



Tracking Progress in Musaceae Genomics with the Banana Genome Hub

Mathieu Rouard
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The Banana Genome Hub

Banana Genome Hub

Home

Genomes

JBrowse

Search

Download

About

Partners



Available Tools



Synteny viewer

Retrieve all syntenic blocks and genes for your [more](#)



Gene search

Search for a gene by name, location, functional [more](#)

```
TGACTCCAT
TGACGCCAT
TGACTCCCT
TGACGCCCT
```

Gigwa

Grow is a web-based tool for the exploration of [I more](#)



Locus Version Converter

This tool allows to convert locus tags names be [more](#)

[See all tools](#)

<https://banana-genome-hub.southgreen.fr/>

Horticulture
Research

Horticulture Research, 2022, 9: uhac21

<https://doi.org/10.1093/hr/uhac21>

Article

The banana genome hub: a community database for genomics in the Musaceae

Gaëtan Droz^{1,2,3,4}, Guillaume Martin^{2,3}, Valentin Caignot^{2,3}, Mathyline Samson^{2,3}, Guilhem Sempere^{5,6,7}, Eloi Duran^{2,3,4}, Alexandre Soriano^{2,3,4}, Franck Christophe Boureau^{2,3}, Alberts Caste^{2,3}, Catherine Bouteux^{2,3}, Thibault Shah², Jean-Marc Aury², Xue-Jun Gu^{2,3,7}, Hai-Hong Hu^{2,3,7}, Nabila Yahiaoui², Angélique D'Honn² and Mathieu Rouzet^{4,8}*

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Abstract

The Banana Genome Hub provides centralized access for genome assemblies, annotations, and the extensive related omics resources available for bananas and banana relatives. A series of tools and unique interfaces are implemented to harness the potential of genomics in bananas, leveraging the power of comparative analysis, while recognizing the differences between datasets. Besides effective genomic tools like BLAST and the JBrowse genome browser, additional interfaces enable advanced gene search and gene family analyses including multiple alignments and phylogenies. A synteny viewer enables the comparison of genome structures between chromosome-scale assemblies. Interfaces for differential expression analyses, metabolic pathways and GO enrichment were also added. A catalogue of variants across the banana diversity is made available for exploration, filtering and export to a wide variety of software. Furthermore, we implemented new ways to graphically explore gene presence-absence in pan-genomes as well as genome ancestry mosaics for cultivated bananas. Besides, to guide the community in future sequencing efforts, we provide recommendations for nomenclature of locus tags and a curated list of public genome resources (assemblies, resequencing, high density genotyping and upcoming resources – planned, ongoing or not yet public). The Banana Genome Hub aims at supporting the banana scientific community for basic, translational, and applied research and can be accessed at <https://banana-genome-hub.southgreen.fr>.

Introduction

The Musaceae, known as the banana family, belongs to the monocotyledons that comprise crops of great economic value as well as ornamental plants. Notably, Musaceae includes the genus *Musa* with bananas, a top ten crop for food security, and arguably the favorite fruit worldwide [1]. Its sister genus, *Ensete*, contains *Ensete ventricosum*, an important crop for food security in Ethiopia [2] and ornamental plants like *Ensete glaucum* widely distributed in Asia. The final monospecific genus in Musaceae includes *Musaella lasiocarpa* from southwest China and possibly extinct in the wild. Wild species within Musaceae are diploids, with basic chromosome numbers of $x=9$, 10 and 11. The *Musa* cultivars grown for fruit result from hybridization between different wild diploid *Musa* species and subspecies. They are parthenocarpic, sterile or poorly fertile and mostly cultivated as vegetatively propagated

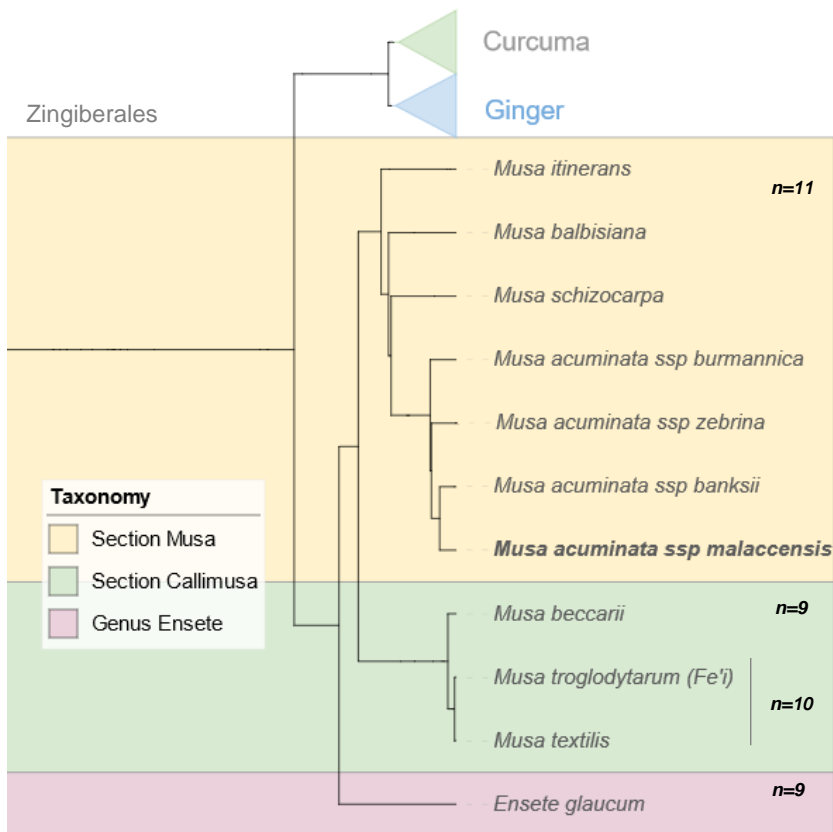
tetraploids ($2n=3x=36$) although some cultivars are diploids or tetraploids, most of cultivars bear large structural variations in their chromosomes, transmitted from different wild ancestors. All these features make banana breeding very complex. Genomic characterization has a great potential to significantly contribute to better conservation strategies, improved use of banana genetic resources and increased sustainability of crop production [3, 4], increasing the availability of genomic resources and facilitating their use has been much needed [5, 6].

