

IT BACKGROUND OF THE MEDIUM-TERM STORAGE OF MARTONVÁSÁR CEREAL GENE BANK RESOURCES IN PHYTOTRON COLD ROOMS

C. KUTI, L. LÁNG, M. MEGYERI, J. BÁNYAI and Z. BEDŐ

AGRICULTURAL INSTITUTE, CENTRE FOR AGRICULTURAL RESEARCH,
HUNGARIAN ACADEMY OF SCIENCES, MARTONVÁSÁR, HUNGARY

Received: ; accepted:

Genebanks are storage facilities designed to maintain the plant genetic resources of crop varieties (and their wild relatives) and to ensure that they are made available and distributed for use by plant breeders, researchers and farmers. The Martonvásár Cereal Genebank (MV-CGB) collection evolved from the working collections of local breeders and consists predominantly of local and regional materials. Established in 1992 by the Agricultural Research Institute of the Hungarian Academy of Sciences (Bedő, 2009), MV-CGB with its over 10,000 accessions of the major species (*Triticum*, *Aegilops*, *Agropyron*, *Elymus*, *Thinopyrum*, *Pseudoroegneria*, *Secale*, *Hordeum*, *Avena*, *Zea mays*), became one of the approx. 80 cereal germplasm collections that exist globally. In Martonvásár breeding is underway on a number of cereal species, and large numbers of genotypes are tested each year in the field and under laboratory conditions. The increasing size of the research programmes assisted by a modern genebank background involve an enormous increase in the quantity of data that must be handled during research activities such as traditional breeding, pre-breeding and organic breeding. A computerized system is of primary importance to synchronize breeding and genebank activities, to monitor the quality and quantity of seed accessions in cold storage, to assist the registration of samples, and to facilitate characterization, regeneration and germplasm distribution.

Key words: agroinformatics, genebank database, breeding software, barcodes

Introduction

An up-to-date (wheat) breeding information system (core system) has been developed and implemented at Martonvásár for the management of large-scale wheat breeding and field research programmes and for the synthesis of the information essential for decision-making (Láng et al., 2001). This system, which has been constantly improved, can be used for keeping records of breeding stock, for planning field and laboratory experiments, for plant performance evaluation, for automated data collection, for the rapid evaluation

of the results and also for the effective management of pedigree, seed exchange and molecular data.

The information systems used by genebanks are becoming increasingly important tools (Crop Gene Bank, 2013) for researchers and breeders seeking data on the distribution of crops and their wild relatives. To accommodate the increasing demand for the storage of the local cereal genebank data (McLaren et al., 2001) and make their practical use possible in management operations, informatics tools (data structure and software) have been developed (Burt and Kinnucan, 1990) as part of the existing Martonvásár wheat breeding information system (Kuti et al., 2008). The aim was to adapt the genebank subsystem to the complex plant breeding data management and experiment evaluation system currently running.

In designing the Martonvásár cereal genebank data model (Herdon, 2009) it was found necessary to estimate the amount and type of present information requirements, to identify future needs and the demand for new functionalities, and to find ways of synchronizing and integrating the genebank data structure and its functionalities with the existing centralized core system data management environment. The genebank database was designed (Hernandez, 2003) with the assumption that the genebank applications will provide access to the corresponding data entities of the existing core system data structure. Important genebank operations and procedures will deploy existing (genealogy, seed shipment, molecular) databases, in order to make full use of the existing services, such as trial and field management, barcode and label generation, data recording system for field and laboratory information, including morphological descriptions, disease evaluation, quality data and agronomic traits.

Materials and methods

The application package of both the core breeding system and the genebank module were developed using the Microsoft® Visual Basic Integrated Development Environment (Aitken, 1999). The applications can be run using various versions of the Windows operational system: Windows® XP®/7®.

