

microsatellite (SSR) markers, 25 Insertion-Deletion (InDel) nuclear markers and four mitochondrial InDel markers were genotyped for 223 accessions. 'Structure' software was applied on nuclear data to check and quantify potential interspecific introgressions in the mandarin germplasm, mainly the pummelo and papeda genomes. Within the mandarin germplasm without identified introgression, seven clusters were revealed by 'Structure' analysis. Five of them should be true basic mandarin groups and the other two include genotypes of known or supposed hybrid origin. The contributions of these seven groups to the mandarin genotypes were estimated. The mitochondrial InDel analysis revealed eight mitotypes, in which the mandarin germplasm was represented in four of them. In this work, new insights in the organization of mandarin germplasm and its structure have been found, and different mandarin core collections were determined. This will allow a better management and use of citrus germplasm collections and to perform genetic association studies.

S01004

Study on genetic diversity of 39 Citron germplasm resources with SCoT and ISSR markers

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The genetic relationships and diversity of 39 citron (*Citrus medica*) germplasm resources were examined by SCoT and ISSR markers in this study. Of the 80 SCoT primers screened, 9 primers gave reproducible, polymorphic DNA amplification patterns with a total 69 amplified bands. The polymorphic percentage was 76.8%. Of the 100 ISSR primers screened, 9 primers gave reproducible, polymorphic DNA amplification patterns with a total 84 of amplified bands. The percentage of polymorphic band was 77.4%. An UPGMA relationship tree was established based on the similarity coefficients. At the coefficient level of 0.85 for SCoT and 0.77 for ISSR, the 39 germplasm resources were divided into six groups and five groups, respectively. The application of SCoT and ISSR markers is discussed in this paper.

S01005

Origin of dwarf, thornless-type trifoliolate orange varieties deduced from genome-wide genotyping analysis

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Trifoliolate orange (*Poncirus trifoliata*) is commonly used as a rootstock in Japan. Several varieties that are different for tree height or tree morphology are recognized. However, origin and phylogenetic relationship among them are not evaluated. We compared genotypes of three varieties, a thornless type trifoliolate orange that lacks thorns at the leaf axil and two dwarf types, 'Hiryu' ('Flying dragon') and 'Unryu' ('Cloudy dragon'), to a reference accession of trifoliolate orange in our citrus collection. Genotyping analysis with 289 genome wide SSR markers gave 265 valid genotypes. Among them, 'Hiryu' lost five loci but 96.2% of genotypes were matched to those of the reference. In contrast, the thornless-type lost 4 loci and 78.8% of genotypes were matched to those of the reference, and 'Unryu' lost 6 loci and 81.4% of genotypes were matched to those of wild type. Assignment of SSR marker genotypes to a citrus linkage map revealed that genotypes of 'Hiryu' were well conserved among all linkage groups. However, loss of heterozygosity (LOH) was observed at various regions of linkage groups for the thornless-type and 'Unryu'. Ratios of homozygous loci of the reference, the thornless-type, 'Hiryu' and 'Unryu' were 70.3%, 88.5%, 69.1%, and 84.9%, respectively. These observations suggested that 'Hiryu' is a sport of trifoliolate orange but the thornless-type and 'Unryu' resulted from trifoliolate orange by self-pollination and mutation at particular loci.

S01006

Multilocus haplotyping by parallel sequencing to decipher the interspecific mosaic genome structure of cultivated citrus

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Recent studies support the theory that four basic taxa (*Citrus medica*, *Citrus maxima*, *Citrus reticulata* and *Citrus micrantha*) have generated all cultivated *Citrus* species. It is supposed that the genomes of most of the actual

citrus cultivars are interspecific mosaics of large DNA fragments issued from a limited number of interspecific meiotic events. In the present work, we analyzed how haplotypic multilocus study of closely linked SNPs allows phylogenetic assignment of DNA fragments for the main cultivated species. We have developed a new method based on universal primers to prepare the amplicons to be analyzed by 454 technology (Roche). It was applied for direct multilocus haplotyping of 12 gene fragments of 48 *Citrus* genotypes. Moreover, Sanger sequencing was performed on a subset of these amplicons (seven gene fragments of 24 citrus genotypes) to validate the 454 results. Consensus haplotype sequences were successfully identified from 454 sequencing. Sanger and 454 results were mostly identical. *C. reticulata* was the most polymorphic basic taxa. The average differentiation between the basic taxa was about 20 SNPs/kb. These polymorphisms were enough for unambiguous multilocus differentiation of the basic species and assignment of phylogenetic origin for each haplotype of the secondary species. Multilocus haplotyping by parallel sequencing will be a powerful tool to decipher the interspecific mosaic genome structure of cultivated citrus.

S01P01

***Citrus ichangensis* in Sichuan and Chongqing**

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Citrus ichangensis from Sichuan and Chongqing Provinces occurs in a wild state in the hills of 42 counties, growing at altitudes of 800 to 2400m with soil pH 5 to 6.5. The dominant vegetation around this species consists of pine, *Chimonobambusa utilis*, plum, kiwifruit, wild cherry, pear, waxberry, fern, rhododendron, couch grass, et cetera. The typical *C. ichangensis* is a shrub or tree, usually 1 to 8 meters high; the corolla of the flowers is purple, light purple, or white; the fruits are ellipsoid, obloid, spheroid or pyriform, 36 to 170 g in weight; the seeds are very large, very numerous (from 20 to 67 in a single fruit), and monoembryonic.

S01P02

Diverse genetic resources of citrus in North-East region of India

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The diverse gene pool of citrus in the North-East India is represented by 23 species, a subspecies, and 68 varieties. Collection, conservation and characterization are necessary for incorporating the useful agronomically important traits present in this large gene pool for breeding of improved citrus rootstocks and cultivars and exploring bioactive compounds present in them. Twenty eight accessions of citrus belonging to different species have been collected and morphologically characterized. Variability observed among the citrus accessions collected is reflected by five different types of fruit shape, five different types of fruit base shape, four different types of fruit apex shape, four types of leaf lamina shape, three different types of petiole wing shape, three types of leaf apex, four different types of leaf margin, two types of leaf lamina attachment and five different types of seed shape. Citrus accessions collected have fruit color ranging from light yellow to yellow and orange to orange red color. Various forms of citrus types such as pummelos, citron, acid lime and other hybrids are available in cultivated, semi-cultivated and wild forms which required immediate intervention of a scientific way of conservation to prevent the continuing threat of genetic erosion.

S01P03

Observations of graft compatibility between *Citrus* spp and related Aurantioideae taxa

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Although *Citrus* has long been known to be graft compatible with the genus *Poncirus*, compatibility between *Citrus* and other genera of the Aurantioideae is less well characterized. Graft compatibility between