In 2012, the first Musaceae reference genome, representative of *Musa acuminata* (A genome), was published [7] alongside the Banana Genome Hub [8] (<https://banana-genome-hub.southgreen.fr>). In the last decade, this reference was iteratively improved [9, 10] while a number of new genome assemblies of different Musaceae species have also been generated. The next

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Recently released genomes



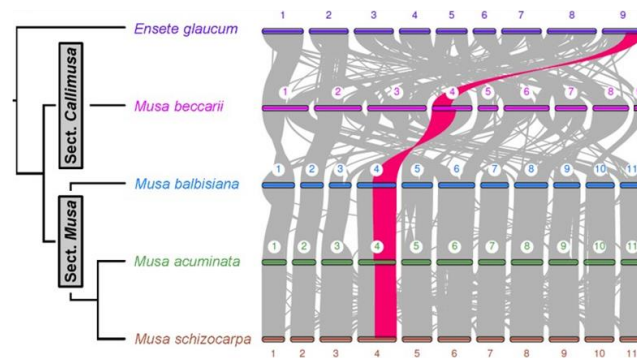
The *Musa troglodytarum* L. genome provides insights into the mechanism of non-climacteric behaviour and enrichment of carotenoids.

Li, Z., Wang, J., Fu, Y. et al. BMC Biol 20, 186 (2022).



Genome assembly of *Musa beccarii* shows extensive chromosomal rearrangements and genome expansion during evolution of Musaceae genomes

Zheng-Feng Wang, Mathieu Rouard; Gaetan Droc, Pat (J.S.) Heslop-Harrison, Xue-Jun Ge (accepted)



JOURNAL ARTICLE

A chromosome-level reference genome of *Ensete glaucum* gives insight into diversity and chromosomal and repetitive sequence evolution in the Musaceae

Ziwei Wang, Mathieu Rouard, Manosh Kumar Biswas, Gaetan Droc, Dongli Cui, Nicolas Roux, Franc-Christophe Baurens, Xue-Jun Ge, Trude Schwarzhacher, Pat (J S) Heslop-Harrison ... Show more

BGH tools



Locus Converter

This tool allows to convert locus tags names between version of the genome assemblies. It supports conversion between v1 and v2 of the DH-Pahang assembly. You can search either by legacy identifiers (SMTUA_Achr3G27160_001) or by RefSeq identifiers (gene708).



Mosaics

Visualize and explore chromosome structure paint with ancestral/parental origins

```
TGACTCCAT
TGACGCCAT
TGACTCCCT
TGACGCCCT
```

Gigwa

Gigwa is a web-based tool for the exploration of large amounts of genotyping data.



Panache

Explore pangenome blocks using Panache



Synteny viewer

Retrieve all syntenic blocks and genes for your regions of interest



Gene search

Search for a gene by name, location, functional annotation keywords...



RNA-Seq count display

Look at gene expression (DEG)



GO enrichment

Perform GO enrichment on list of genes



Primer Blaster

This tool was designed to test the specificity of any primer pair on the musa genome by using BLAST. Make sure primers have the same id in both cases. As a result, a table displays all tested primers with primer name and positions, location on chromosome, amplicon size and number of hits on the musa genome. If the primer pair is really specific, this status is clearly marked as 'ok' in the table.



Primer Designer

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MusaCyc

Look at metabolic pathways



JBrowse

Visualize data using an interactive genome browser.



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RNA-Seq data analysis using Diane

Analyse your own transcriptomics data

Explore banana genomes with Synvisio



- Custom genome comparison 2x2 or global
- Filtering options by chromosomes
- Synteny colored scheme or orientation



