

Databases for managing genetic resources collections and mapping populations of forage and related species

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Introduction Effective management of plant material used in crop improvement and underpinning research is greatly facilitated by a properly designed data structure accessible by all those working with the material. At IGER we have developed the Aberystwyth Genetic Resources Information System, AGRIS, for managing genetic resources acquired through collecting trips, seed exchange, breeding and transgenic programmes. Recently this has been complemented by MaPIS, a Mapping Populations Information System, which links with AGRIS and allows for storage and documentation of information about plant mapping populations, including pedigrees, status and physical locations of accessions and individual genotypes. IGER also maintains the European Central Crop Databases for *Lolium* species and *Trifolium repens*, and the UK National Inventory of all plant genetic resources conserved *ex situ* in the UK; by November 2004, the UKNI had contributed over 220000 accessions to the 900000 in the Europe-wide database EURISCO.

Methodology and databases AGRIS and MaPIS are currently based on the Microsoft Access relational database management system, with user-friendly forms and reports for easy and accurate data input and generation of plant labels, data summaries etc.(Figure 1) Data in AGRIS use an extended version of the FAO / International Plant Genetic Resources Institute's Multi-crop Passport Descriptors (Maggioni *et al.*, 1998). The UKNI and the *Lolium* and *T. repens* databases (<http://www.igergru.bbsrc.ac.uk/Welcome/ECCDB/eccdb.htm>) also currently use Access. However we propose to migrate all our existing Access databases to Microsoft SQL server in order to accommodate the rising level of usage and increasing data volumes now being experienced.

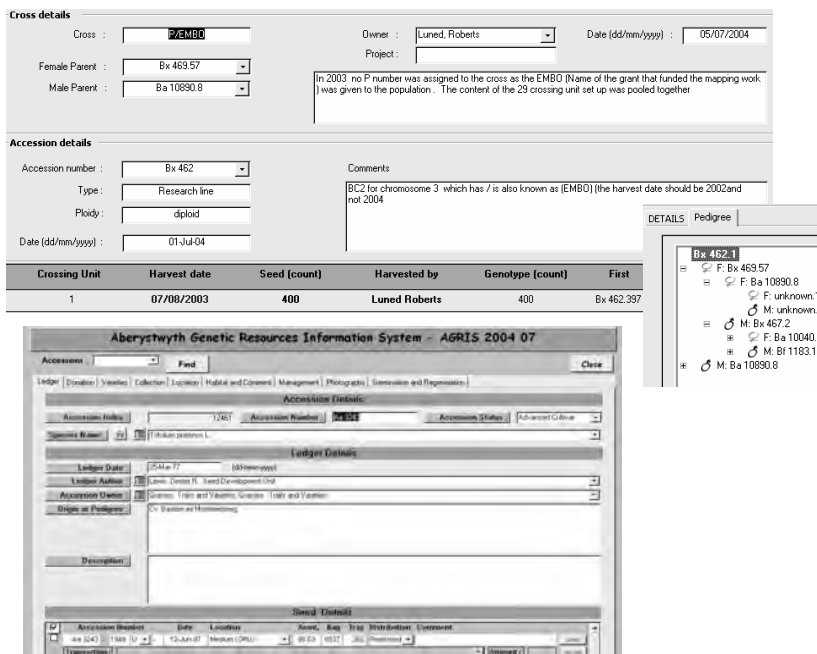


Figure 1 MAPIS (illustrating pedigree, cross and accession details) and AGRIS (showing ledger details)

Computer demonstrations of the databases described in this paper are taking place at the 4th International Symposium on the Molecular Breeding of Forage and Turf, Aberystwyth, 3-7 July 2005.

References

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