

In this Issue

This issue of *Plant Genetic Resources: Characterization & Utilization* comprises nine full research papers, four short communications and a commentary on a recent PGR symposium. As is the common pattern for the journal, the majority of the papers cover widely grown food crops: pulses (groundnut faba bean and chickpea), cereals (rice, maize and sorghum), oilcrops (sunflower) and fruit (grape), along with a discussion of the contribution of crop wild relatives. While much of arable production is dedicated to these mainstream crops, other species have importance too – here the garden plant lilac. A final paper introduces software to aid the management of germination data, the bread-and-butter trait used by *ex situ* genebanks, and another of single nucleotide polymorphism (SNP) data, the data type which is rapidly coming to dominate discussions surrounding the genotypic characterization of genebank accessions.

This issue marks something of a watershed for the journal in two ways. First, we have now acquired our initial impact factor, which has been accompanied by a marked up-tick in the rate of manuscript submission. Meanwhile, perhaps regrettably in the eyes of some of us (but cheered on by others), this will be the last issue for which a conventional hard copy will be produced. From 2014, the journal will appear online only – meaning the lifting of restrictions on the use of colour for illustration and the accelerated ‘publication’ of the paginated version of the journal. Not even PGR is immune, it seems, from the brave new digital world.

Full research papers

Genetic variability of phytic acid phosphorus and inorganic phosphorus in cultivated groundnut (*Arachis hypogaea* L.)

In excess, phytic acid can act as an anti-nutritional factor. Poonam *et al.* analyses the accumulation of phytic acid in the seed of a set of 40 groundnut cultivars, and are able to show that they displayed a considerable level of genotypic variation. The range of phytic acid phosphorus content was about two-fold, averaging about 225 mg per 100 g. The inorganic phosphorus content of the seed was also variable, once again by about two-fold, averaging about 83 mg per 100 g. Some of the lines had a high content of both inorganic phosphorus and phytic acid.

Morphology and fitness components of wild × crop F₁ hybrids of *Sorghum bicolor* (L.) in Ethiopia: implications for survival and introgression of crop genes in the wild pool

Natural hybrids between a crop and one of its wild relatives can generate forms that are weedy and difficult to control. Adugna and Bekele set out to assess the fitness of seven wild × cultivated sorghum hybrids based on seedling survival and the fertility of the adult plant. The hybrids were fertile, and most of them were as fit as either of their parents. The data highlighted a potential risk posed by the case of natural hybrids that carry genes inherited from the cultivated type (and especially a herbicide resistance transgene). Such forms may be highly weedy, and the presence of herbicide resistance would make them very difficult to control.

Association of qLTG3-1 with germination stage cold tolerance in diverse rice germplasm from the Indian subcontinent

Low temperature is a major constraint for crop productivity. In rice, so far, just one quantitative trait locus (QTL) has been described for determining tolerance to low temperature at germination. Challam *et al.* exploit an established indel marker to screen a panel of rice accessions adapted to the cooler climate typical of North and Northeastern India to validate its association with low-temperature germinability. About one-half of the entries carried the allele associated with the known QTL. Several rice accessions known to be either drought or salinity tolerant, and which were not selected in a low-temperature environment, also carried the critical indel.

Introgression of *Botrytis* grey mould resistance genes from *Cicer reticulatum* (bgmr1_{cr}) and *C. echinospermum* (bgmr1_{ce}) to chickpea (*C. arietinum*)

Botrytis grey mould (BGM) causes significant economic losses to chickpea crops, and no sources of genetic resistance have been located in the primary gene pool. *Cicer echinospermum* and *C. reticulatum*, the only two sexually compatible annual wild relatives of chickpea, are known to show resistance to BGM. Hence, Ramgopal *et al.* develop

populations bred from a cross between a cultivated type and either *C. echinospermum* or *C. reticulatum*. A genetic analysis of these interspecific populations showed that BGM resistance was controlled by a single gene acting additively, and this gene can be introgressed via a conventional backcross breeding strategy.

Microsatellite analysis to rationalize grape germplasm in India and development of a molecular database

A set of 317 grape accessions curated by the Indian National Active Grape Germplasm Site were genotyped by Upadhyay *et al.* at 25 microsatellite loci. About 42% of the alleles detected were classified as rare, and some were unique to a specific accession. The genotypic data identified 63 putatively duplicated accessions. Several cases of misnomers, synonymy and homonymy were identified, and the likely parentage of a few selections was ascertained. A phylogenetic analysis grouped the 254 distinct accessions into four major clusters. A core collection, comprising 80 entries, was defined.

