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Next Generation Genebanking

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Genomics and genebanks

Next Generation Sequencing (NGS) and subsequent X-omics technologies will enable genebanks to optimize the conservation of plant genetic resources and to provide better services to its users. Based on large-scale DNA sequence information of accessions, curators will eventually be able to (1) make better founded management decisions concerning collection composition, and (2) mine their collections for allelic variants of useful genes.

The wealth of genetic information will open the door for new concepts of collection management, one that is based on genotype composition or allelic richness, rather than on taxonomic and origin data. This will also allow genebanks to improve their services to users by providing well documented or newly identified alleles for the traits of interest.

Initiatives in which large numbers of genebank accessions are sequenced have started. The International Rice Research institute (IRRI) is leading the way as thousands of rice lines have been sequenced (McCouch *et al.*, 2012). Similar activities are on-going in maize, wheat and barley, and on a smaller scale in many other crops (Kilian & Graner 2012).

It is expected that the sequencing of complete crop collections against affordable prices will become reality within a few years.

New technologies develop rapidly, the picture shows a portable $900 disposable Oxford Nanopore sequencer, with USB support.

To anticipate on these developments, genebanks have to reconsider their role, and develop novel methods to best use the new wealth of information to improve genebank management and user support.

Paradigm change

Genebanks conserve accessions of cultivars, landraces, and crop wild relatives, which may represent variable populations with a variety of alleles.

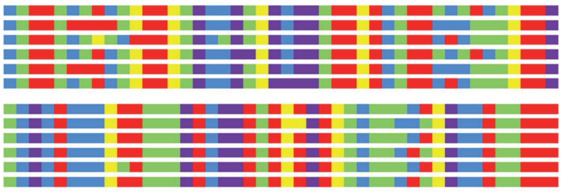

Fig. 1 Two classical genebank accessions: mixtures of lines that differ per generation and have at best indicative characterisation and evaluation data. (Columns refer to genes, different colours in a column to alleles of a gene.)

Parallel to the conservation of diversity in the classical way (Fig. 1), next generation genebanks will also develop user collections in the form of homogeneous lines with well characterised alleles (Fig. 2). These collections allow users to order an allele or a set of alleles with flanking sequences, which are distributed as seed or DNA.

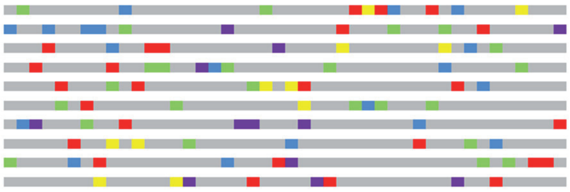

Fig. 2 Ten new genebank user samples with well characterised alleles in known genetic backgrounds, reliable characterisation and evaluation data. (Columns refer to genes, different colours in a column to alleles of a gene, grey can be any colour.)

Changing genebanking

Genebanks are conservative by nature. They are usually established as service departments, maintaining and distributing seeds. In that setting incentives to innovate are rare, therefore implementing a paradigm shift by adopting the Next Generation Genebank concept will not happen naturally. It will require a few advanced genebanks to initiate this development, not only through developing concepts and methods, but also by strongly promoting the new opportunities offered by scientific developments.

References

Kilian B, Graner A (2012) NGS technologies for analyzing germplasm diversity in genebanks. Briefings in functional genomics 11:38-50

McCouch SR, McNally KL, Wang W, Sackville Hamilton R (2012) Genomics of gene banks: A case study in rice. Am J Bot 99:407-423

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