The computers involved in the system include standard office equipment and data collectors with the minimum configuration required for Windows XP/7. Requests from the workstations are processed by a central database server (IBM eSeries 200); the combined size of the databases (accumulated since 1984) is approximately 1 GB. Data identification takes place using the barcode technology. This requires barcode readers (BCH5X49 / Motorola-Symbol LS2208), thermo-printers (TTX350 / Avery AP 4.4) and conventional laser printers for printing self-adhesive labels.

Results and discussion

Right from the beginning, the main feature of the Martonvásár cereal genebank data management system was the ability to share functionality with the relevant services of the existing breeding core system. This means using the

same genealogical database (Kuti et al., 2006), the same partner list for seed source and seed dispatch, the same data structure for recording characterization information and some of the passport information. New functions have been designed, however, to integrate and synthesize information related to certain genebank operations (Regeneration, Characterization) with the existing core system operations. Special functions for tracking dispatched material, maintaining accurate inventories, checking quantity and year of regeneration have been developed and added to both systems (core / genebank).

The genebank data structure, which houses relevant information about over 10,000 accessions, only includes data elements that have not already been defined in the implemented core system: accession ID, donor's details, ancestral pedigree, cross data, selection history data, date of regenerations, weight or estimated number of seeds, position of the sample in the storage facility, accessibility (free/limited/not accessible), etc. All genebank operations are assisted either by the specific genebank module or by the appropriate modules and functions of the implemented core system application package.

Registration

Samples newly entering the genebank have basically two origins: a) from the Martonvásár (wheat) breeding programme, b) from foreign donor resources. In both cases the first step is registration. Using the [*selection function*] of the core system (Fig. 1, v), it is possible to transfer genotypes directly from the core system to the genebank (Fig. 1, ii). The benefit of using integrated genebank data management lies in that it allows the automatic delivery of passport information on the genotypes (donor's details, data and location of regenerations, botanical status, genealogical information) (Fig. 1, i) from the core system to the genebank. In the second case the procedure is similar, but with the difference that information on the incoming seed must first be stored in the core system (Fig. 1, iii, iv), in order for it to be transferred subsequently to the genebank, using the core system's built-in [*seed exchange*] management function.

Regeneration

The genebank data management system can be searched by the genebank operators. Along with the selection of candidates for the breeding programmes (classical, pre-breeding, organic) using the [*select from genebank*] function menu (Fig. 2, i), limit criteria for quantity and regeneration year can be used to create (sql) queries and execute them against the genebank database to define target groups for germplasm regeneration. This makes it possible to ensure that a sufficient quantity of material (seed number) is maintained in the cold rooms, and that the minimum germination (viability) rate is preserved for the accessions. Selected germplasm is automatically included (Fig. 2, ii) in specific, single replication field trials, with the advantage that the trial design and analysis methods can be accessed, together with the field management practices of the core system: *field book, sowing list, Bar-coding, labelling*.

