

P3.30 - Genome-wide variation from the wild to the cultivated and its implications to study on germplasm of soybeans

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After the domestication of cultivated soybean (*Glycine max* (L.) Merr.) in China from its annual wild relative *Glycine soja* Sieb. & Zucc., thousands and thousands of landraces were developed by the ancient Chinese farmers during the long history, based on which more than 1300 improved cultivars were released in China since 1923. From studies on large samples of wild accessions, landraces and released cultivars by using genome-wide SSR markers, it was found that the genetic diversity in terms of genetic richness and genetic dispersion decreased obviously from the wild to the cultivated landraces and in turn to the released cultivars, which showed obviously two stages of bottlenecks, but with a great number of new alleles emerged during human being's artificial improvement. In fact, the parental materials used in breeding programs are mainly released cultivars or related breeding lines which provide more than 90% of the germplasm to the newly released cultivars. Therefore, to evaluate the genome-wide genetic structure of breeding target traits of the released cultivars should be the number one task in the study of soybean germplasm. By means of linkage mapping and association mapping the elite genes and their alleles for traits related to yield, quality and tolerance to abiotic and biotic stresses in the released cultivar population were detected and evaluated. The results imply that for a better utilization of the elite germplasm, genes and alleles, the pyramiding technology of genes and alleles needs to be further studied since to pyramid individual major gene(s) with the help of marker-assisted selection is usual, but to pyramid a number of minor genes is rather difficult.

P3.31 - Analysis of genetic diversity and population structure of *Citrus* Germplasm using nuclear (SSRs, INDELS) and mitochondrial markers

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Previous studies with molecular markers (ISSR, RAPD, SCAR, AFLP and SSR) have shown that most of the genetic diversity of cultivated *Citrus* (except *C. aurantifolia*) comes from the recombination between three main species: *C. medica* (citron), *C. reticulata* (mandarin) and *C. maxima* (pummelo). However, the precise contribution of these basic species to the genome constitution of secondary species (*C. sinensis*, *C. limon*, *C. aurantium*, *C. paradisi*) and recent hybrids is not known. In this study, 58 nuclear and four mitochondrial markers were used to investigate the genetic diversity among 106 *Citrus* accessions, representing the three main ancestors groups, secondary species and several hybrids from the 20th century breeding programs. For the nuclear analysis, 50 simple sequence repeats (SSRs) developed from genomic libraries and ESTs databases were used. Moreover, 10 Insertion-Deletion (INDEL) markers were developed from genomic sequences of some primary and secondary metabolites determining the citrus fruit quality (sugars, acids, flavonoids and carotenoids). All the SSR markers and one INDEL are included in a consensus genetic map of clementine and pummelo Chandler and are distributed along the nine linkage groups, representing positively the global genome of *Citrus*. Genetic diversity statistics were calculated for each SSR and INDEL marker, within the entire population and within and between the different specified *Citrus* groups. The organizations of the genetic diversity among all the accessions were determined by constructing neighbor-joining trees for the different sets of primers. INDEL markers are less polymorphic than SSRs, display a higher organization of genetic diversity and appear to be better phylogenetic markers to trace the contribution of the three ancestral species. Population structure was studied using the Structure software, version 2.2.3, (<http://cbsuapps.tc.cornell.edu/structure>) which implements a model-based clustering method for inferring population structure using genotype data. The relative proportion of ancestral taxa genomes in the secondary species and recent hybrids was assigned. Mitochondrial markers revealed a maternal phylogeny of citrus germplasm accessions in agreement with previous studies with chloroplastic markers. This analysis allowed a better understanding of the genetic diversity organization among citrus cultivars, opening the way for a better management of citrus germplasm banks and breeding programs.