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In this Issue

This issue, the first to appear exclusively in electronic form, of *Plant Genetic Resources: Characterization & Utilization* comprises ten full research papers and two short communications. Similar to its predecessors, the range of species covered is large and not restricted to the major crops (although there are papers concerned with rice and wheat). As noted in my previous *In this Issue* piece, the journal is experiencing a continued increase in manuscript submission, which is raising the bar on acceptance. Reflecting this, the journal's second impact factor, which is shortly to be published, has risen by 50% and now is likely to exceed 1.0. From 2015, the Editorship of the journal is likely to pass (after a 10-year stint) to a new person, but before this, a manuscript online submission system will be put in place, sadly marking the end of a successful personalized service. *O tempora, o mores!*

Full research papers

Genetic diversity and adaptive variations under static and dynamic management: a case of rice landraces from parts of Odisha in India

A comparison of the static and dynamic management of diversity in Indian rice landraces has been undertaken by Priyan *et al.* based on the allelic state at 14 simple sequence repeat (SSR) loci. Of the 64 alleles uncovered, 60 were common and four were rare. An analysis of molecular variance showed that the management system accounted for over 75% of the molecular variance. Although the evidence was that the landraces shared only a limited degree of the overall genetic diversity, there was little differentiation at the phenotypic level as a result of the management system.

Comparative tolerances of two Cucumis *species to salinity,* Rhizoctonia solani *and* Meloidogyne incognita

Barakat *et al.* have shown that accessions of the wild melon species *Cucumis prophetarum* are relatively more tolerant to salinity stress (whether exerted by NaCl or $CaSO_4$) and more resistant to both the fungus *Rhizoctonia solani* and the root knot nematode *Meloidogyne incognita* than the cultivated cucumber *C. sativus*. The suggestion is that the wild species represents a major source of beneficial genetic variation for cucumber improvement.

An analysis of genetic differentiation and geographical variation of spinach germplasm using SSR markers

A spinach germplasm panel consisting of 250 plants sampled from 50 accessions collected from diverse locations worldwide has been SSR genotyped by Kuwahara *et al.* The overall level of genetic diversity uncovered was high, particularly in materials derived from West Asia. The result is consistent with the supposed centre of origin of the species in West Asia. The provenance of the material accounted for over a quarter of the overall genetic variance. The differentiation between the East Asian and European gene pools is probably attributable to a founder effect associated with crop dissemination, although subsequent selection and genetic drift during breeding are likely to have contributed.

Characterization of high-molecular-weight glutenin subunit Bx7OE and its distribution in common wheat and related species

The *Bx7OE* allele drives the overexpression of the wheat Bx7 high-molecular-weight glutenin subunit (HMW-GS). Li *et al.* have assembled a collection of 31 wheat cultivars and related species carrying *Bx7OE*. Reversed-phase high-performance liquid chromatography analysis revealed that the Bx7 subunit contributed over 40% of the total HMW-GS content of the flour, compared with about 30% in the flour of wheats carrying a normal *Bx7* allele. A quality analysis of the flour of seven representative *Bx7OE* cultivars and three *Bx7* cultivars showed that the presence of *Bx7OE* is associated with higher gluten strength. A polymerase chain reaction-based survey of near relatives indicated that the retroelement-mediated recombination at the *Glu-B1* locus responsible for the allele was a relatively recent event, after the formation of hexaploid wheat.

Amplified fragment length polymorphism and poly(butylene adipate) polymorphism in an endangered medicinal plant **Rhazya stricta** *in Pakistan*

Gilani *et al.* have studied habitat fragmentation in the Pakistani Himalaya in six populations of the endangered medicinal plant *Rhazya stricta*. The plant material was subjected to P450-based analogue functional genomic marker and amplified fragment length polymorphism (AFLP) genotyping. Both marker types revealed a low level of genetic differentiation between the populations and a more pronounced differentiation within the populations, reflecting a high rate of gene flow. The results confirmed that habitat fragmentation is being caused by anthropogenic activity, and although signs of genetic erosion are not yet visible, they are likely to be manifested in the near future.

