



Press release

Banana genome is sequenced.

Cirad and Genoscope have just achieved the complete sequencing of the banana genome, with the financial support of the ANR. The results are published online today, Wednesday, July 11th 2012 in the prestigious scientific magazine *Nature*. This constitutes a major scientific progress in the understanding of the genetics and breeding of this species. This is as well a major achievement for the Global Musa Genomics Consortium, whose teams collaborated in the data mining.

After 10 years of efforts, banana now delivers to geneticists the deciphered secrets encompassed in its 520 million bases. A wild banana of the *Musa acuminata* species has been sequenced. Every edible banana, either dessert bananas or cooked bananas, has been derived from this species.

A major breakthrough to help improve varieties.

Banana is unavoidable in food supply and economic activity for over 400 million people living in developing countries; meanwhile, banana plants undergo permanent threats from pathogens. This stress is especially important in plantations which produce the « exported » bananas that are displayed in our supermarkets. The creation of new varieties exhibiting better resistances is a real need, even if the very low level of fertility among cultivated banana plants makes breeding quite sophisticated.

The sequence is from now on fully available and will allow accessing the full set of genes –over 36,000- which have been identified and located accurately along the eleven chromosomes. This knowledge will greatly help identify genes which govern traits like resistance to pathogens and fruit quality. These data will finally provide an efficient tool to improve banana varieties by using the large panel of genetic resources available worldwide.

A new insight on the evolution of the genome.

Banana is the first plant among the monocots, aside from the cereals, for which a genome sequence fully anchored on chromosomes has been gained. This sequence constitutes a high value reference to study the evolution of the genomes. Scientists have indeed already found that banana underwent three steps of whole-genome duplications, independently from the duplications which took place within the gramineae lineage. While most genes brought on by these rounds of duplication are subsequently lost, some do persist and lead to the emergence of new biological functions. A set of regulation factors (transcription factors) peculiarly abundant in banana have been already identified, and govern key processes like the fruit maturation.

The sequence of the banana genome with the gene annotation and complementary information are freely accessible on the website <http://banana-genome.cirad.fr>.

Link to the publication in Nature:

‘The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants’
10.1038/nature11241. Advance Online Publication (AOP) on <http://www.nature.com/nature>

