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In this Issue

This issue of Plant *Genetic Resources: Characterization & Utilization* comprises 14 full research papers and six short communications. This is a rather larger collection of materials than usual, and marks the transformation of the journal from a print plus electronic publication into a fully electronic one. The papers' topics range widely both species-wise and geographically wise, spanning oilseed rape cultivars from Canada to wild plant populations in Antarctica, and from the major crops rice, wheat, maize and potato to lesser crops such as mulberry, sesame and *Desmodium* spp. and very minor ones such as *Luffa* spp. and the bottle gourd.

As noted in the previous issue of *Plant Genetic Resources: Characterization & Utilization*, the journal has experienced a marked increase in the submission of articles, which are now running at about 50% above the levels experienced from 2009 to 2012. Since there is no intention as yet to increase the output of the journal, the result is that the quality of the material accepted for publication will rise.

Full research papers

Variation for selected morphological and quality-related traits among 178 faba bean landraces collected from Turkey

Faba bean is cultivated worldwide, especially in the Mediterranean Basin, but the breeding effort dedicated to this ancient crop is relatively limited. Karaköy *et al.* describe a mini-core collection comprising entries from 178 landraces and four cultivars. The landraces were acquired from a diversity of locations in Turkey. The collection displayed substantial variation for a number of morphological and end-use quality traits. Some of the entries performed very well for key agronomic traits. Inter-trait correlations have been detailed. The landraces clustered into four groups, but these groups were not fully congruent with geographical origin. The collection captured a wide range of phenotypic variations, which should provide ideal foundation material for a focused breeding programme.

Genetic diversity analyses of Brassica napus *accessions using SRAP molecular markers*

Ahmad *et al.* have genotyped a collection of 60 spring-type canola accessions with 20 SRAP (sequence-related amplified polymorphism) primers, an assay which preferentially amplifies coding sequence. The profiling identified 162 polymorphic fragments. Genetic similarity estimates ranged from 40 to 100%. A cluster analysis resulted in the recognition of five groups; the first captured 23 accessions, mostly of Australian origin, and the second 13 accessions mostly of Canadian origin. The two male fertility restorer lines R-111 and R-101 along with their corresponding backcross progeny constituted a third cluster, and a set of Scandinavian cultivars the fourth. Some variation in the number of markers was noted between open-pollinated cultivars and inbred lines. The clustering pattern was largely consistent with pedigree relationships.

Agro-morphological variability of rice species collected from Niger

African rice (*Oryza glaberrima*) and other related wild species are endemic to Niger. Sow *et al.* report the outcome of a collection mission across a range of growing regions and agricultural systems in Niger. The collection assembled 177 Asian rice (*O. sativa*) cultivars, 65 *O. glaberrima* landraces, 27 *O. barthii* accessions and one *O. longistaminata* accession. Apart from the *O. barthii* accessions, which originated from around Lake Chad, the collection site of most of the material was along the Niger River. The naming of landraces by farmers was consistent within a region but seldom across regions. The phenotypic variability of the collection, as measured by the Shannon–Weaver diversity index, was relatively high, with accessions originating from irrigated areas being less diverse than those collected from traditional farming systems. There was no significant difference in the magnitude of the diversity between the major eco-geographical zones or between clusters. However, the traits contributing most strongly to diversity varied. There was evidence for frequent exchange of germplasm between regions.

Characterization of Sudanese pearl millet germplasm for agro-morphological traits and grain nutritional values

The potential of Sudanese pearl millet landraces as a source of desirable traits for crop improvement was assessed by Bashir *et al.* based on a set of 225 Sudanese accessions. The assessment comprised the measurement of key agro-morphological traits and grain nutrient content. Genetic variation was relatively limited for days to flowering, plant height and panicle length. However, the iron and zinc content of the grain varied widely. Positive correlations among many of the nutritional traits suggested that the enhancement of a few of them should produce a simultaneous improvement in the others. No associations were noted between the nutritional and agro-morphological traits. There was no evidence for geographical differentiation for any of the traits.

Plant and fruit trait variations among four Capsicum *species in a Caribbean germplasm collection*

Despite the importance of *Capsicum* in the Caribbean diet, the diversity of the species has not been well studied in this region. Bharath *et al.* have evaluated 37 traits (seedling, vegetative and reproductive) across 201 accessions belonging to four *Capsicum* species. A multivariate analysis revealed that 54% of the quantitative and 64% of the qualitative variation in flower and fruit morphology could be captured by the first two principal components. Three major clusters were identified. The southern Caribbean accessions were rather homogeneous (if not identical to one another), providing an opportunity to identify and exclude duplicates from the collection. Their similarity with material originating from the Upper Amazon implied that they were brought to the Caribbean from there. The Upper and Lower Amazon accessions were well differentiated from one another. The Central American, Greater Antilles/ Bahamas and Guiana Shield accessions shared similarities with both the Upper and Lower Amazon populations, hinting at a process of introduction from both Amazon regions.

