

Not Drowning But Waving - Surfing The European Barley Gene Pool

Dirk Enneking

Genebank, Institute for Plant Genetics and Cultivated Plants Research (IPK), Corrensstrasse 3, D-06466 Gatersleben, Germany, enneking@ipk-gatersleben.de

Twenty-eight partners from 12 European countries (AUT(1), BEL(1), DEU(9), DNK(4), ESP(1), FIN(1), FRA(2), GBR(2), GRC(1), ITA(2), NLD(1), SWE(3)) are joining their efforts and expertise to improve the utilisation of barley genetic resources in Europe (<http://barley.ipk-gatersleben.de>). Co-ordinated and standardised multiple site evaluation for resistance against biotic and abiotic stress factors is the main feature of the project, with emphasis on the international Barley Core Collection (BCC) (Knüpfper and Hintum 1995). Diffusion of the results is coupled to the development of an information system for barley genetic resources in Europe. IPK is responsible for project co-ordination and documentation. The latter is subject of this contribution.

The European Barley Database (EBDB) was developed by Knüpfper *et al.* since 1983 (Knüpfper 1988, Knüpfper and López 1999). At present it documents ca. 90.000 accessions in 29 European gene banks, representing a quarter of the global *ex situ* gene pool. It is now being extended through inclusion of evaluation data and links to off-shore information.

Current developments: Data contributed to EBDB are being converted to uniform codes (e.g. IPGRI Multi-crop descriptors, IPGRI/FAO Institute codes, barley descriptors) and standardised with regard to botanical nomenclature. This transformation is being communicated back to data donors; interfacing native codes with standardised format, thus providing conversion tables for future updates and dynamic linking. Linking with databases outside Europe was advocated by Knüpfper and López (1999) to aid identification of unique germplasm and to reduce redundancy between collections. Half of the global *ex situ* barley gene pool, estimated at 373.000 accessions (Hintum and Menting, in press) is kept in 17 collections (WIEWS and EBDB data; IPGRI IINSTCODE (total number of accessions >5000); **EBDB contributors** in bold type script): AUS003 (6000); BGR001 (5120); BRA003 (18210); CAN002 (5455); CAN004 (39347); CHN001 (14268); **DEU001** (7467); **DEU146** (12360); ETH001 (12648); GBR011 (*H. spontaneum*, 14648); **ISR003** (6652, *H. spontaneum*); JPN003 (6236); JPN108 (5130); **RUS001** (19437) SYR002 (25370); UKR044 (8000); USA029 (24847).

Links from EBDB to USA029 and SYR002 have been generated using donor and synonymous IDs. Such lists of corresponding synonyms are the boot- or **octopus straps (sticky tails** if you are a molecular biologist) to knit together a global information system. This idea is further discussed for selected collections.

RUS001 (VIR, St. Petersburg) collection: Integrated into EBDB, information on collection sites and expeditions, donors and donor ID numbers is lacking, since not yet computerised. Translation, extracting or reviewing published and internal barley evaluation reports from VIR, coupled with consultation of archived documents, is considered most cost-effective to access these data, since raw data is currently hidden in field books and introduction journals.

DEU001 (BAZ Genebank, Braunschweig) & DEU146 (IPK Genebank, Gatersleben): Both are integral part of EBDB. Characterisation and evaluation data since 1948 are available and partly searchable (<http://www.dainet.de/genres/eva/>). Numerous gene banks have received Gatersleben HOR accessions. Linkage through HOR numbers thus provides added value and has been generated.

USA029 (USDA): Major off-shore donor. USDA accessions are present in virtually every genebank. A list of 5458 unique USDA accession IDs has been generated matching a total of 6387 lines documented in EBDB. This allows access to the exhaustive passport, characterisation and evaluation data in GRIN that is readily available through a WWW interface and in the pcGRIN barley packages.

SYR002 (ICARDA): The data of 1995 include 2993 HOR and 16108 USDA accessions. The corresponding IG numbers provide a link to evaluation information generated in the ICARDA network.

The International Crop Information System (ICIS, CIMMYT, CGIAR centres) developed the concept of global identifier (GID) to tag unique accessions. Version 1.0 features the incipient International Barley Information System (IBIS) (S. Grando, ICARDA). The feature to handle up to 30 pedigree generations is of particular interest to breeders. IBIS comprises 28773 unique accessions (assigned GIDs). Interfacing these GIDs with accession IDs of individual collections, and assignment of GIDs to other unique accessions is needed.

To aid further global data integration, the creation of an online register for cultivars with information on pedigrees, breeder and principal attribute, and standardisation of collection site information would be desirable. Existing compilations of barley cultivars (ie. Arias *et al.* 1983, Baum *et al.* 1985, Baumer and Cais 2000) provide detailed information that is presently being integrated in EBDB.

Tracking of the most original ID numbers (through feedback loops amongst databases and curators), standardisation of accession names (via reference to a cultivar register), assignment of GIDs and integration into IBIS, will pave the way towards a truly global inventory for barley genetic resources. More generally, the above concepts are also applicable to the linking between complete PGR collections, and to the compilation of a global system for the documentation of plant genetic resources.

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