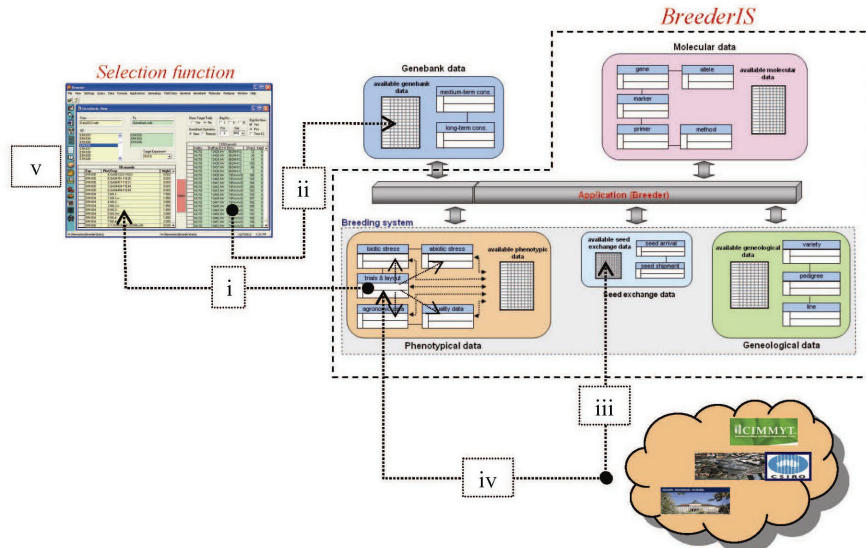


Fig. 1. Registration of accessions in the Martonvásár Cereal Genebank

Characterization

The characterization of the germplasm is essential to provide information on the traits of the accessions, thus enabling valuable germplasm to be retrieved for future plant breeding programmes. The recording and compilation of data on the most important characteristics is facilitated by direct access to the central database, which permits the core data structure (Fig. 2, iv) to serve as a repository for data from agronomical and morphological observations and laboratory analysis. The description of the plant germplasm can be supplemented later with the results of the molecular characterization of the most important genomes (Fig. 2, v), thus assuring the successful utilization of the germplasm collection for breeding, pre-breeding and organic breeding purposes.

Distribution

The genebank system also manages germplasm orders, shipment-related information and information on genebank partners. Accessions with free or limited accessibility can be distributed from MV-CGB (Fig. 2, iii) to germplasm users using the [seed exchange] module of the core system. Apart from creating automatic lists (in-house, recipient), label editing and label printing, another important characteristic of the genebank system is the ability to track dispatched material, which greatly contributes to keeping an accurate inventory. Once the destination of the germplasm is selected, the system will automatically display a detailed list of previous seed deliveries to the selected partner.

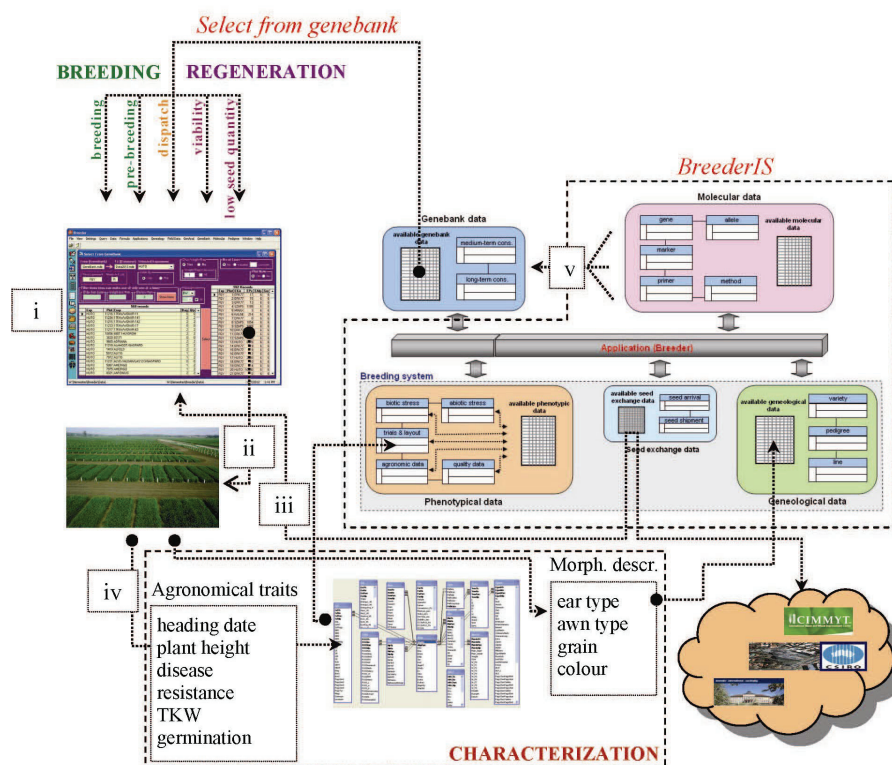


Fig. 2. Regeneration, characterization and distribution in the Martonvásár Cereal Genebank

Barcoding

Barcoding is a useful tool that can reduce errors and facilitate computerized management and control. The barcoding of individual packets/containers facilitates genebank management and limits human error. Built-in barcoding is widely utilized throughout the whole genebank management work. Different label types (self-adhesive/plastic) are used for different purposes (laboratory/field); various label formats can be created and used to produce diverse label layouts. The information content of the labels (accession number, accession name, weight, registration year, etc.) is directly transferred from the corporate database.

