

DOCUMENTATION AND EVALUATION OF BARLEY GENETIC RESOURCES IN EUROPE

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Thirty-five European Institutions participate in the EU-funded GENRES CT-98-104 project and its ECP/GR-funded complementary Non-EU module (see <http://barley.ipk-gatersleben.de>). Documentation of collections holding barley genetic resources in Europe, and the standardised evaluation of *Hordeum* spp. germplasm for resistance against biotic and abiotic stress factors are the objectives of this initiative. The International Barley Core Collection (BCC) is the major focus of the screening for stress resistance. Resistances against *Pyrenophora teres* and *Rhynchosporium secalis* and the virus diseases (BaYMV complex, BYDV) have been observed in accessions of the BCC. Resistance to *Erysiphe graminis* and *Puccinia hordei* is limited in the *H. vulgare* germplasm of the BCC and mainly restricted to well characterised cultivars. It appears that the BCC subset from ICARDA (incl. *H. vulgare* ssp. *spontaneum*) includes promising germplasm for resistance against leaf rust and powdery mildew. Observations made during pre-screening are being verified by multi-location testing. The European Barley Database is evolving into an information system providing geo-referenced passport, characterisation and evaluation data.

1. INTRODUCTION

The EU GENRES CT-98-104 project [1] is concerned with improved access to, and utilisation of, barley germplasm in Europe. The three year project began in 1999 with 28 partners (Breeders, Genebanks, Public Research Institutions).

In 2001 an additional 7 partners from non-EU countries, including several EU candidates, joined the project in its final phase (Fig. 1).

Our activities are focussed on two areas:

- Development of an information system for European barley collections comprising passport, characterisation and evaluation data.
- Evaluation of barley germplasm for resistance against biotic and abiotic stresses

2. THE EUROPEAN BARLEY DATABASE

The basis for the information system is an updated version of the European barley database (EBDB)[2, 3]. This is being developed as a backbone to link with information related to individual accessions.

The database is an inventory for barley germplasm held in 35 genebanks and for the barley core collection (BCC, 1126 accessions), totalling 137445 accessions. Two collections from outside of Europe, those of the International Center for Research in the Dry Areas, ICARDA and the Australian Winter Cereals Collection, Tamworth are also included.

For the passport data emphasis is being placed on improvement of geo-referencing (Fig. 2), standardisation of accession names according to published cultivar inventories [4, 5, 6] and compilation of synonymous accession numbers.

Accession numbers are stored in a maximum of three columns, separating prefix, numerical part and, if present, suffix. This format allows flexibility in linking with data files containing characterisation and evaluation information from individual collections and thus provides the primary key to related information about an accession.

3. EVALUATION OF THE BARLEY CORE COLLECTION FOR RESISTANCE AGAINST AND TOLERANCE TO BIOTIC STRESSES

The BCC has been conceived as a representative sample of the genetic diversity in the barley gene pool to provide a manageable set of genetically well defined accessions (maximum 2000 entries) for genetic, characterisation, and evaluation studies.

Screening for resistance against, in the European context, economically important fungal and viral diseases was carried on its complete East Asian, American, European, and partial South-West Asian subsets.

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 gene pool for further detailed evaluation.

For the years 1999, 2001 and 2000, 23899 observations were provided by partners of project GENRES CT98-104, funded by the European Union. These data were collected during three spring and two winter seasons. 22571 observations on BCC material were used as the basis for a first analysis. Two further seasons observations (winter 2000 and spring 2001) have been carried out but were not completely included in the present analysis.

Enneking, D.; Schliephake, E., and Knüpffer, H. (2002) Documentation and evaluation of barley genetic resources in Europe. Hernández, P.; Moreno, M. T.; Cubero, J. I., and Martin, A. Triticeae IV. Proceedings of the 4th International Triticeae Symposium; Cordoba, Spain. Cordoba: Junta de Andalucía. Consejera de Agricultura y Pesca; 183-186.

