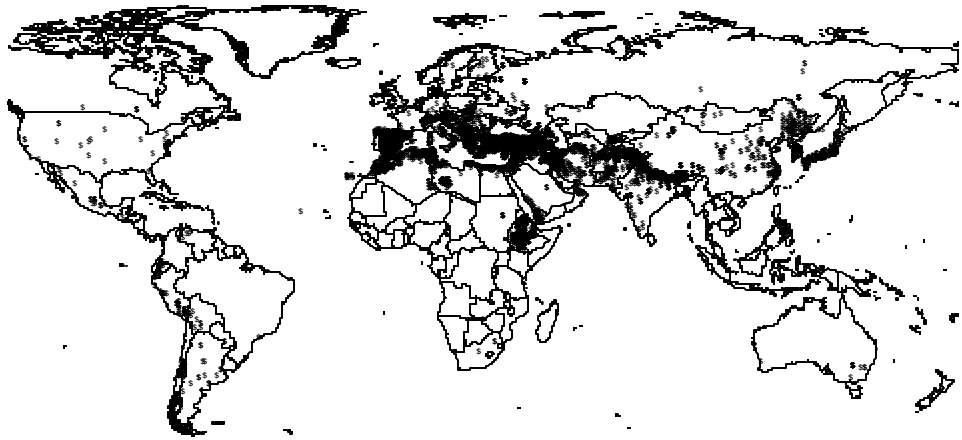
Documentation of collections holding barley genetic resources in Europe, and the standardised evaluation of germplasm for resistance against biotic and abiotic stress factors were the objectives of the recently completed EU-funded GENRES 104 project on barley (<http://barley.ipk-gatersleben.de>).

Comprehensive information about traits, or targeted evaluations, are a prerequisite for utilisation of genetic resources by breeders to achieve specific goals. Due to the large size of European and global genebank collections, representative subsets sampled from the genepool are desirable, covering the variability for traits of interest to allow rapid and efficient evaluations. The Barley Core Collection (BCC, Knüpfper & Hintum 2003) attempts to represent the genetic diversity in the barley gene pool, with up to 2000 genetically well defined accessions for genetic, characterisation, and evaluation studies. The entire East Asian, American, European, and part of the West Asian/North African BCC subsets were screened for resistance against fungal and viral diseases of economic importance in the European context, supplemented by additional genebank material to utilise the additional screening capacities provided by project partners. The aim of this study is to provide an overview of the available genetic diversity for disease resistance and to pinpoint particular parts of the genepool for further detailed evaluation.

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The European Barley Database

The EBDB is an inventory of barley germplasm held in 42 collections and the BCC (1,363 accessions), totalling 188,815 accessions. Four collections from outside of Europe, namely those of the International Center for Research in the Dry Areas (ICARDA), the Australian Winter Cereals Collection, Tamworth, the National Small Grains Collection, Aberdeen, USA, and Okayama University, Japan, are also included. Exclusion of reference standards, dead accessions, and



US accessions still leaves 161,072 inventoried samples. For passport data, emphasis was placed on improvement of geo-referencing (34,218 accessions=18%, Fig. 1; with substantial contributions by Jan Konopka, ICARDA), standardisation of accession names, compilation of synonymous accession numbers and their subsequent use for the linking and knitting together of related information. The compiled data can now be verified with molecular tools. The use of unambiguous accession identifiers is important for linking to reference collections and genebanks. A graphical information system for presentation of the results and navigation of the database was developed with assistance of Morten Huldén and Dag Terje Endresen (Nordic Gene Bank). Initially, biotic stress data from the GENRES barley project were integrated into the system (<http://barley.ipk-gatersleben.de/genres/>) The data structures developed in accordance with the IPGRI descriptor list for barley, allow the addition of further characterisation and evaluation data sets. Informed sampling of the barley gene pool is now possible. The database is ready to be merged with the remainder of public data sets to create a global inventory for barley.

Evaluation of barley germplasm against biotic stresses with standardised methods

The methodology (http://barley.ipk-gatersleben.de/EU_methods.htm) for field observations of fungal diseases is based on multiple assessments of the percentage of infected leaf area during the course of infection. Discrete observations and time intervals between them were then used to calculate a disease progression curve, from which an average ordinate (AO) is estimated. Finally, an average score is calculated (logarithmic intervals, 1=0% infection, 9=100% infection). This scoring system helps to detect genotypes with effective combinations of minor resistance genes, the so-called horizontal or quantitative resistance. The number of genotypes evaluated by individual project partners varied from 60 to 400. In the first season, the available accessions were evaluated in at least three different sites for each disease. The most promising material was re-tested during the following season. The large screening capacities available at some sites allowed a rapid pre-screening for several diseases. Due to lack of natural infection pressure, not all the planned evaluation activities could be carried out. Standard susceptible and resistant test varieties were used for a comparison between results from different sites and years. Virulence (differential) standards with differing resistance genes allow an assessment of the effectiveness of individual genes at individual experimental locations. They are being used to monitor virulences for leaf rust, powdery mildew, net blotch and scald in continuation of the COST 817 action. For future evaluation work a close co-ordination with this ongoing initiative is highly recommended.