The synchronization between the two systems (core/genebank) permits the genebank data to be kept up-to-date. In this way it is possible for the [crossing] application to automatically determine whether or not the parents are to be found in the genebank when new crosses are created from the source germplasm. If they are not, the system issues a warning message, and offers the possibility for the item in question to be selected into the genebank. A similar thing happens when sharing breeding and genetic resources with partners and when seed

samples of breeding lines are sent to designated receiving stations. The [seed exchange] application notifies the sender if an attempt is made to send germplasm which is not duplicated in the base collection.

Summary

An up-to-date information system (Breeder Core System) has been developed and implemented at Martonvásár for the management of large-scale wheat breeding and field research programmes and for the synthesis of the information essential for decision-making. In designing the Martonvásár genebank data model an estimate was made of current and future information requirements and a preliminary analysis was made of the possibilities for synchronizing and integrating its functionalities with the existing core system applications. The specific database for genebank activities was constructed with the assumption that genebank applications will provide access to the corresponding data entities of the existent core system data structure. Thus, important genebank operations and procedures will make full use of the existing genealogy, seed shipment and molecular data structure and will deploy existing services: trial and field management, barcoding, data recording systems for quality and agronomic trait data, for morphological description data and for disease evaluation data.

Acknowledgements

The present work was financed from NKTH grants (TECH-08-A3/2-2008-0397 – CONFU_08 and OM00363 – ALKOBEEER).

References

- Aitken, P. G. (1999): *Programozás Visual Basic 6 nyelven*. (Visual Basic 6 Programming Blue Book). Coriolis Kiadó, Budapest.
- Bedő, Z. (2009): Tudományos műhelyek: Az MTA Mezőgazdasági Kutatóintézete. (Scientific workshops. Agricultural Research Institute of the Hungarian Academy of Sciences.) *Növénytermelés*, **58**, 185–190.
- Burt, P., Kinnucan, M. (1990): Models and Modeling Techniques for Information-Systems. *Review of Information Science and Technology*, **25**, 175–208.
- Crop Gene Bank (2013): http://croptgenebank.sgrp.cgiar.org/index.php?option=com_content&view=article&id=16&Itemid=37&lang=english, valid on January 25th 2013
- Herdon, M. (2009): *Informatika agrárgazdasági alkalmazásokkal*. (IT for use in agricultural economics.) Szaktudás Kiadó Ház. Budapest, pp. 217–252.
- Hernandez, J. M. (2003): *Database Design for Mere Mortals*. Addison Wesley Professional, Indianapolis.
- Kuti, C., Láng, L., Bedő, Z. (2006): Pedigree records in plant breeding: from independent data to interdependent data structures. *Cereal Res. Commun.*, **34**, 911–918.
- Kuti, C., Láng, L., Bedő, Z. (2008): Informatical background of field experiments. *Cereal Res. Commun.*, **36**, 171–174.

- Láng, L., Kuti, C., Bedő, Z. (2001): Computerised data management system for cereal breeding. *Euphytica*, **119**, 235–240.
- McLaren, C. G., Portugal, A., Lieshout, J. G. F. (2001): Design of the data management system (DMS). *International Crop Information System. Technical Development Manual*. http://www.icis.cgiar.org/icis/index.php/TDM_Data_Management_System_5.5, valid on January 25th 2013.

Corresponding author: C. Kuti
Phone: +36-22-569560
Fax: +36-22-460213
E-mail: kuti.csaba@agrar.mta.hu