Fig 1. Distribution of Evaluation sites and Partner Institutes of the EU barley project in 2001

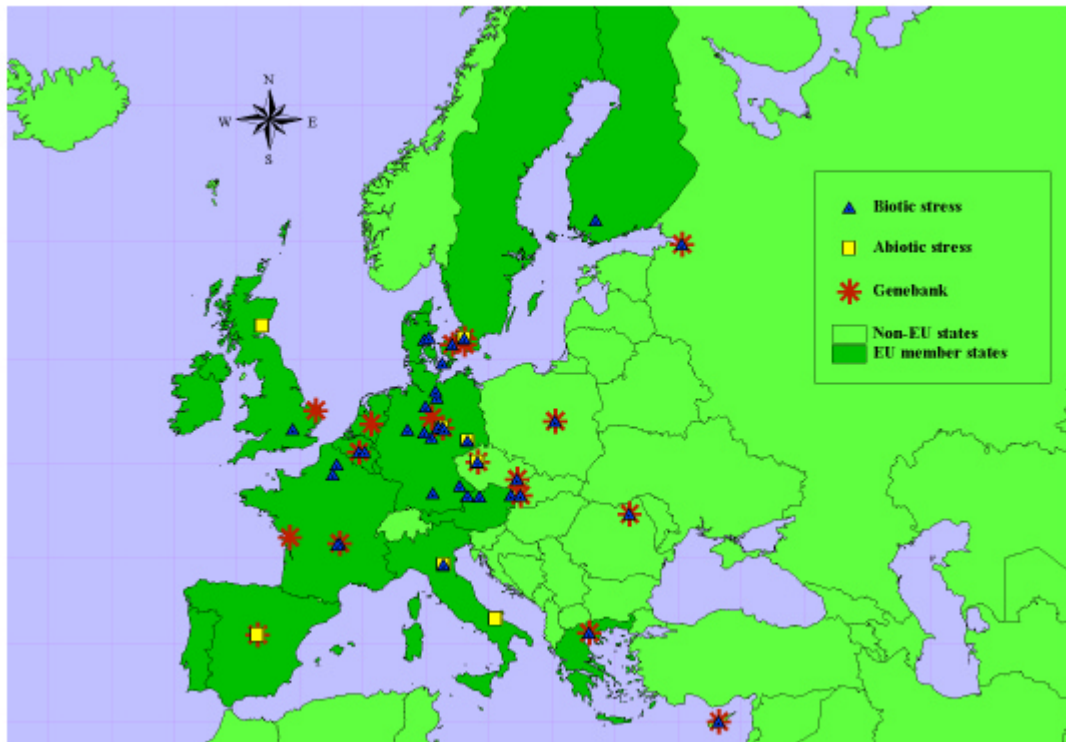
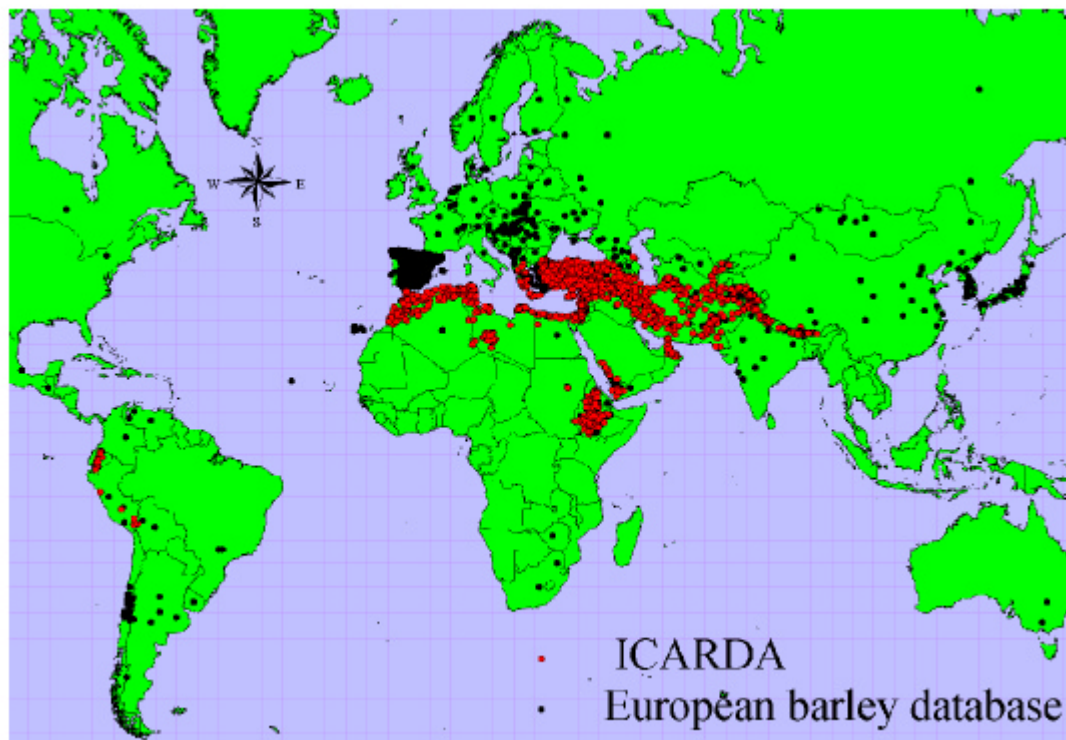