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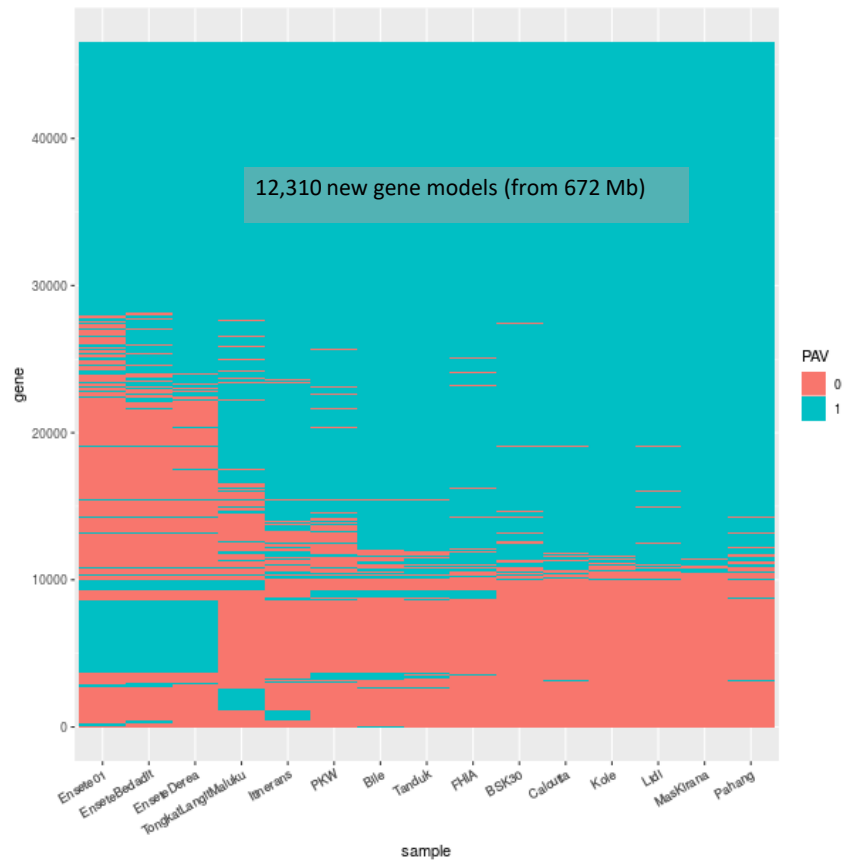
The pangenome of banana highlights differences between genera and genomes

Habib Rijzaani, Philipp E. Bayer, Mathieu Rouard, Jaroslav Doležel, Jacqueline Batley, David Edwards

First published: 05 July 2021 | <https://doi.org/10.1002/tpg2.20100> | Citations: 6

Core Ideas

- We assembled the first banana pangenome across two genera.
- The two genera exhibit high levels of divergence.
- The banana pangenome contains very few novel disease resistance genes.



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Panache: Pangenomics-related interface

- Pan chromosomes comparison
- Track sorting by genes, phylogeny...
- Automatic PAV detection
- Core/dispensable ration threshold



A digital catalog of high-density markers for banana germplasm collections

Mathieu Rouard¹ | Julie Sardos¹ | Guilhem Sempéré^{2,3} | Catherine Breton¹ | Valentin Guignon⁴ | Ines Van den Houwe⁴ | Sebastien C. Carpentier^{4,5} | Nicolas Roux¹

¹Biodiversity International, Parc Scientifique Agropolis II, Montpellier, France

²CIRAD, UMR INTERTRYP, Montpellier, France

³INTERTRYP, Univ Montpellier, CIRAD, Montpellier, France

⁴Biodiversity International, Leuven, Belgium

⁵Laboratory of Tropical Crop Improvement, Division of Crop Biotechnics, Leuven, Belgium

Correspondence

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Societal Impact Statement

Global production of bananas, among the top 10 food crops worldwide, is under threat. Increasing the use of germplasm conserved in genebanks is crucial. However, the lack of or difficult access to genetic diversity information limits the efficient utilization of these valuable resources. Here, we present a digital catalog of high-density markers for banana germplasm conserved at the international banana collection. By facilitating access to subsets of genetic diversity information, the catalog has potential to maximize conservation and use of climate-ready varieties and to optimize breeding strategies. The catalog is extendable with data from any banana collection and the software is easily deployable in other crop genebanks.

KEYWORDS

banana, data management, digital genebank, high-density markers, plant conservation

1 | INTRODUCTION

Crop plant diversity managed by genebanks is of great value in the context of the changing needs of agriculture (Smale & Juma, 2020), but genetic and phenotypic information on this diversity is insufficiently available for most genebanks (McCouch et al., 2013, 2020). The advent of Next Generation Sequencing has enabled—at an ever-decreasing cost—the sequencing of reference genomes of many crops as well as high-density genotyping for large numbers of samples per crop. Genotyping is a powerful tool to help identify gaps or redundancies in germplasm collections, and when combined with phenotyping data, can be used to detect correlations between genome regions and agronomic traits. For some crops, massive sequencing and data processing have been undertaken, as shown in the rice, wheat and barley germplasm collections (Milner et al., 2019; Sansaloni et al., 2020; Wang et al., 2018). These approaches represent increasingly reachable targets for many genebanks worldwide,

including the CGIAR international collections (Halewood, Lopez Noriega et al., 2018).

For bananas (*Musa* spp.), the largest ex situ collection is maintained in vitro at one of the CGIAR international genebanks, the International Musa Germplasm Transit Centre (ITC), comprised of more than 1,600 accessions (Van den houwe et al., 2020). Then, over 60 national collections worldwide conserve banana diversity and conduct-related research (Figure 1). Bananas (including Plantains) are arguably the world's most important fresh fruit and are a major staple food for hundreds of millions of people in low-income countries. With an estimated world production of 158 million tons annually, the volume of gross banana exports is worth US\$12.8 billion to exporting countries (FAOSTAT 2019). Furthermore, most of the global production is by smallholders for their own consumption or for local trade, making it the fourth-most important food crop in the least developed countries (LDCs) as defined by the United Nations, ranked by total production and food consumption.

