January 9-13, 2016 San Diego, CA

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Meeting Information

When: January 08 - 13, 2016 Where: San Diego, CA

W075

One Hundred and Six Diploids to Unravel the Genetics of Traits in Banana: A Panel for Genome-Wide

Association Study and its Application to the Seedless Phenotype

Date: Tuesday, January 12, 2016

Time: 10:50 AM

Room: Pacific Salon 6-7 (2nd Floor)

Julie Sardos , Bioversity International, Montpellier, France Mathieu Rouard , Bioversity International, Montpellier, France Yann Hueber , Bioversity International, Montpellier, France Alberto Cenci , Bioversity International, Montpellier, France Katie Hyma , Genomic Diversity Facility, Cornell University, Ithaca, NY

Ines Van den houwe, Bioversity International Transit Center, Heverlee, Belgium Eva Hřibov , Institute of Experimental Botany, Prague, Czech Republic

Brigitte Courtois , CIRAD, Montpellier Cedex 5, France

Nicolas Roux, Bioversity International, Montpellier, France

Banana is a fruit crop with a complex diversity pattern resulting from a complex domestication scheme. Due to the availability of plant genome sequences and to the accessibility of next-generation genotyping technologies, Genome-Wide Association Studies (GWAS) have been increasingly performed in crop plants as a start to resolve genetic architecture of traits. The GWAS method was developed to perform association studies between phenotypes such as diseases and genotypes in Humans and is now successfully applied to many plants and animals to support the breeding process. However, there are prerequisites for such methods as it has been designed for populations of diploids organisms which follow the mendelian genetics model (i.e. "infinite" population and panmixia). In banana, the most popular cultivars are triploids, often hybrids between different species, and due to the absence of seeds in the fruit, a wide amount of the diversity observed ensues from the clonal diversification of a few initial genotypes. Therefore, the application of such approach to the crop is challenging and innovative. We selected a set of 106 diploid accessions with pure *M. acuminata* background avoiding clone duplicates and generated the appropriate molecular markers to support GWAS for any given trait. Finally, we validated the approach on the major domestication syndrome in banana, the seedless phenotype, and identified six candidate regions in which are located two strong candidate genes for female sterility.

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