Fig 2. Geo-referenced accessions in the European barley database



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3.1 Methods

The methodology [7] used for field observations of fungal diseases is based on multiple assessments of the percentage of infected leaf area during the course of infection. The discrete observations and time intervals between them are then used to calculate a disease progression curve, from which an average ordinate is derived. Finally an average score is calculated (logarithmic intervals 1=0% infection, 9=100% infection)

With this scoring system it is possible to detect genotypes with effective combinations of minor resistance genes, the so called horizontal or quantitative resistance. This type of resistance is considered more durable in the long term. The potential utility of such genetically broadly based resistance provides the stimulus to carry out the more labour intensive multiple scoring method.

The number of genotypes evaluated by individual partners varied from 60 to 400. In the first season the available accessions were distributed so that each would be evaluated at at least three different sites for each disease. The most promising material was provided to each experimenter during the second season. With capacities available to screen 300 to 400 accessions at some sites for several diseases, rapid pre-screening was possible.

Not all the planned activities regarding evaluation for particular resistances could be carried out. This is due to lack of natural infection pressure by some diseases as influenced by climatic conditions.

3.2 Fungal diseases

Differences between spring and winter barley, with higher frequency of susceptible scores for spring types, appear to relate more to increased infection pressure than to lower resistance levels.

Table 1. Frequency of infection scores in BCC winter barley accessions

Score	BaMMV	BYDV	leafrust	mildew	netblotch	scald	BaMMV +	BaYMV_1 +	BaMMV +	BaYMV_1+ BaYMV_2
1	61	0	0	0	2	25	57	82		
2	0	1	2	0	107	7	11	13		
3	12	1	31	54	136	44	12	3		
4	0	7	84	158	64	90	26	9		
5	0	62	111	114	6	124	13	19		
6	0	98	88	40	0	116	7	4		
7	0	80	8	8	0	40	19	51		
8	0	41	0	2	1	20	10	7		
9	27	9	0	0	0	5	32	111		
Σ	100	299	324	376	316	471	187	299		

Table 2. Frequency of infection scores in BCC spring barley accessions

Score	leafrust	mildew	netblotch	ramularia	scald
1	7	6	0	6	1
2	10	13	6	14	4
3	14	18	361	17	36
4	37	64	456	13	270
5	91	209	64	3	216
6	178	218	8	4	148
7	210	225	1	1	60
8	205	127	0	0	16
9	19	29	0	0	0
Σ	771	909	896	58	751

Tables 1 and 2 show the distribution of scores from evaluations of winter and spring barleys, respectively.

Resistances against *Pyrenophora teres* (netblotch) and *Rhynchosporium secalis* (scald) and the virus diseases (BaYMV complex, BYDV) have been observed in accessions of the BCC. Resistance to *Blumeria graminis* (mildew) and *Puccinia hordei* (leafrust) is limited in the *H. vulgare* germplasm of the BCC and mainly restricted to well characterised cultivars. It appears that the BCC subset from ICARDA (incl. *H. vulgare* ssp. *spontaneum*) includes promising germplasm for resistance against leaf rust and powdery mildew.

3.3 Viral diseases

Some genotypes with tolerance against BYDV were identified. No completely resistant forms were found so far.

A different picture has emerged for soil borne viruses belonging to the BaMMV - BaYMV complex. A high portion of genotypes with qualitative resistance could be identified, amongst these several with combined resistance against BaMMV, BaYMV type 1 and BaYMV type 2.

These accessions are now being assessed for the presence of known resistance genes using established molecular markers.

Detailed results, including accession numbers are to be published following 12 months after completion of the project.

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