Acuminata genome

The **acuminata genome**, designated by the letter A in the nomenclature system used to classify edible bananas, is the genome of *Musa acuminata*, a species of wild bananas that has been involved in the domestication of the vast majority of edible bananas. It is also the first genome to be sequenced in the genus *Musa*. The sequenced genome was an haploid version of the subspecies *malaccensis*, DH Pahang. At the time of the release of the genome sequence, 91% of the genome had been sequenced and 92% of the predicted 36,542 genes had been positioned on the 11 chromosomes[1].

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### Genome size

The haploid genome size is 600 Mb[2]. It is larger than the genome of *Musa balbisiana*, which donated the B genome found in many edible bananas. The genome is larger than the genome of rice and Arabidopsis but smaller than the one of maize and wheat.

### Genome composition

Plant genomes consists largely of repetitive DNA including include transposable elements, satellite DNAs, simple sequences and tandem repeats which represents approximately 30% of the A genome[3]. These genome features might be responsible for the variation in genome size observed in *Musa* species.

### Comparison with B genome

Depending on the study, the A and B genomes have diverged 4.6[4] or 27.9 million years ago[5].

In 2013, a team of Belgian and Malaysian scientists sequenced the genome of a *Musa balbisiana* accession and used the *acuminata* reference sequence as a template onto which they aligned their fragments of *balbisiana* DNA. The resulting B genome was 79% the size of the A genome. The number of genes was predicted to be 36,638[6].
References

1. The banana (Musa acuminata) genome and the evolution of monocotyledonous plants in the 9 August 2012 issue of Nature.

Further reading


Also on this website

First glimpse at the banana genome in News and analysis (11 July 2012).
A tale of two banana sequences in the ProMusa blog (7 November 2013).

External Links

The Global Musa Genomics Consortium

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