

In this Issue

This issue of *Plant Genetic Resources: Characterization & Utilization* comprises ten full research papers and two short communications. The contributions cover a number of the world's leading cereal (wheat, rice, barley, millet) and pulse (chickpea) crop species, as well as the brassicaceous species pepperwort (*Lepidium latifolium*), a species which can be found from the Mediterranean to the Himalayas; here though, the focus is on populations adapted to the extremely cold and arid environment of Ladakh.

Full research papers

Powdery mildew resistance in some new wheat amphiploids (2n = 6x = 42) derived from A- and B-genome diploid progenitors

Tetraploid (durum) bread wheat is a hybrid product of two distinct, but related grasses. These grasses represent a secondary gene pool for the crop's improvement. Here, Rafique *et al.* describe sources of resistance against the foliar pathogen powdery mildew expressed in synthetic hybrids made between a donor (or a near donor) diploid species and tetraploid wheat. A substantial proportion of the derived amphiploids showed resistance against the pathogen, although in some cases, resistant donors produced non-resistant hybrids, which was taken as an example of suppression.

Evaluation of cowpea (*Vigna unguiculata* (L.) Walp.) germplasm lines for tolerance to drought

Cowpea provides an important dietary source of protein to the human population of sub-Saharan Africa. Much of the area sown to the crop lies in the dry savanna belt, where drought stress is commonplace. Fatokun *et al.* have outlined the progress made by the IITA towards enhancing the level of drought tolerance in cowpea, based on large-scale experiments involving ~1300 random selections made from the IITA germplasm collection. Their observation is that the imposition of drought accelerates flowering time and grain yield, but not seed size or seed number per pod. A small number of lines do display a 'stay green' phenotype, but not all of these can produce pods when irrigation is withheld.

Genetic diversity among forty-four accessions from *Solanum aethiopicum* L. subgroups based on agronomic traits

The Ethiopian eggplant *Solanum aethiopicum* is little known outside of Africa, but within Africa, it is a significant fruit and leaf vegetable. Here, Adeniji *et al.* have investigated diversity at the morphological level among a collection of germplasm, with the aim of identifying discriminatory traits and suitable parents for use in the crop's improvement. Fruit length proved to be correlated with leaf length, fruit calyx length and width. Promising donors of multiple traits were identified. Earliness and fruit length were highly variable.

Genetic diversity and structure of indica rice varieties in South China and IRRI

Xie *et al.* report the patterns of genetic diversity and relationships to be found among 215 widely cultivated *indica* rice varieties developed in southern China and IRRI, using a SNP oligonucleotide pooled assay. They show that the Chinese material was more diverse than the IRRI-bred varieties. Although the genotyping of the Chinese varieties allowed them to be clustered into distinct groups, there was no correlation of these groups with geographic origin, suggesting that gene flow through germplasm exchange has been commonplace in Chinese rice breeding.

Genetic variability and inter-relationships of phenological, physicochemical and cooking quality traits in chickpea

Tripathi *et al.* provide a characterization of the diversity represented in a collection of chickpea germplasm, based on the variation in phenology, and physicochemical and cooking quality traits. The two major types of chickpea ('Desi' and 'Kabuli') differed significantly from one another for almost all the traits assessed. Many of the traits were associated with high heritability, and informative trait correlations could be drawn. Cooking time was not correlated with any other trait, showing that it should be possible to breed either Kabuli or Desi cultivars which produce seed with a rapid cooking independent of seed size.

Identification of gaps in pearl millet germplasm from East and Southern Africa conserved at the ICRISAT genebank

ICRISAT maintains a major collection of pearl millet germplasm, but gaps in the collection remain. Upadhyaya *et al.* have applied FloraMap software to reveal collection gaps in four East African and seven Southern African countries.

Assessing genetic diversity, allelic richness and genetic relationship among races in a foxtail millet core collection

Foxtail millet is a relatively neglected tropical cereal species, despite it being a short duration crop which does not suffer too much from pests and diseases. Its yield tends, however, to be low. Here, Vetriventhan *et al.* describe the assembly of a core collection comprising 155 accessions, and have applied a set of DNA markers to characterize the allele diversity captured within it. The markers detected a mean of ~16 alleles per locus, although about one-third of these alleles were rare. Some alleles were even specific to a particular accession.

Random genomic scans in cold-adapted *Lepidium latifolium* for identifying regions of allele excess

Pepperwort has a wide geographic distribution, and populations can be found which are adapted to the high-altitude cold arid environment of Ladakh. Grover *et al.* sought to develop some microsatellite resources for the species by exploiting a genome walker library approach. Their aim was to identify a genetic signature of natural selection in response to abiotic stress. The genotyping was complemented by scanning for variation at two genes known to be involved in abiotic stress tolerance. A low level of heterozygosity at one of these genes suggested that low temperature has exerted positive selection on the pepperwort populations.

Elucidation of identities in an international cacao germplasm collection

Cacao conservation relies on living collections of trees, and a major collection is housed at the International Cocoa Genebank in Trinidad. Motilal *et al.* set out to identify mislabelling and to characterize the population structure and genetic diversity of a subset of the

collection. Microsatellite genotyping revealed a synonymous rate of 7.5% and an error rate of 39.4%. Refractorio accessions could be grouped into four subclusters.

Genetic gap analysis of *Hordeum taxa*

Vincent *et al.* have undertaken an updating of *in situ* and *ex situ* conservation strategies for wild barley, by combining an ecogeographic survey with a gap analysis. The analysis was based on the large collection of wild *Hordeum* spp. housed by ICARDA. The major conclusion was that a genetic reserve should be established in the Mendoza area of Argentina, as this appears to be globally the most species-rich area. Meanwhile, a network of reserves needs to be established across the Fertile Crescent to provide effective conservation within specific centres of diversity. Most of the species were deemed to be under-collected.

Short communications

Genetic diversity of native cultivated cacao accessions (*Theobroma cacao* L.) in Nicaragua assessed using microsatellite markers

Aragon *et al.* describe the microsatellite variation present within a set of 60 farmer's accessions from Nicaragua. Comparisons were made with a panel of breeder's accessions. There was rather a low level of differentiation among the farmer's accessions. Six distinct accessions showing a measure of resistance against black pod disease were nevertheless identified in the germplasm set.

Sources of resistance to *Fusarium* wilt and root-knot nematode in indigenous chickpea germplasm

Fusarium wilt is a ubiquitous and devastating disease almost wherever chickpea is cultivated. Mohar Singh *et al.* tested 70 indigenous lines and were able to show that four of these were highly resistant against the disease, and a further six possessed an intermediate level of resistance. The same germplasm set was also screened for reaction against the root-knot nematode *M. incognita*, and one accession appeared to express a significant level of resistance.

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