W077

Investigating Chromosomal Structural Variations in *Musa acuminata* using NGS Approaches

Date: Tuesday, January 14, 2014
Time: 11:10 AM
Room: Pacific Salon 6-7 (2nd Floor)

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Structural heterozygosity is thought to be one of the main causes of sterility in banana (*Musa* spp.) hybrids. These structural variations impact chromosomal segregation and recombination, limiting crossing possibilities and complicating genetic analyses. It is thus important to better understand their nature and location in the genome.
For the production of the *Musa accuminata* reference genome sequence (D'Hont et al., Nature, 2012), we generated a genetic map that allowed anchoring 70% of the genome assembly on the 11 *Musa* chromosomes. The genetic map was based on a self progeny of the wild diploid *Musa acuminata* 'Pahang', the parent of the sequenced doubled haploid DH-Pahang. Strongly distorted markers were found on linkage group 1 and part of linkage group 4 that might indicate a structural rearrangement affecting these two linkage groups.
We have developed a bioinformatic pipeline to help characterize structural variation based on resequencing approaches. We are using this pipeline on resequencing data of DH-Pahang and its parent and are densifying the genetic map with DArTseq markers to better understand the causes of the strong markers distortions and their link with structural variation.

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Meeting Information

When:
January 10 - 15, 2014
Where:
San Diego, CA