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Using Genotyping-By-Sequencing to Understand *Musa* Diversity*Date: Monday, January 13, 2014**Room: Grand Exhibit Hall**Agnes P. Chan , J. Craig Venter Institute, Rockville, MD**Xavier Perrier , CIRAD, Montpellier, France**Julie Sardos , Bioversity International, Montpellier, France**Christophe Jenny , CIRAD, UMR AGAP, Montpellier, France**Jean-Pierre Jacquemoud-Collet , CIRAD, Montpellier, France**Nicolas Roux , Bioversity International, Montpellier, France***Christopher D. Town** , J. Craig Venter Institute, Rockville, MD

This project is part of a larger effort to apply genomics technologies to assess genetic diversity and to advance genetic improvement efforts in *Musa* (banana and plantain), a major staple food crop in the developing world. Most cultivated varieties of bananas result from intra- or inter-specific crosses of the wild diploid species, *Musa acuminata* (A genome) and *Musa balbisiana* (B genome). Somaclonal mutation and human selection has resulted in current day bananas with a wide morphological diversity. The Cavendish (AAA) subgroups are believed to have derived from an individual unique initial genotype, and similarly for the subgroup plantain (AAB). However, little or no genetic diversity can be detected within these groups using conventional molecular markers such as RFLP, SSR, DArT.

To assess genetic diversity with an improved resolution, we have selected 65 accessions with diploid and triploid combinations of the A and/or B genomes including AAB plantains and AAA Cavendish, and cultivated or wild *Musa* accessions from the core collection at the Global Musa Genomics Consortium (GMGC) (<http://www.musagenomics.org>). We have used a high-throughput reduced representation genome sequencing approach - genotyping-by-sequencing (GBS) to obtain high density sequence markers. Genotypes are determined for each diploid and triploid accession, and dissimilarity computed across all accessions. We will discuss the value of GBS markers to characterize the genetic diversity of individual *Musa* subgroups with high resolution.

This work is funded by the USAID linkage funds.

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Meeting Information**When:**

January 10 - 15, 2014

Where:

San Diego, CA