*Phenotypic characterization of indigenous rice (*Oryza sativa *L.) germplasm collected from the state of Nagaland, India*

Nagaland (northeastern India) harbours a considerable diversity in cultivated rice. Roy *et al.* have provided a morpho-agronomic characterization of 124 rice landraces collected from tribal areas, and have shown that these materials vary considerably with respect to plant architecture, grain morphology and grain quality. A multivariate analysis was used to assess the patterns of morphological variation. A set of 12 principal components explained 75.4% of the total variation for the 38 measured traits. The landraces clustered into five groups. Inter-trait correlations were noted. The landrace materials have been conserved in the national genebank.

SSR-based and carotenoid diversity assessment of tropical yellow endosperm maize inbred lines

The consumption of yellow endosperm maize could reduce vitamin A deficiency among many pre-school children and women of reproductive age in sub-Saharan Africa. Adeyemo *et al.* screened 122 tropical yellow endosperm maize inbred lines using 62 SSR markers, of which 51 were informative. In total, 190 alleles were detected. The genetic distance between pairs of inbred lines varied from 0.02 to 0.61. Carotenoid content was also used to derive genetic distances. A principal coordinate analysis separated the inbred lines into both SSR-based and carotenoid-based groupings. Clusters based on the SSR genotype were largely consistent with known pedigree relationships.

*Genetic diversity analysis of a potato (*Solanum tuberosum *L.) collection including Chiloé Island landraces and a large panel of worldwide cultivars*

An analysis of the diversity of Chilean potato germplasm, which included 30 Chiloé Island landraces along with representatives of global varieties and breeders' lines, used SSR markers, as reported by Esnault *et al.* The close genetic proximity of the Chiloé Island landraces to modern germplasm was confirmed in an analysis that combined principal coordinate analysis, hierarchical clustering, analysis of molecular variance and Bayesian model-based clustering. The latter, in particular, revealed no clear genetic structure between the modern group and the Chiloé Island landraces. The Chiloé Island germplasm appears to represent an interesting gene pool that could be exploited in potato breeding programmes.

*Exploitation of forage attribute-based variations in Sudan pearl millet [*Pennisetum glaucum *(L.) R. Br.] collections*

Babiker *et al.* studied phenotypic diversity in a collection of 100 accessions of pearl millet originating from Sudan. The material differed widely with respect to total dry forage yield, days to harvest, plant height, number of tillers/plant and leaf/stem ratio. During the rainy and winter seasons, many of the accessions produced a forage yield of over 5 t/ha, while over three quarters of them yielded less than 5 t/ha during the summer season. Two accessions performed well with respect to dry matter yield in all three seasons, and 11 were consistent in at least two seasons. The results suggest that it should be possible to develop pearl millet cultivars suitable for forage purposes.

Latitudinal patterns of diversity in the world collection of pearl millet landraces at the ICRISAT genebank

The ICRISAT genebank curates nearly 20,000 pearl millet landraces collected from latitudes ranging from 33°S to 34°N. Upadhyaya *et al.* have attempted to correlate latitude of collection site with trait diversity. Landraces collected from sites in the range of 5°–10°N tended to be late flowering with thick panicles, heavily tillering and tall, independent of sowing time. Those originating from a latitude range of 10°–15°N tended to be sparsely tillering but formed long, thick panicles bearing large seeds. Long-bristled, bird-resistant landraces were most frequent from sites at higher latitudes. Late maturing, tall and high tillering landraces from lower latitudes were the most suitable for fodder production. Early maturing, large-seeded landraces from mid-latitudes (15°–20°) in both hemispheres should be useful for the development of high-yielding cultivars.

A preliminary investigation of cultivated and wild species of Luffa *for oil and protein contents*

Prakash *et al.* have reported the variability in size, colour, coat surface, weight, along with the oil and protein contents, of the seed of wild and cultivated species of *Luffa*. A panel of 71 accessions drawn from three cultivated species, plus a further nine accessions (three wild species), were sampled. The material originated from all over India. Both inter- and intra-specific variations were present. Seed oil and soluble protein content were greatest in accessions of the cultivated species, reaching, respectively, 27 and 10%. Correlations between seed morphology and biochemical traits should inform the choice of *Luffa* accessions used for cropping purposes.

*Assessment of molecular genetic diversity and population structure of sesame (*Sesamum indicum *L.) core collection accessions using simple sequence repeat markers*

Sesame is an ancient oil crop, which is widely cultivated in Asia and Africa. Park *et al.* set out to assess the genetic diversity, phylogenetic relationships and population structure of a 277 accession sesame core collection, originating from countries in four continents. SSR analysis identified 158 alleles at 14 loci, with the number of alleles per locus varying from 3 to 25. The polymorphism information content of the SSRs ranged from 0.34 to 0.84. Accession-specific alleles were identified at 12 of the SSR loci. The core collection was separable into four clusters, without any evidence for a correlation between cluster and geographical origin.