Purpose of the study / Dataset	Number of accessions (samples)	Collection	Taxonomical coverage	Number of markers	Sequencing Technologies	References	Sequence data availability
GWAS panel for parthenocarpy and sterility	106	ITC	<i>M. acuminata</i> (wild) and AA (cultivated)	7,079,397	Genotyping by Sequencing (GBS)	(Sardos et al., 2016)	PRJNA305234
Genome constitution of ABB, AB	83	ITC	ABB, M, acuminata and balbisiana	683,264	RAD sequencing	(Cenci et al., 2020)	PRJNA450532
Genome constitution of AAB	118	ITC	AAB, M, acuminata and balbisiana	3,315,168	RAD sequencing	Publication in preparation	PRJNA450532
Panel evaluated for drought tolerance	10 (60)	ITC	AAA, AAB, ABB	6,951,307	RNA sequencing	(Cenci et al., 2019)	PRJNA305241
Domestication and acuminata subspecies	254	ITC	<i>M. acuminata</i> and AA	245,285	RAD sequencing	Publication in preparation	PRJNA450532
A/B Structural variations	207	CRB-PT	Breeding population	148,329	RAD sequencing	(Baurens et al., 2019)	PRJNA448968 PRJEB28077
Genome ancestry mosaics	25	CRB-PT, CARBAP	<i>M. acuminata</i> , AA, AAA	191,876	RNA sequencing	(Martin et al., 2020b)	SRR956987
Chromosome reciprocal translocations	155	CRB-PT, ITC	Breeding populations, <i>M. acuminata</i> , AA	120,111	Genotyping by Sequencing (GBS)	(Martin et al., 2020a)	PRJNA667853

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Blast Search

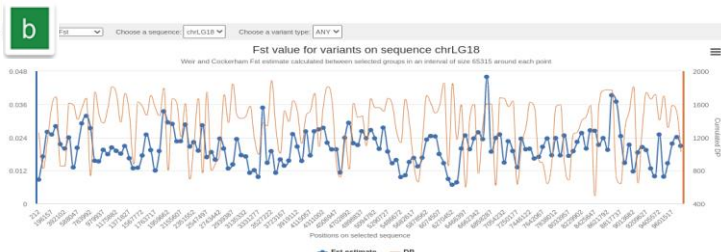
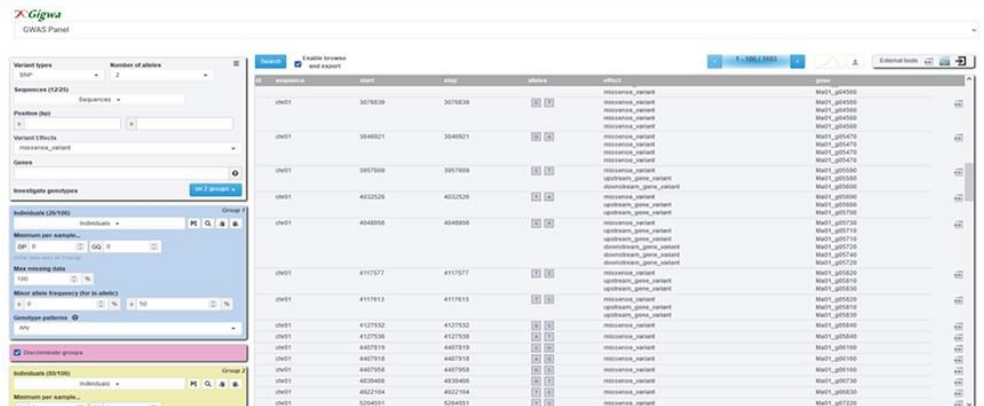
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RNA-Seq data analysis using Diane

Analyse your own transcriptomics data

SNP markers with GIGWA



Customisation options

Number of intervals: (Between 50 and 300)

Individuals accounted for: (From groups: (1/37 selected))

Additional series based on VCF genotype metadata:

Cumulated DP data

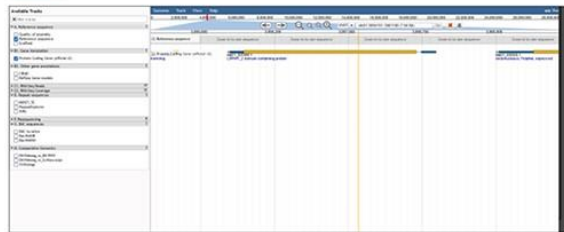
Cumulated GQ data

Show Fst significance threshold with value:

Group Fst by:

c

Facilitated link with external tools (IGV, JBrowse)



d



Dynamic graph display:
variant density, Fst, Tajima's D

Embedded third-party visualization tools:

- Flapjack-Bytes
- IGV.js (online genome browser)

Genome ancestry mosaics reveal multiple and cryptic contributors to cultivated banana