*Genetic diversity and population structure of a roselle (***Hibiscus sabdariffa** *L.) collection from Niger*

Little is known concerning the genetic diversity and population structure of roselle in Niger. Bakasso *et al.* have characterized the diversity present in a set of 124 roselle accessions and 16 accessions of its close relatives *Hibiscus cannabinus* and *Abelmoschus esculentus*. On the basis of ten agromorphological traits and 267 AFLP markers, two major clusters of roselle were recognized, associated with the number of days required to reach flowering, seed weight and calyx size. Calyx colour, the character used frequently to classify ecotypes, was not informative.

Bottleneck and gene flow effects impact the genetic structure of seed-propagated apricot populations in Moroccan oasis agroecosystems

To highlight the genetic status and origin of Moroccan apricot populations, Mamouni *et al.* have sampled trees from ten oasis agroecosystems and analysed their DNA by AFLP fingerprinting. The extent of genetic diversity in Maghreb apricot was limited. A similar situation was illustrated at a finer geographical scale through an analysis of trees originating in the Moroccan Draa Valley. The data were suggestive of substantial gene flow into traditional types from recently introduced cultivars. Morocco appears to be a secondary centre of diversification for apricot.

Diversity and gaps in **Pennisetum glaucum** *subsp.* **monodii** *(Maire) Br. germplasm conserved at the ICRISAT genebank*

The ICRISAT collection of *Pennisetum glaucum* subsp. *monodii* comprises 335 accessions originating from 13 countries. Upadhyaya *et al.* have assessed the diversity present in the material in an attempt to identify geographical gaps in the collection. Morphological variation was extensive for most traits, and the analysis pointed to regions in eight countries belonging to the primary centre of origin of pearl millet. The limited collection of germplasm emphasizes the need for collection missions to be mounted to fill the taxonomic and geographical gaps in the collection.

*Seasonal and genetic variation of water-soluble carbohydrates and other quality traits in ecotypes and cultivars of perennial ryegrass (***Lolium perenne** *L.)*

McGrath *et al.* have reported their phenotyping of perennial ryegrass, with a focus on water-soluble carbohydrate (WSC), crude protein and dry matter content. A set of 1320 plants was pooled into 132 samples belonging to 33 ecotypes/cultivars and the material was sampled at five time points. Although, in general, the cultivars had a higher WSC content than the ecotypes, some ecotypes performed well enough to be considered as potential breeding lines. A positive correlation was established between dry matter and glucose content both early and late in the growing season. The time of cutting was the most significant factor influencing variation in the traits.

Genetic diversity and structure of improved indica rice germplasm

Wang *et al.* have described the single-nucleotide polymorphism genotyping of 737 improved *indica* rice materials. A model-based population structure analysis revealed the presence of two major clusters and six subclusters, with no clear relationship being identified between cluster/subcluster membership and provenance or breeding programme. The groupings indicated plentiful gene flow within *indica* germplasm. A distance-based clustering exercise showed that Latin American cultivated *indica* lines formed a distinct ecological cline, which could be exploited as a potential heterotic ecotype in the context of hybrid rice breeding. African cultivated *indica* types, on the other hand, have not yet formed any recognizable ecological cline. The heavily exploited hybrid rice parents Zhenshan97B and Minghui63 unexpectedly clustered within the same subgroup, which indicates that a significant genetic distance between parents is not necessarily required to generate high levels of heterosis.

Short communications

Interspecific hybridization between Cajanus cajan *(L.) Millsp. and* Cajanus lanceolatus

The cultivated pigeon pea has a narrow genetic base. Herein, van der Maesen *et al.* have reported their successful wide-cross between the cultivated pigeon pea and a wild relative from the secondary gene pool, native to Australia, featuring desirable traits including frost and drought resistance. The hybrid plants set mature pods and seeds and displayed an intermediate morphology. All the hybrids flowered profusely; some were fully male sterile, but others were partially fertile. A meiotic analysis of fertile hybrids revealed a high degree of chromosome pairing, while in the sterile hybrids there was a breakdown in microsporogenesis after the formation of tetrads.

*Two fruits per pedicel in cacao (*Theobroma cacao *L.) – a rare phenotype*

A rare aberrant cacao fruit phenotype noted in Trinidad has been described by Bhola *et al.* Double, rather than single, fructification occurred on a single pedicel. The aberration probably arose as a result of the formation of two pistils in a single flower. Fruits matured as normal, and both fruit morphology and seed number were within the normal range.

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