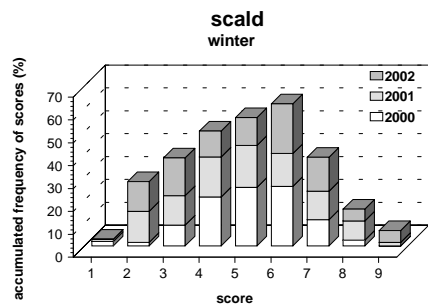
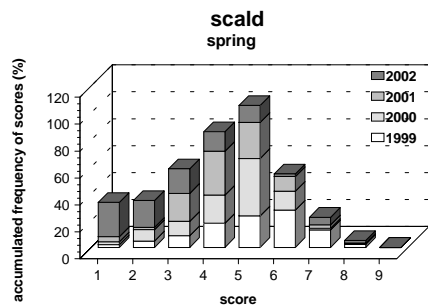
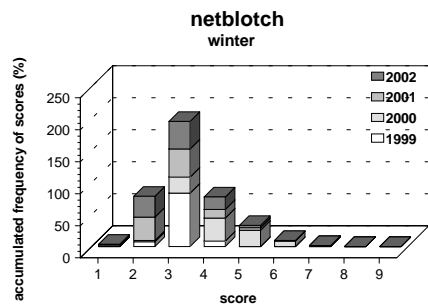
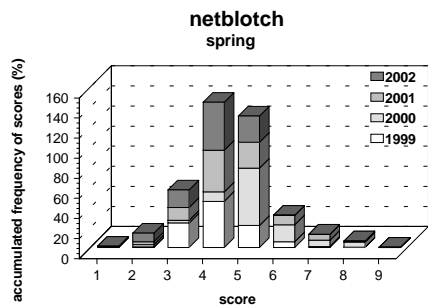
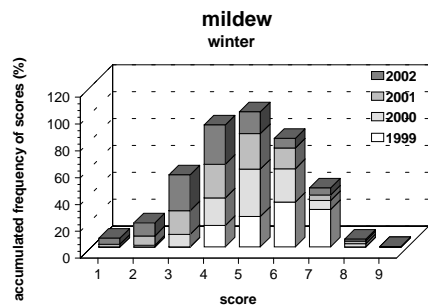
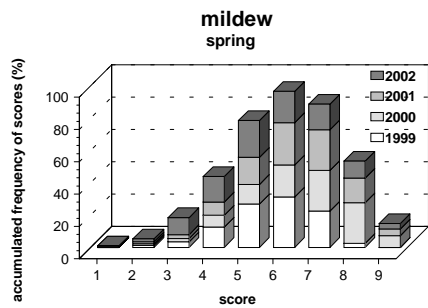
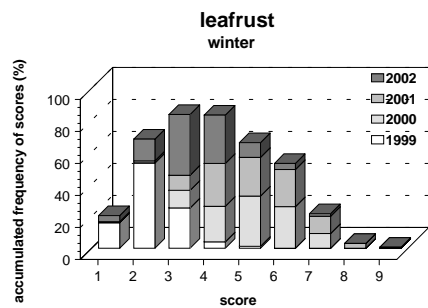
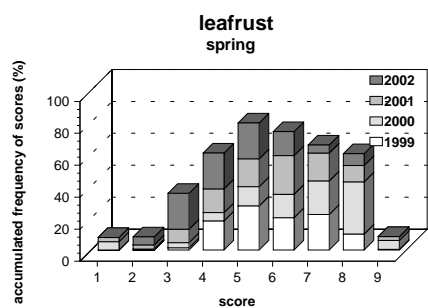
Results

The frequencies of resistance reactions against individual diseases (powdery mildew, leaf rust, scald, net blotch) show a close to normal distribution for both winter and spring barleys (Figs. 2 - 9), suggesting that the material tested was a representative sample of the available diversity. A number of accessions with relatively good average scores (AO's) was found, particularly for powdery mildew. Statistical analysis of the complete field data set without exclusion of low infection sites, using locations as replicates and years as factors, shows no significant differences to the resistant standard, but several accessions, which are on average better than the susceptible standard. In addition, there are numerous accessions with average values within the range of those with statistical significance. A geographical analysis of accession origin and

evaluation results from both field and glasshouse was presented at the meeting. High frequencies for powdery mildew and leaf rust resistances from *H. vulgare* ssp. *spontaneum* were shown in the Levant. Geospatial analysis of germplasm characteristics is a promising tool.

References

Knüpffer, H., and Th.J.L. van Hintum, 2003. Summarised diversity – the Barley Core Collection. In: R. von Bothmer, Th.J.L. van Hintum, H. Knüpffer and K. Sato (eds), *Diversity in Barley (Hordeum vulgare)*, pp. 259-267. Elsevier Science B.V., Amsterdam, The Netherlands.



Figs 2 to 9 frequency of scores in barley for the evaluated fungal diseases