Genetic characterization of sunflower breeding resources from Argentina: assessing diversity in key open-pollinated and composite populations

Open-pollinated and composite populations are valuable resources for sunflower breeding, but little is known concerning the level and distribution of genetic variation within them. Moreno *et al.* present an analysis of quantitative and qualitative traits (including microsatellites) to evaluate 14 populations used in the INTA sunflower breeding programme. The mean gene diversity was 0.56 and the average number of alleles per locus 6.25. No statistically significant differences in genetic diversity were detected between the open-pollinated and composite populations. The outcome of the study was that high levels of global diversity have been preserved.

A baseline study of vicine–convicine levels in faba bean (*Vicia faba L.*) germplasm

The anti-nutritional compounds vicine and convicine both accumulate in the faba bean cotyledon, so there is an increasing level of interest in developing low-vicine and -convicine faba bean germplasm. Khamassi *et al.* describe a rapid and robust screening method for vicine and convicine content. The method allows an efficient means of scanning germplasm for parental materials appropriate for faba beans bred for human consumption.

Variation in inflorescence architecture associated with yield components in a sorghum germplasm

Witt Hmon *et al.* report the variation in various panicle-related traits of 206 sorghum accessions. The distribution of several components of inflorescence architecture influenced yield components. No clear separation between Asian and African accessions was observed. Panicle length, the total number of branches, rachis length and panicle width all exerted a positive effect on grain yield. The variation in inflorescence architecture was dependent not just on panicle length, but also on the total branch number, the maximum length of the primary branch, the rachis length and the panicle diameter and width.

Perceptual distinctiveness in Native American maize (*Zea mays L.*) landraces has practical implications

The observed variation in non-adaptive kernel colour displayed by Native American maize landraces is an evidence of recurring selection for perceptual distinctiveness. Jaradat describes the use of multivariate statistical procedures to quantify variation and interrelationships between grain colour and various physical traits, the C:N ratio, protein content and micro- and macronutrient concentrations. A hierarchical and joint clustering procedure was developed to facilitate the selection of single or multiple traits based on kernel colour traits.

Short communications

Microsatellite markers for common lilac (*Syringa vulgaris L.*)

Common lilac is a popular landscape plant represented by nearly 2000 cultivars. Palovaara *et al.* develop nine informative microsatellite markers, and apply these to a set of 75 accessions, including 17 named cultivars. Each of the nine markers revealed two to five alleles. The resulting phylogenetic analysis concurred well with a grouping made on the basis of morphological traits, and also agreed with whatever pedigree information could be obtained.

Genebank data-management software incorporating seed-viability test results

The Japanese NIAS genebank is responsible for the conservation of plant, microorganism and animal genetic resources related to food and agriculture. Genebanks are obliged to maintain the viability of the seed they conserve, and they

mostly achieve this via low-temperature and low-humidity storage. Takeya *et al.* describe a data-management software package designed to manage germination testing data. It monitors the loss of seed viability of each accession and thereby identifies accessions that require regeneration.

NIASGBsnp: integration of single nucleotide polymorphism data of rice (*Oryza sativa* L.) genetic resources

The NIASGBsnp database manages SNP data collected for rice accessions held by the NIAS Genebank. Currently, the level of data comprises the allelic status of 768 SNP loci across 301 accessions, although its capacity is much greater than this. The database can be used to display pairwise differences between accessions using graphical genotyping. At the same time, the accession's passport data, morphological description and any evaluation data can be readily retrieved.

Climate change and crop wild relatives: can species track their suitable environment, and what do they lose in the process?

Crop wild relatives are recognized as a vital source of genetic variation for crop improvement. Here, Cobben *et al.* suggest that two important aspects,

namely dispersal capacity and founder effects, are currently seldom taken into account. Neglecting these aspects can lead to an underestimate of the climate change-induced threat to the extent of the species range and the conservation of range-wide levels of genetic diversity. Their paper proposes that the integration of process-based simulation models and statistical species distribution models will facilitate the inclusion of dispersal processes and founder effects in future assessments of the resilience of plant genetic resources under climate change.

Commentary

Fishing in the gene pool – how useful was the catch?

Koebner and Ortiz provide a snapshot of the EUCARPIA Plant Genetic Resources Section meeting held at the Swedish University of Agricultural Sciences (SLU) in Alnarp in June 2013. The central theme of the meeting was the use of plant genetic resources in pre-breeding, particularly in the context of incipient climate change and human population pressure.

Robert Koebner
Editor-In-Chief
plantgeneticresources@gmail.com