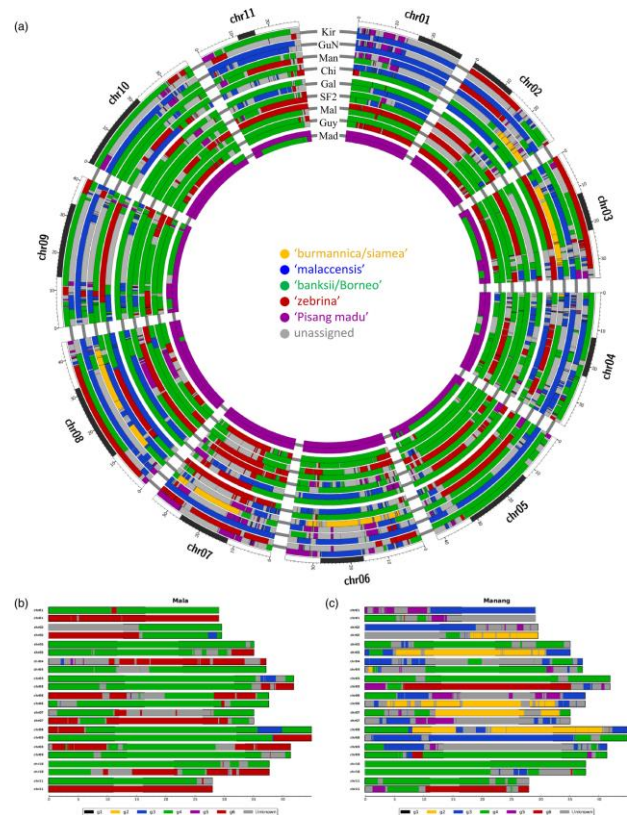
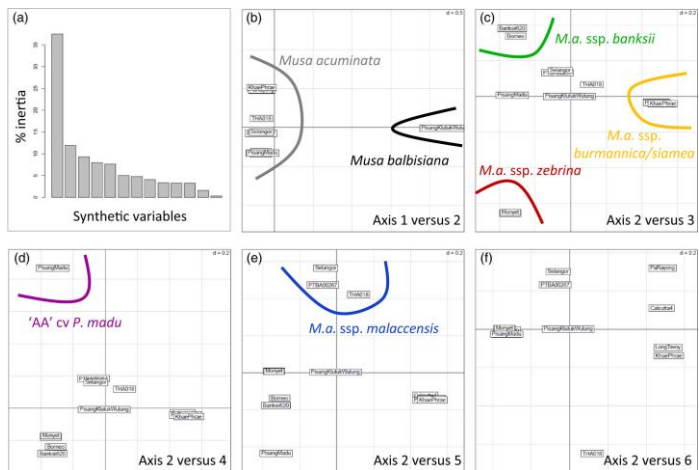
Guillaume Martin^{1,2,*}, Céline Cardin^{1,2}, Gautier Sarah², Sébastien Ricc^{2,3,4}, Christophe Jenny^{1,2}, Emmanuel Fond², Xavier Perrier^{1,2}, Jean-Christophe Glaszmann^{1,2}, Angélique D'Hont^{1,2} and Nabila Yahiaoui^{1,2}

¹CIRAD, UMR AGAP, F-34398 Montpellier, France,

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³CARBAP, Rue Dinde, No. 110, Bonanjo, BP 832 Douala, Cameroon, and

⁴CIRAD, UMR AGAP, F-97130 Capestanne Belle Eau, France



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GeMo: a web-based platform for the visualization and curation of genome ancestry mosaics

Marilyn Summo ✉, Aurore Comte, Guillaume Martin, Pierrick Perelle, Eric M Weitz, Gaëtan Droc, Mathieu Rouard ✉

Database, Volume 2022, 2022, baac057, <https://doi.org/10.1093/database/baac057>

Published: 14 July 2022 Article history ▾

Home

Chromosome Painting

Pre-loaded examples ⓘ

Banana (Musa spp. ▾) GrandeNaine ▾

With your own data ⓘ

Input files ⓘ

chr	haplotype	start	end
ancestral_group			
01	0	1	914859 g3
01	0	935898	945410 g7

Choose file Browse

Chromosomes size and labels ⓘ

Choose organism ▾

or upload your own

chr	len	centromereInf	centromeresup	label
chr01	29878452	21245289		
chr02	29511734	6858044		

