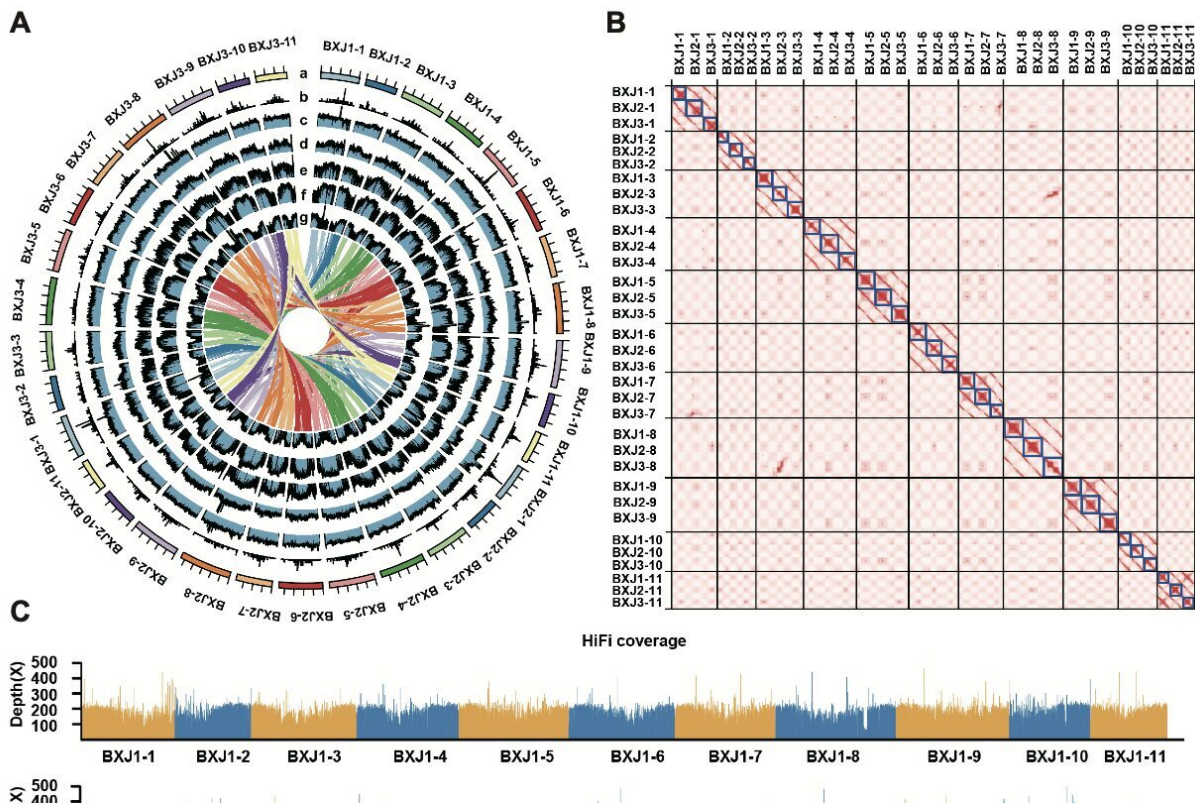


The first telomere-to-telomere haplotype-resolved reference genome of triploid banana

