

GPGR3 – Session II, Plant Genome Diversity

Abstract

Genome Configuration and Breeding Strategies in Three Tropical Polyploid Crops

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Breeding polyploid crops induces a broad diversity of situations that generally require specific adaptations for each instance. Our work provides illustration of genomics-assisted breeding strategies for banana, sugarcane and groundnut.

The *Musa* genome has been sequenced recently, opening many new perspectives. Yet bananas are seedless triploids and recurrent selection has a limited efficiency. Recent work using molecular markers highlighted the probable genealogy that led to THE current leading variety worldwide, and guided priorities to recombining useful genes within ancestral fertile diploid populations prior to genome re-assembling. GISH has recently demonstrated effective interspecific pairing between chromosomes from the ancestral species involved in plantain.

Sequencing the *Saccharum* genome is most challenging. Analyses focussed on specific regions suggest a high conservation of gene content and structure among all homologs and homeologs and a close similarity to the reference genome of sorghum. Sugarcane diversity can be profusely reshuffled through large and easy-to-generate progenies. Chromosome pairing depends on the context. Recombination occurs between the genome of parental species. The early bottleneck that occurred with interspecific crosses a century ago created linkage disequilibrium that is highly valuable for genetic analysis using panels of modern cultivars, both for quantitative traits and for allele differentiation at major loci.

The *Arachis* genome sequence is still awaited. Recent years have seen population development from crosses between the cultivated allotetraploid groundnut and synthetic amphiploids. These are fertile inbreds produced from MA-introgression in order to derive chromosome segment substitution lines in an elite background, which reveal considerable, useful and genetically-resolvable, phenotypic variation.

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