pairing irregularities in meiosis of inter-sub-specific hybrids suggested the presence of large chromosomal structural variations. Genetic linkage analysis in a self-progeny of in the *M. acuminata* ssp. *burmannicoides* 'Calcutta 4' accession and mate-pair sequencing were used to search for chromosomal rearrangements in comparison to the standard structure of the *M. acuminata* genome reference sequence (accession DH Pahang, ssp. *malaccensis)*. Two large reciprocal translocations were characterized in 'Calcutta 4' accession. One involved a 240 kb distal region of chromosome 2 and a 7.2 Mb distal region of chromosome 8. The other involved a 20.8 Mb distal region of chromosome 1 and a 11.6 Mb distal region of chromosome 9. Signature segment junctions of these translocations were searched in whole-genome sequencing data from 123 wild and cultivated *Musa* accessions. Both translocations were found only in wild accessions belonging to the *burmannica* genetic group suggesting that they originated in this genetic group. Only two of the 87 cultivars analyzed displayed the 2/8 translocation, while none displayed the 1/9 translocation. Chromosomes segregation was studied in a diploid population involving a structurally heterozygous parent for these translocations. In the case of the 1/9 translocation, the two chromosome structures were found to be mutually exclusive in gametes and the rearranged structures (1T9 and 9T1) were preferentially transmitted to the progeny. In the case of translocation 2/8, the two chromosome structures were also generally found to be mutually exclusive, although a few individuals with chromosomes 8 and 2T8 were observed, and the rearranged structures (2T8 and 8T2) were preferentially transmitted to the progeny. These results should help genetic analysis interpretation and breeding programs involving this disease resistance-rich *burmannica* group.

## W098: Banana Genomics

### *In-vitro* Activation of Retro-Transposable Elements as an Effective Mode of mutagenesis in Musa

**Eli Khayat**, Rahan Meristem (1998) LTD, Goleta, CA

The majority of triploid banana and plantains are sterile and contain a stagnant genome, while microbial pathogens evolve rapidly. Recently we have shown that by demethylation of specific loci in the chromatin it is possible to diversify banana genomes and modify important characteristics. Using the demethylation compounds 5-Aza-2′-deoxycytidine it is possible to control DNA methylation of plant meristems. This induces activation of retro-transposable elements (RE) and generation of new genotypes. Given the new insertions of the RE the mutations remain stable for many generations. Employing this technique, we have mutated GAL cultivar and tested the plants for resistance/tolerance to TR4. From a population of 9640 in vitro-mutated plants that have been inoculated with TR4, we selected 514 lines that were asymptomatic. These were evaluated in a field trial in an infected area in the Philippines. An analysis of the mutated genotypes demonstrated sensitivity of particular chromatin regions to the demethylation. We have targeted and selected genotypes with TR4 resistance, altered plant stature and early flowering We analyzed the polymorphic regions following demethylation. An entire genome sequence analysis comparison between the resistant genotype and its precursor mother clone revealed changes in various parts of the genome including a QTL of clustered "R-genes" but not in the coding sequences.

## W099: Banana Genomics

### The Complex Story of Intergenomic Recombination in ABB Allotriploid Bananas

Alberto Cenci[1], Julie Sardos[1], Guillaume Martin[2], Catherine Breton[1], Nicolas Roux[1], Rony Swennen[3], Sebastien Carpentier[4] and **Mathieu Rouard**[1], (1)Bioversity International, Montpellier, France, (2)CIRAD, Montpellier, France, (3)KU Leuven, Leuven, Belgium, (4)Bioversity International, Leuven, Belgium

Bananas (*Musa* spp.) are a major staple food for hundreds of millions of people in developing countries. The cultivated varieties are seedless and parthenocarpic clones of which the ancestral origin remains to be clarified. The most important cultivars are triploids with an AAA, AAB, or ABB genome constitution, with A and B genomes provided by *M. acuminata* and *M. balbisiana*, respectively. Previous studies suggested that inter-genome recombinations were relatively common in banana cultivars and that triploids were more likely to have passed through an intermediate hybrid. In this study, we investigated the chromosome structure within the ABB group, composed of starchy cooking bananas that play an important role in food security. Using SNP markers called from RAD-Seq data, we studied the chromosome structure of 36 ABB genotypes spanning defined taxonomic subgroups. To complement our understanding, we search for similar events within nine AB hybrid genotypes.Recurrent Homoeologous Exchanges (HEs), i.e. chromatin exchanges between A and B subgenomes were unraveled with at least 9 founding events at the origin of the ABB bananas prior to the clonal diversification. The discovery of this

