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Insights Into The Genome Of Musa (Banana), A Giant Herb Bearing Fleshy Fruits

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Musa species, comprising dessert and cooking bananas, represent the fourth most important crop in developing countries. They are monocotyledons of the Musa species, comprising dessert and cooking bananas, represent the fourth most important crop in developing countries. They are monocotyledons of the Zingiberales order and the Musaceae family. We have compared genomic sequence in two Musa species with orthologous regions in the rice genome. We produced 1.4 Mb of Musa sequence from 13 BAC clones, annotated and analyzed them along with 4 previously sequenced BACs. The 443 predicted genes revealed that Zingiberales genes share GC content and distribution characteristics with eudicot and Poaceae genomes. Comparison with rice revealed microsynteny regions that have persisted since the divergence of the Commelinid orders Poales and Zingiberales at least 117 Mya. The previously hypothesized large-scale duplication event in the common ancestor of major cereal lineages within the Poaceae was verified. The divergence time distributions for Musa-Zingiber (Zingiberaceae, Zingiberales) orthologs and paralogs provide strong

evidence for a large-scale duplication event in the *Musa* lineage after its divergence from the Zingiberaceae approximately 61 Mya. Comparisons of genomic regions from *M. acuminata* and *M. balbisiana* revealed highly conserved genome structure, and indicated that these genomes diverged circa 4.6 Mya. Further sequencing efforts should be focused first on the A genome of *M. acuminata*, which has a major contribution to banana and plantain diversity. This will enable:

- alignment of the *Musa* genome in relation to major grasses, including rice and sorghum
- phylogenomic analysis of gene families and metabolic pathways among monocots
- use as a template for positional cloning of genes of agricultural interest
- use as a support to develop genomic tools for whole-genome expression analysis
- use as a template for re-sequencing and deep diversity analysis in the *Musa* gene pool.