Choose file Browse

Global ploidy 3 ▾

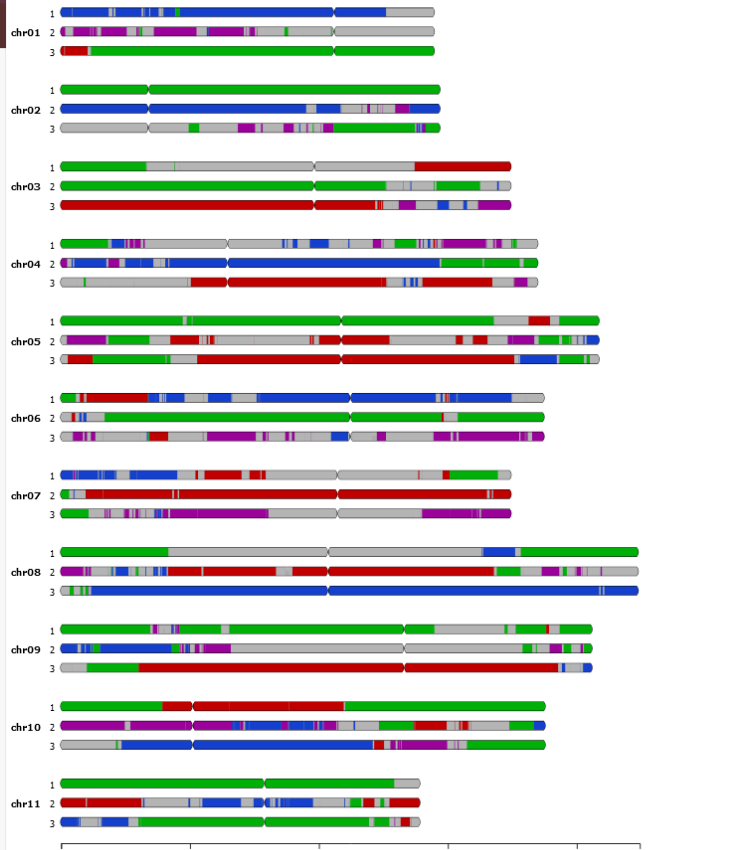
Show Labels

Colors (optional) ⓘ

Choose existing palette

or enter your own color data

group	name	hex
g6	zebrina	#c00000
g5	unknown	#9a029a
g3	malaccensis	#1448cd



Legend

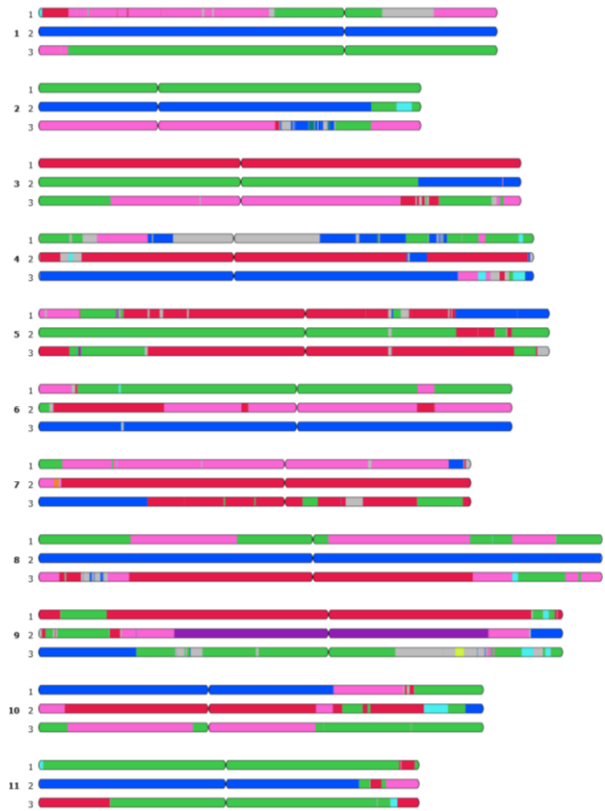
- No data
- zebrina
- unknown
- malaccensis
- burmannica
- banksii
- unassigned
- balbisiana

24 accessions (RNAseq)

175 accessions (WGS)

~600 accessions (HTG - planned)

Cavendish



Martin et al, 2023

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BEATRICE SIRINUNTANON/SHUTTERSTOCK

TRILOBITES

The Search Is on for Mysterious Banana Ancestors

A new study shows that domesticated bananas have genetic markers tying them to three types of wild bananas that have not yet been found.

Sardos et al, 2022

Chromosome reciprocal translocations have accompanied subspecies evolution in bananas

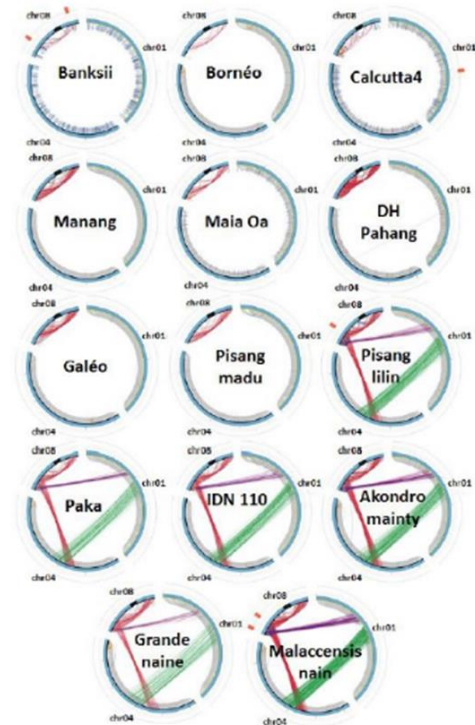
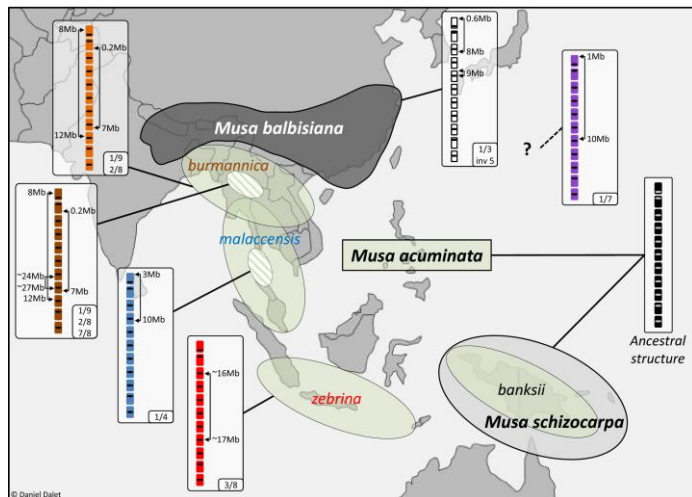
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³CIRAD, UMR AGAP, Capesterre-Belle-Eau, Guadeloupe F-97130, France, and

