

9- Characterization of large chromosomal structural variations between *Musa acuminata* sub-species by NGS re-sequencing.

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Bananas are Monocotyledons from the Zingiberales order and Musaceae family originating from south East-Asia. *Musa acuminata* (A genome, $2n = 2x = 22$, $1C = 500-600$ Mbp) and *M. balbisiana* (B genome, $2n = 2x = 22$, $1C = 550$ Mbp) are the two main *Musa* species involved in cultivated bananas.

M. acuminata has evolved in several sub-species that have been geographically isolated on various archipelagos, and have accumulated large structural variations. Domestication of banana involving hybridization between these subspecies has been made possible by human migration and selection of diploid and triploid inter-sub-specific hybrids with seedless parthenocarpic fruits. Large structural variations within *M. acuminata* have been hypothesized based on chromosome pairing analysis and genetic mapping. These structural variations are suspected to be at least partially responsible for *M. acuminata* hybrids sterility. This sterility allows the production of seedless fruits but complicates breeding programs by limiting crossing possibilities. These structural variations also impact chromosomal segregation and recombination, complicating the transmission of agronomical traits of interest and genetic analyses. There is thus a strong need to characterize these structural variations within the *Musa acuminata* sub-species. A re-sequencing approach to characterize these structural variations is currently being tested. It is based on paired-end sequencing of genomic fragments of known sizes from banana accessions, and comparison to the *Musa acuminata* reference genome to detect discrepancies in paired-read mapping. A specific bioinformatics pipeline has been developed to detect different types of structural variations, and validated on simulated data. The pipeline is currently being tested on diploid banana accessions using various DNA fragment sizes (5kb to 15kb) in order to optimize the detection of large structural variations.