Desmodium *genetic resources for improving flavonoid concentrations, oil content and fatty acid compositions*

The flavonoid concentrations, oil content and fatty acid compositions of 25 *Desmodium* spp. accessions belonging to five species (*D. discolor*, *D. incanum*, *D. intortum*, *D. sandwicense* and *D. tortuosum*) were analysed by Morris *et al.* using high-performance liquid chromatography, nuclear magnetic resonance and gas chromatography, respectively. Some of the accessions produced seed with a marked concentration of quercetin and kaempferol, and all of them produced notable concentrations of isorhamnetin and luteolin. The contents of linoleic (18:2) and behenic (22:0) acids were higher than those in *D. incanum* check accessions. A significant positive correlation was noted between the contents of quercetin and kaempferol, while quercetin content was negatively correlated with isorhamnetin content. The seed oil was dominated by palmitic, stearic, linolenic and lignoceric acids.

Microsatellite marker analysis reveals the events of the introduction and spread of cultivated mulberry in the Indian subcontinent

Krishnan *et al.* investigated a set of 36 leading mulberry accessions of historical importance, since they have been frequently used in Indian crop improvement programmes over the last five decades. A panel of 70 informative SSRs was employed to elucidate the diversity, structure and breeding history of the accessions. Cluster and STRUCTURE analysis produced a picture consistent with the known genetic relationships and origin of the collection. The study revealed the history of the introduction of mulberry into and its spread across the Indian subcontinent.

Short communications

Establishment of the core collection of Ziziphus mauritiana *Lam. from India*

Ziziphus mauritiana is a fruit crop exploited in the Thar Desert of India. Some 330 accessions and cultivars collected from various parts of India are currently maintained at the Central Institute for Arid Horticulture's farm. Sivalingam *et al.* have used a heuristic approach based on phenotypic characters to identify 52 accessions as representing a representative core collection. No significant difference was observed with respect to either the Shannon–Weaver or the Nei diversity index for qualitative traits, mean and range of quantitative traits or clustering pattern between the core set and the whole collection.

The relationship between national plant genetic resources programmes and practitioners promoting on-farm management: results from a global survey

A global survey was conducted among a wide range of stakeholders to gain insight into the state of on-farm management (OFM) as a strategy for enhancing the conservation and sustainable use of plant genetic resources for food and agriculture (PGRFA). The results reported by Nilsen *et al.* show that OFM is not considered a priority in national PGRFA programmes (NPGRPs), and that OFM practitioners and their organizations are not always aware of or involved in the NPGRPs. The survey also highlighted the lack of awareness, understanding and collaboration between OFM practitioners and the managers and policy-makers associated with NPGRPs. The outcome of the analysis supports a hypothesis that OFM is, to a large extent, supported by stakeholders who are not directly engaged in PGRFA conservation and use, and are therefore not associated with NPGRPs.

Genetic diversity of Colobanthus quitensis *across the Drake Passage*

The Drake Passage represents a likely route for gene flow into Antarctica, as it is the shortest path between this continent and other land masses. To compare the levels of genetic diversity between Antarctic and South American populations of the Antarctic pearlwort *Colobanthus quitensis*, Acuña-Rodríguez *et al.* have conducted an AFLP analysis of the genetic diversity in four populations. Differences among genetic diversity levels were found between tested populations, as well as between their allelic identities. However, most interestingly, their spatial distribution across the Drake Passage suggests a north-to-south gradient of increasing genetic diversity.

Genetic diversity and structure found in samples of Eritrean bread wheat

Abera *et al.* analysed the genetic diversity and structure of a set of 284 Eritrean bread wheat accessions using 30 SSR markers. In total, 539 alleles were recognized, with the number of alleles per locus ranging from 2 to 21. The average genetic diversity index was 0.66, with values ranging from 0.01 to 0.89. Comparing the three genomes of wheat, the B genome had the highest genetic diversity (0.66) and the D genome the lowest (0.61). A STRUCTURE-based analysis revealed the distinct partition of the Eritrean wheat accessions into two major groups.

Microsatellite-based DNA fingerprinting and genetic diversity of bottle gourd genotypes

Distinctness, uniformity and stability (DUS) tests of morphological characters are used for varietal registration, but these traits usually cannot resolve closely related individuals. Sarao *et al.* have applied ten informative SSR assays to a set of 20 bottle gourd accessions; the number of alleles per locus ranged from 2 to 4. Unique DNA profiles of each accession were produced by as few as five primer pairs.

Microsatellite high-resolution melting (SSR-HRM) analysis for identification of sweet cherry rootstocks in Greece

When sweet cherry scions are grafted onto one of a wide range of *Prunus* sp. rootstocks, the identification of the rootstocks based on plant morphology is almost impossible, particularly during the winter season. DNA-based molecular analysis carried out on actively growing shoot tips, leaves or dormant buds offers a good opportunity to reliably distinguish rootstocks. Ioannis *et al.* report a high-resolution melting (HRM) protocol based on five SSR markers, which allowed for the identification of the most popular sweet cherry rootstocks used in Greece. One of the markers produced six HRM profiles, which was enough to discriminate all the rootstocks studied. The assay provided a flexible, cost-effective and closed-tube microsatellite genotyping method well suited to the identification of sweet cherry rootstocks.

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