⁴Genoscope, Institut de biologie François Jacob, Commissariat à l'Énergie Atomique (CEA), Université Paris-Saclay, Evry, France

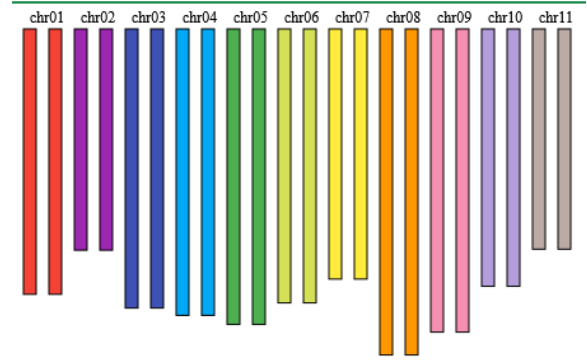
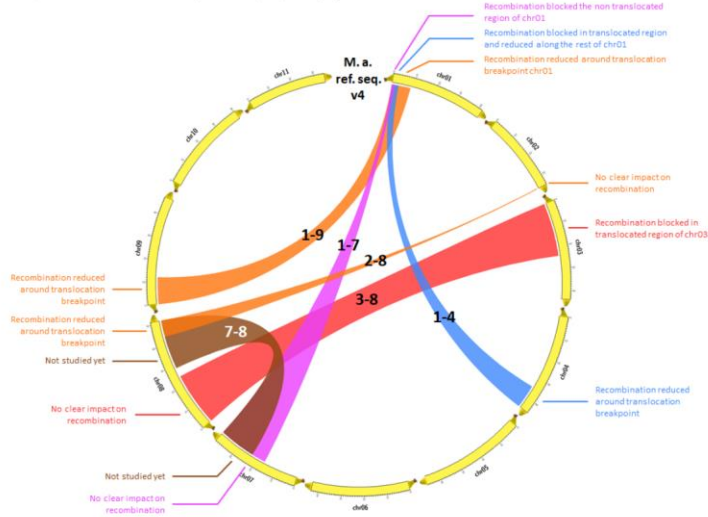


Translocations

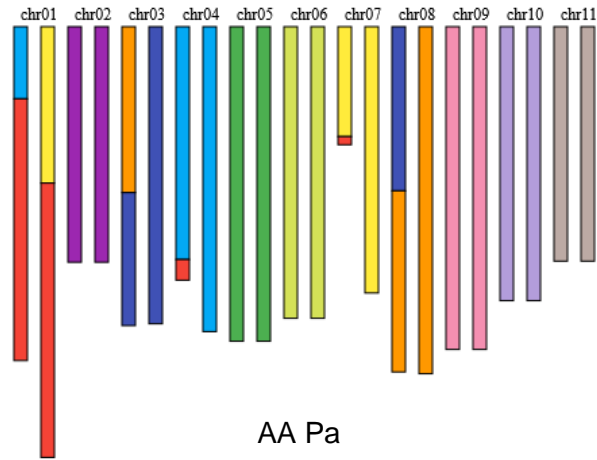
Translocation

Musa chromosome structure database

Martin et al. 2017. Evolution of the Banana Genome (*Musa acuminata*) Is Impacted by Large Chromosomal Translocations.



AA Hawain2



AA Pa

Search [input] [button] [button] [button] [button]

Name	Accession Name	Genome ^a	Species/Phylogenetic cluster ^b	Status ^c	1-4	3-8	1-7	2-8	1-9	7-8
Ambly P1	NA ^{***}	AA	-	wild accession	2	1	0	0	0	0
Pisang Segun	PT-BA-00319	AA	-	wild accession	0	0	0	0	0	0
Hawain 2	PT-BA-00113	AA	<i>Musa acuminata</i> ssp. bankii	wild accession	0	0	0	0	0	0
Waligo	PT-BA-00412	AA	<i>Musa acuminata</i> ssp. bankii	wild accession	0	0	0	0	0	0
Bankii	PT-BA-00024	AA	<i>Musa acuminata</i> ssp. bankii	wild accession	0	0	0	0	0	0
M. a. ssp bankii	ITC0897	AA	<i>Musa acuminata</i> ssp. bankii	wild accession	0	0	0	0	0	0



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Comparative Analysis the Complete Chloroplast Genomes of Nine *Musa* Species: Genomic Features, Comparative Analysis, and Phylogenetic Implications.

