



AGROPOLIS  
LES DOSSIERS

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Genetic  
resources  
*Genomics*  
Plant  
biotechnology



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# Genomics applied *to agronomic* traits

*Genetic improvement is founded on better understanding of the characteristics and functioning of individual plants and on a finer perception of the diversity present in the genetic resources of the cultivated species. The various technologies of genomics should make a major contribution to the characterization of genes and their functions.*

## Team and co-ordinator

The "Genomics applied to agronomic traits" research group (UMR GACA) comprises 13 researchers from Agro.M, Cirad and INRA.

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**G**enomics offers various ways of acquiring knowledge on cultivated plants and of improving them:

- molecular physiology, which uses functional genomics to identify agronomically valuable traits,
  - genetic mixing, which enables the creation of new varieties based on better genome mapping of factors that govern the agronomic characteristics.
- Genomics is applied to:
- general agronomic characteristics, which can be studied in model plants such as rice (model plant for monocotyledons),
  - specific agronomic traits, which should be studied in the different species of agronomic value, as done for twenty or so Mediterranean and tropical plants.

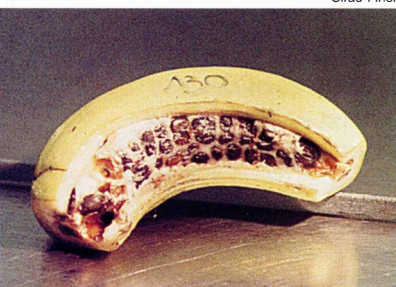
Genomics is based on recent progress in molecular biology, which has led

to the development of a whole range of new methods and improved precision of existing methods.

## Mapping and sequencing of genomes

• **Genetic mapping** uses labelling with molecular markers to map the genetic factors responsible for certain agronomic traits of interest (such as resistance to disease or a criterion of the technological quality of the plant). Offspring are generated by controlled crosses and then analyzed, using molecular markers and agronomic assessment in the field. This molecular characterization yields a detailed genetic map of the genome of the species. Fine mapping, based on the analysis of more offspring then locates these genetic factors precisely enough to allow physical mapping.

Cirad-Filhor



*Wild banana with seeds to improve crop varieties*

## A BAC library for the study of the structure of banana plant chromosomes

The banana is a giant herbaceous plant that may grow to between 1.5 and 8 metres in height. The fruit of cultivated banana (cultivars) are the only ones to be eaten.

They are seedless, whereas the fruits of wild banana plants contain

seeds about 5 mm in diameter. The cultivars are divided into two subgroups: sweet bananas (or dessert bananas) and cooking bananas, among which plantains are the most important.

The cultivars, of interspecific origin, are classified according to their ploidy level (number of chromosomes) and the relative contribution of the species *Musa acuminata* (genome A) and *Musa balbisiana* (genome B) to the characteristics of the clone considered. All the wild *acuminata* and *balbisiana*

forms are diploid,  $2n=2x=22$ . There are six main genomic groups: AA, AAA, AB, AAB, ABB, ABBB. In addition to the contribution (different proportions) of genomes A and B, there are also translocations, exchanges and inversions in each of the two genomes, although their frequency is unknown. The availability of large fragments of DNA combined with in situ hybridization to chromosomes (FISH, Fluorescent In Situ Hybridization) should lead to characterization of variations in genome structure in the banana plant. A BAC (Bacterial Artificial Chromosome) library constructed from the cultivar Calcutta 4 (AA) is used for this purpose. This research will clarify the relative structure of banana cultivars and the impact of translocations on their diversity, and open up new ways to improvement.

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