August 28 2023



Overview of the Cavendish reference genome. Credit: *Horticulture Research*

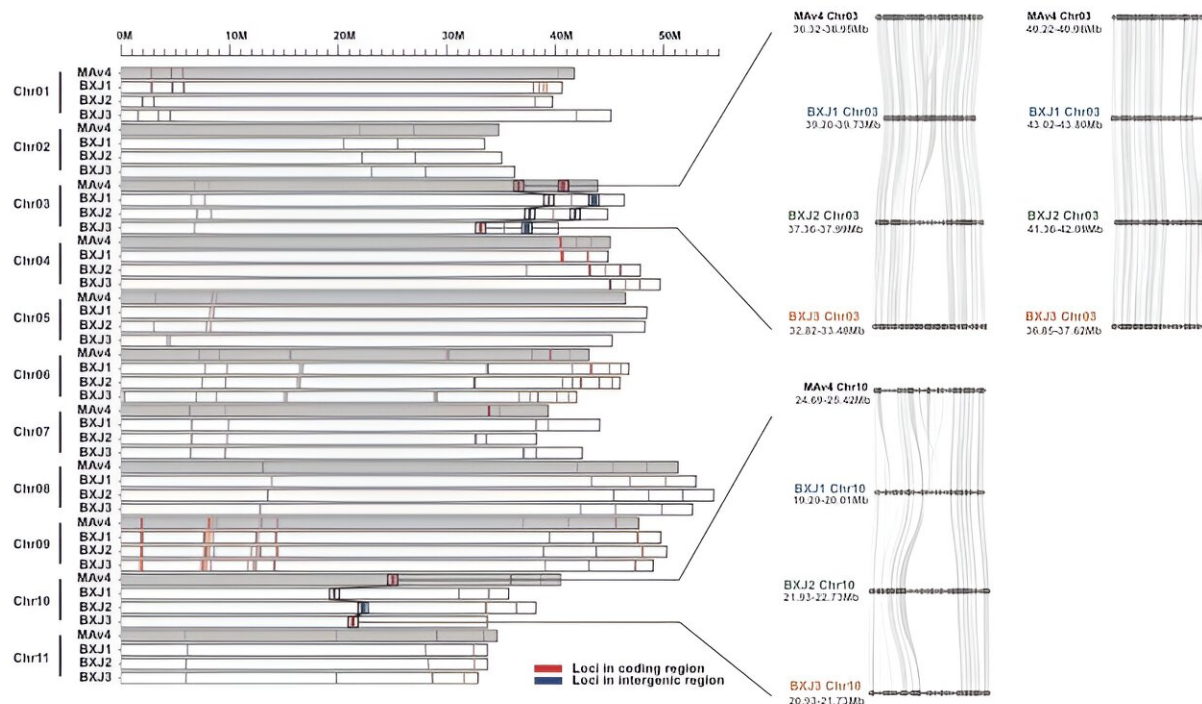
Banana is one of the most important crops of the world. The demand for cultivated bananas continues to grow; however, their production is greatly affected by a complex of biotic and abiotic stresses. For instance,

banana yields are severely threatened by the disease fusarium wilt, which is caused by the fungus *Fusarium oxysporum* f. sp. *cubense*.

Therefore, breeding new banana cultivars with improved traits, particularly [genetic resistance](#) to a wide and diverse group of pathogens, is crucial for future banana production; and a high-quality banana genome would no doubt facilitate such genetic manipulation.

Cavendish-type bananas, which have a monospecific *Musa acuminata* origin (AAA), account for around half of the global banana production, thereby are of great significance for human societies. However, until now, the high-quality haplotype-resolved reference genome was still undecoded for banana cultivars. In this study, the telomere-to-telomere (T2T) and haplotype-resolved reference genome of 'Baxijiao' (Cavendish) was reported.

This reference genome consists of three haploid assemblies, the sizes of which were estimated to be 477.16 Mb, 477.18 Mb, and 469.57 Mb, respectively. Genome quality assessments confirmed the contiguity (LAI: 19.84, 20.65 and 20.22) and completeness (BUSCOs: 97.40%, 97.80% and 93.80%) of the genome. Within the three haploid assemblies, 19, 17 and 17 telomeres were identified, respectively. In terms of repetitive regions, 256.48 Mb (53.76%), 258.29 Mb (54.14%), and 258.84 Mb (55.13%) were identified.



The distribution of NLR loci in *Musa acuminata* (MAv4) and 'Baxijiao' genomes. Credit: *Horticulture Research*

In addition, a total of 37,185, 37,241, and 37,178 high-confidence protein-coding genes were predicted from each assembly. Although with monospecific origins, the three haploid assemblies showed great differences with low levels of sequence collinearity. Several large reciprocal translocations were identified among chromosomes 1, 4 and 7.

An expansion of gene families that might affect fruit quality and aroma was detected, such as those belonging to sucrose/disaccharide/oligosaccharide catabolic processes, sucrose

metabolic process, starch metabolic process, and aromatic compound biosynthetic process. Besides, an expansion of gene families related to anther and pollen development was observed, which could be associated with parthenocarpy and sterility of the Cavendish cultivar.

Finally, much fewer resistance genes were identified in 'Baxijiao' than in *M. acuminata*, particularly in the gene clusters in chromosomes 3 and 10, providing potential targets to explore for molecular analysis of [disease resistance](#) in banana. This T2T haplotype-resolved reference genome will thus be a valuable genetic resource for biological studies, molecular breeding and genetic improvement of banana.

The article "Telomere-to-telomere haplotype-resolved reference [genome](#) reveals subgenome divergence and disease resistance in triploid Cavendish banana" has been published in *Horticulture Research*.

More information: Hui-Run Huang et al, Telomere-to-telomere haplotype-resolved reference genome reveals subgenome divergence and disease resistance in triploid Cavendish banana, *Horticulture Research* (2023). [DOI: 10.1093/hr/uhad153](https://doi.org/10.1093/hr/uhad153)

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