Summary

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In this study, the nine species of *Musa* were collected from Plant Germplasm and Genomics Center, Kunming Institute of Botany, the Chinese Academy of Sciences, and was approved by Kunming Institute of Botany and local policy. The complete chloroplast genome was further validated and calibrated by using *de novo* splicing script NOVOpIsty 4.2 (Dierckxsens et al., 2017)

Display name ▲	created	size
Musa ingens.fa	Fri, 04/08/2022 - 14:32	169.28 KB
Musa jackeyi.fa	Fri, 04/08/2022 - 14:32	168.78 KB
Musa laterita.fa	Fri, 04/08/2022 - 14:32	171.38 KB
Musa lolodensis.fa	Fri, 04/08/2022 - 14:32	169.35 KB
Musa mannii.fa	Fri, 04/08/2022 - 14:32	171.52 KB
Musa nagensium.fa	Fri, 04/08/2022 - 14:32	171.12 KB
Musa rubinea.fa	Fri, 04/08/2022 - 14:32	173.48 KB
Musa troglodytarum.fa	Fri, 04/08/2022 - 14:32	168.93 KB
Musa yunnanensis.fa	Fri, 04/08/2022 - 14:32	170.63 KB

9 files - 1.5 MB



Sequencing status curat



56 leaf transcriptomes



Sequencing	A	B	C	D	E	F
	Genus	Section	Species/gr...	Subspecies/s...	Collection	Name
	Musa	Musa	acuminata	burmannica	SCBG	n/a
	Musa	Musa	acuminata	burmannica	SCBG	n/a
	Musa	Musa	acuminata	burmannica	IAARD	Calcutta 4
	Musa	Musa	acuminata	burmannica	CRB-PT	Calcutta 4
	Musa	Musa	acuminata	burmannica	CRB-PT	Calcutta 4
	Musa	Musa	acuminata	burmannica	CRB-PT	Calcutta 4
	Musa	Musa	acuminata	burmannica	Unal	Calcutta 4
	Musa	Musa	acuminata	burmannica	CRB-PT	Long Tavoy
	Musa	Musa	acuminata	halabanensis	SCBG	n/a
	Musa	Musa	acuminata	halabanensis	SCBG	n/a
	Musa	Musa	acuminata	malaccensis	ITC	n/a
	Musa	Musa	acuminata	malaccensis	CRB-F	n/a
	Musa	Musa	acuminata	malaccensis	CRB-F	n/a
	Musa	Musa	acuminata	malaccensis	ITC	n/a
	Musa	Musa	acuminata	malaccensis	CRB-F	n/a
	Musa	Musa	AA	n/a	ITC	n/a
	Musa	Musa	acuminata	malaccensis	ITC	n/a
	Musa	Musa	acuminata	malaccensis	CRB-F	n/a
	Musa	Musa	acuminata	malaccensis	CRB-F	n/a
	Musa	Musa	acuminata	malaccensis	ITC	n/a
	Musa	Musa	acuminata	banksii	ITC	n/a
	Musa	Musa	acuminata	microcarpa	SCBG	n/a
	Musa	Musa	acuminata	microcarpa	SCBG	n/a
	Musa	Musa	acuminata	microcarpa	TBRI	n/a
	Musa	Musa	acuminata	microcarpa	TBRI	n/a

Validation of high throughput sequencing as virus indexing test for Musa germplasm: performance criteria evaluation and contamination monitoring using an alien control

Wei Rong, Johan Rollin, Marwa Hanafi, Nicolas Roux, and Sebastien Massart

Published Online: 4 Oct 2022 | <https://doi.org/10.1094/PHYTOFR-03-22-0030-F1>

Accession	Method	Availability	Project ID
PT-BA-00051	WGS - reads	Public	PRJNA532826
PT-BA-00051	WGS - Chromosome scale assembly	Not public yet	
n/a	RNAseq - reads	Public	SRR13836930-941
PT-BA-00178	RNAseq - reads	Public	SRR11197801
V45	Chloroplast - assembly	Public	OK012357
	proplast - reads	Public	SRR8879212
	proplast - assembly	Public	HF677508
	S - reads	Public	ERR3606950
	S - Chromosome scale assembly	Public	ERR3606951
	seq - reads	Public	ERR5455028
	seq - reads	Public	BGH
	seq - reads	Public	SRR7691539-543
	seq - reads	Public	SRR9203049
	S - reads	Not public yet	
	seq - reads	Public	SRR11197800
	seq - reads	Public	SRR11197798
	seq - reads	Public	SRR9203050
	S - reads	Not public yet	
	proplast - assembly	Public	OK012347
	proplast - reads	Public	SRR8879213
	proplast - assembly	Public	LC609621
	Chloroplast - reads	Public	SRR15112712

- To be released
- Chromosome-scale genomes assemblies
 - Plantain (AAB)
 - Textilis
 - zebriana
 - Calcutta 4
 - Banksii
 - E. ventricosum
 - Etc.

Take home messages

- The banana genome hub serves the community
 - Large number of tools for comparative and functional genomics
 - Promotes interoperability using BrAPI with genebanks and breeding (MGIS, Musabase) - Source of material can be important
 - Designed to hold more genomes: data from publications or by authors
- don't hesitate to contact us early in the process for data entering (Blast, Jbrowse, synteny, transcriptomics)



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