

In this Issue

This issue of *Plant Genetic Resources: Characterization & Utilization* comprises nine full research papers and one short communication. Most of the material relates to widely grown food crops: olive, tomato, bean, potato, pumpkin, cassava, oil palm and grape. However, in one paper, the net is thrown much wider, considering whether there are any as yet non-domesticated legume species that could be better exploited either in their region of origin in Africa or as introductions to what is deemed to be a similar climatic environment in Australia. A final paper charts the progress made by a mutagenesis programme targeting the improvement of fodder sorghum.

Full research papers

Genetic diversity of on-farm selected olive trees in Moroccan traditional olive orchards

Most olive orchards have been established for a long period, and so capture a past snapshot of genetic diversity. El Bakkali *et al.* set out to use microsatellites to determine whether the same range of diversity is present in traditional orchards across Morocco. A sample size of 88 trees, selected from such orchards sited in the northern and central part of the country, was genotyped with respect to 12 SSR loci. About half of the trees appeared to be genetically identical to the variety called ‘Picholine Marocaine’, but the other half comprised 27 distinct genotypes. The former are thought to reflect the heavy use of ‘Picholine Marocaine’ as a source of vegetative propagules, while the others are likely to represent sexual progeny.

Evaluation of tomato accessions for flavour and flavour-contributing components

Flavour is, of course, a highly relevant consumer trait in tomato, and many commercial varieties have attracted unfavourable opinions of their flavour. From a breeder's point of view, therefore, there is some importance in incorporating desirable fruit flavour along with other producer and consumer traits, and this demands an understanding of what variability exists for the content of those compounds that contribute most to flavour. Total soluble sugar (TSS) and total titratable acid (TTA) contents are both correlated with flavour, and Panthee *et al.* showed that it was possible to select both high TTA or high TSS

types among a core collection of 173 accessions maintained by the USDA-ARS Plant Genetic Resources Unit.

Inducing variability in multi-cut forage sorghum through mutagenesis

Improving performance with respect to fodder yield and quality of multi-cut sorghum varieties has proved to be hard to achieve, with the variety SSG 59-3, a sweet sudangrass released in 1974, remaining as the benchmark for breeding. Pahuja *et al.* describe the use of mutagenesis to improve the performance of SSG 59-3. A set of mutagenesis-derived selections was evaluated in several locations over 2 years, and a considerable amount of variability was observed for flowering time, fodder protein content and *in vitro* dry matter digestibility. Some of the selections also showed favourably low levels of the major anti-nutritional factor HCN.

Genetic diversity of two Indian common bean germplasm collections based on morphological and microsatellite markers

The common bean is more associated with Central/South America and Africa than with India, but it, nevertheless, represents a significant grain legume there. Sharma *et al.* have analysed a collection of Indian landraces by genotyping with a panel of 24 microsatellites. A population structure analysis was used to find groups in each collection, and this was compared across collections. The analysis successfully identified the two major common bean types: Andean and Mesoamerican. Andean types dominated the collection based on the north-western Himalayan region, while the FAO-protected accessions were predominantly Mesoamerican. Little evidence for introgression between the two gene pools was noted.

Genetic diversity among potato species as revealed by disease and stress resistance and microsatellites

The diversity among wild potato species offers opportunities for widening the genetic basis of the cultivated potato. Here, Carputo *et al.* surveyed variation in the resistance against *Ralstonia solanacearum*, potato virus Y and low temperature among a set of 21 clones (12 species), and determined the level of microsatellite

variation present. Sources of resistance were identified, with variation shown both within and between species. Some clones showed multiple disease/stress resistance. The genotypic analysis over 12 loci uncovered 46 alleles, with both unique and rare alleles being present. The presence of resistance in different genotype-based clusters suggested that genetically distinct resistant genes were represented.

Molecular characterization of oil palm from Cameroon

Commercial oil palm production rests on a very narrow genetic base. Arias *et al.* have conducted a genotypic survey of an *ex situ* collection of materials originating in Cameroon. A set of 31 microsatellites all showed some polymorphism, with many of the 223 alleles uncovered being only present at a low frequency. Genetic differentiation between geographic regions was low, suggesting that the oil palm population in Cameroon consists of a single diverse population. It was concluded that a set of 120 accessions would capture almost the entire genetic diversity of the species in Cameroon.

Seed oil content and fatty acid composition in a genebank collection of *Cucurbita moschata* and *C. argyrosperma*

The levels of intraspecific variability present for seed oil content, physical characteristics and fatty acid composition in *C. moschata* and *C. argyrosperma* have not been well described. Jarret *et al.* characterized variation for these traits among 528 genebank accessions of *C. moschata* and 166 genebank accessions of *C. argyrosperma*. The oil of both species had near identical viscosity, colour and oxidative stability, but that from *C. argyrosperma* had a slightly higher pour point, cloud point, acid value and free fatty acid content. Their mean oil content was similar, but that of *C. argyrosperma* subsp. *argyrosperma* var. *palmeri* was rather higher. Linoleic acid was universally the predominant fatty acid.

Exploring the wider potential of forage legumes collected from the highlands of Eritrea

Snowball *et al.* provide a preliminary view of the outcomes of a pasture plant collecting mission in the highlands of Eritrea, made with a view to identifying species that could potentially thrive in southern Australia. Seeds of 53 legume species and *Rhizobium* strains associated with 18 of these species were collected, and some were established in nurseries in Western Australia for assessing growth,

flowering and seed production. Based on a climate match analysis and nursery observations, the most promising species for southern Australia were the annual legume *Biserrula pelecinus* ssp. *leiocarpa* and the perennial shrub *Colutea abyssinica*, but the greatest potential was associated with use within Eritrea itself, where animal husbandry would probably benefit from better utilization of these species through replanting, careful grazing management and a demonstration of the benefits of increasing the native legume component of local wild pastures.

Genetic diversity of cassava landraces and cultivars from southern, eastern and central Africa

Cassava is a key food crop in sub-Saharan Africa, but the extent of genetic variation available within national breeding programmes has not been well characterized. Kawuki *et al.* document the nature and extent of genetic variation among a collection of 1401 varieties originating from seven countries. Few of these accessions are held in formal collections, as they were selected from farmers' fields and national breeding programmes. The survey was based on genotyping at 26 microsatellite loci, and this analysis demonstrated a moderate degree of genetic variation. Some differentiation was observed among countries, but pivotal populations were those from Tanzania. The complexity of the genetic relationships between cultivars and landraces reflects a history of germplasm introduction, gene flow, disease pandemics, past breeding programmes and the major influence of the activities carried out by the International Institute of Tropical Agriculture.

Short communication

Direct-multiplex PCR for grapevine genotyping and varietal identification

Grapevine cultivar identification is conventionally based on a combination of microsatellite genotyping and ampelography. Migliaro *et al.* describe a direct-multiplex PCR assay, in which 11 microsatellite loci are co-amplified from a crude DNA extract. The bypassing of normal DNA extraction is achieved by using an engineered DNA polymerase. Amplification was achieved from leaf, root, wood, berry flesh and skin, stalk and must. The method is quicker and cheaper than currently employed ones and has provided a high level of accuracy.

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