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W46 : Banana (Musa) Genomics

### Musa Genetic Mapping

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We report a reference map of *Musa acuminata* from 180 individuals of BORLI population. This F1 population derived from the cross between M.a. 'Borneo' x M.a. 'Pisang Lilin' which was chosen for mapping mainly because of the great heterozygosity of both parents (76 % each). For map construction we genotyped 180 SSR markers on 180 individuals, 12 RGA-RFLP probes on 112 individuals and 380 DArT markers on 92 individuals. Using the software Joinmap 4 at LOD 5, Kosambi calculation distance and the regression mapping algorithm, we defined 11 main linkage groups, as expected, on Borneo parent and 10 on Pisang lilin due to one translocation event in the male parent. Despite structural differences between the parents, a consensus map was built. In order to check genotyping results and to analyse structural rearrangements, we developed an original method using Neighbor Joining algorithm implemented in the genetic diversity software Darwin5. It allows visualizing graphically disruptions in alignments arising from these structural rearrangements.