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CIRAD's goal was to streamline the banana breeding process. This project is being carried out within the framework of the Global *Musa* Genomic Consortium coordinated by Biodiversity International under the PROMUSA programme.

The research was aimed at identifying and characterizing translocations in banana so as to enhance genetic analyses and gain insight into the hereditary factors controlling target traits.

Plant material studied

Two banana cultivars were studied:

• **The Calcutta 4 clone *(Musa acuminata burmannicoides)*:** diploid (2n=2x=22) belonging to the North-A translocation group, structurally homozygous (no structural difference between homologous chromosomes), differing from the Central group by two translocations. Banana varieties were classified in different groups according to the chromosome pairing pattern observed during meiosis in hybrids. The absence of translocation or the presence of one to two translocations was typical in these groups.

• **The Madang clone (*Musa acuminata banksii*)**: diploid (2n=2x=22), structurally homozygous, belonging to the Central translocation group, i.e. the control group without any translocations.

Project goals

The project was aimed at developing tools to map translocations in banana and applying these tools to map translocations in order to differentiate Calcutta 4 and Madang clones.

Different technologies had to be developed and/or adapted to be able to meet these objectives, mainly:
• the construction of a library of large banana DNA fragments or a bacterial artificial chromosome (BAC) library;
• the development of cytogenetic mapping via *in situ* fluorescent hybridization of BAC clones for translocation mapping.

The project was also based on a genetic map constructed at CIRAD from an F2 population (second generation obtained by selfing) derived from a cross [Calcutta 4 x Madang] between two fertile and highly homozygotic varieties.

Banana

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▶ *Bunches of cv. Bluggoe (cooking) bananas that are triploid and interspecific* (M. acuminata/M. balbisiana)

Bananas are currently cropped in around 100 tropical and subtropical countries (India Uganda, Ecuador and Brazil are top producing countries). Banana is a food product (a low-fat nutritious edible fruit with a high sugar, potassium, vitamin A, B6 and C content) which produces fibres that are used industrially (paper, cardboard, rope) and generates considerable income due to the low production expenditures. Banana cropping consolidates the economy in European overseas regions (Guadeloupe, Martinique) where exports of bananas (over 80% cv. Cavendish) generate substantial income.

Bananas belong to the Musaceae family. They are high monocotyledon herbaceous plants that are monocarpic (only flower once) and the pseudostem is formed by the coiling of leaf sheaths around each other, with an edible flower (bunch) emerging from the centre. Banana breeding programmes have been set up to create new varieties, especially lines that are resistant to the many pest infestations affecting this fruit. Genetic variations concern the plant size, sucker vigour, number of hands per bunch, fruit size and sources of resistance to the main pests and diseases. Problems associated with typical characteristics of cultivated bananas must be overcome through the different breeding phases, i.e. sterility, triploidy (threefold more chromosomes than in common plants of close species) and the multispecific origin.

In banana, fertility has been counterselected by breeders for generations in order to obtain seedless and very pulpy edible fruits. Cultivated bananas are parthenocarpic (bulkier fruits develop without fertilized ovules or their transformation into embryonic seeds) and preserved cultivars therefore have to be vegetatively propagated from suckers. Cultivars are di-, tri- (the most numerous as they are the hardiest) or tetraploid and their genomes differ (denoted A and/or B). Most cultivars derive from haploid (11 chromosomes) wild species, i.e. *Musa balbisiana* (one B genome) and *Musa acuminata* (one A genome).

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