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W075: Banana (Musa) Genomics

MusaTract: Sequencing Of The Banana (Musa acuminata) Whole Genome

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Genoscope (French National Sequencing Center) and the CIRAD are engaged in the complete sequencing of the banana genome in the framework of the Global Musa Genomics Consortium. The banana accession chosen is a doubled haploid (Musa acuminata, subspecies malaccensis, accession Pahang DH). M acuminata represents the main species that enters into the composition of dessert and cooking bananas; its genome consists of 500 to 600 million base pairs, depending of the subspecies, spread over 11 different chromosomes. The sequencing strategy is a mixed approach combining the Sanger, 454 and Solexa technologies. A high-density map is currently being developed for scaffold anchoring. The sequencing phase will be completed in early 2010 and automatic annotation will take place during the first semester of 2010. An update on the progress will be presented.

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