nine founding events allows discussing the possible routes that led to the creation of the different subgroups and formulate new hypotheses. Based on our observations, we suggest different routes that gave rise to the current diversity in the ABB cultivars. Routes involving primary AB hybrids, routes leading to shared HEs and routes leading to a B excess ratio. Genetic fluxes took place between *M. acuminata* and *M. balbisiana*, particularly in India, where these unbalanced AB hybrids and ABB allotriploid originated and where cultivated *M. balbisiana* are abundant. The result of this study clarifies the classification of ABB cultivars and leading possibly to the revision of the classification of this subgroup. This is an important step to unravel the origin of polyploid bananas, and contributes to possible scenarios on the origin. ABB bananas are hypothesized to be more drought tolerant. Knowing the origin of our current cultivars and so their potential parents will help breeders to make the right choices for future crosses. The *M. balbisiana* genome is a good source to create new cultivars able to answer the numerous challenges of banana breeding.

## W100: Banana Genomics

### New Insight for Banana Resistance to *Xanthomonas vasicola* pv. m*usacearum*

**Valentine Nakato**, International Institute of Tropical Agriculture,, Kampala, Uganda

Xanthomonas wilt caused by *Xanthomonas vasicola* pv. *musacearum* (Xvm) is one of the most devastating disease of banana in East and Central Africa. All banana varieties, except the wild *Musa balbisiana*, were reported susceptible to Xvm. However, *M. balbisiana* is not ideal for breeding since it has the B genome (BB subgroup), while most edible banana have the A genome. To further confirm whether all banana varieties were susceptible to Xvm, we evaluated a broader range of banana varieties, that represented the entire genetic diversity of banana. 72 banana accessions were artificially inoculated with a virulent Xvm isolate. *M. balbisiana* was confirmed as resistant. We further identified Monyet, Zebrina, Saba, Buitenzorg, Tani, IC2, Pelipita, Kikundi, Cameroun, P. Raja and Maia Oa as potential sources of resistance to Xvm. This finding unlocks doors for using genetic resistance to manage Xvm and contribute to food security for millions of smallholder banana farmers in the region who are dependent on the crop for livelihoods. We are in the process of elucidating the genetics of resistance and development of markers to expedite transfer of resistance to susceptible but preferred east African highland bananas.

## W101: BER Plant Genomic Science

### Introduction and Overview of KBase and Joint Genome Institute Plant Program

**Robert W. Cottingham**, Oak Ridge National Laboratory, Oak Ridge, TN and Jeremy Schmutz, HudsonAlpha Institute for Biotechnology, Huntsville, AL

The Department of Energy Biological and Environmental Research (DOE-BER, www.energy.gov/science/ber) program supports research and facilities to achieve a predictive understanding of complex biological, earth, and environmental systems with the aim of advancing the nation's energy and infrastructure security. The program seeks to discover the underlying biology of plants and microbes as they respond to and modify their environments. This knowledge enables the reengineering of microbes and plants for energy and other applications. BER research also advances understanding of the dynamic processes needed to model the Earth system, including atmospheric, land masses, ocean, sea ice, and subsurface processes.

BER funds both a large scale user facility for plant genomics at the DOE Joint Genome Institute (www.JGI.doe.gov), and an open and collaborative computational resource for predictive systems biology of microbes, plants and their communities called the DOE Systems Biology Knowledgebase (www.KBase.us). Both endeavor to help scientists conduct experiments and analyses in areas such as improving biofuel development, understanding plant model systems, advancing plant comparative science and investigating global carbon cycling. In this annual workshop, speakers present current and ongoing developments in their research enabled by JGI and KBase toward Increasingly large-scale and integrative biology relevant to DOE-BER mission. We will also give a brief introduction describing how to apply for access to the JGI Community Science Program, and how you can use KBase to accelerate your plant genomics research.