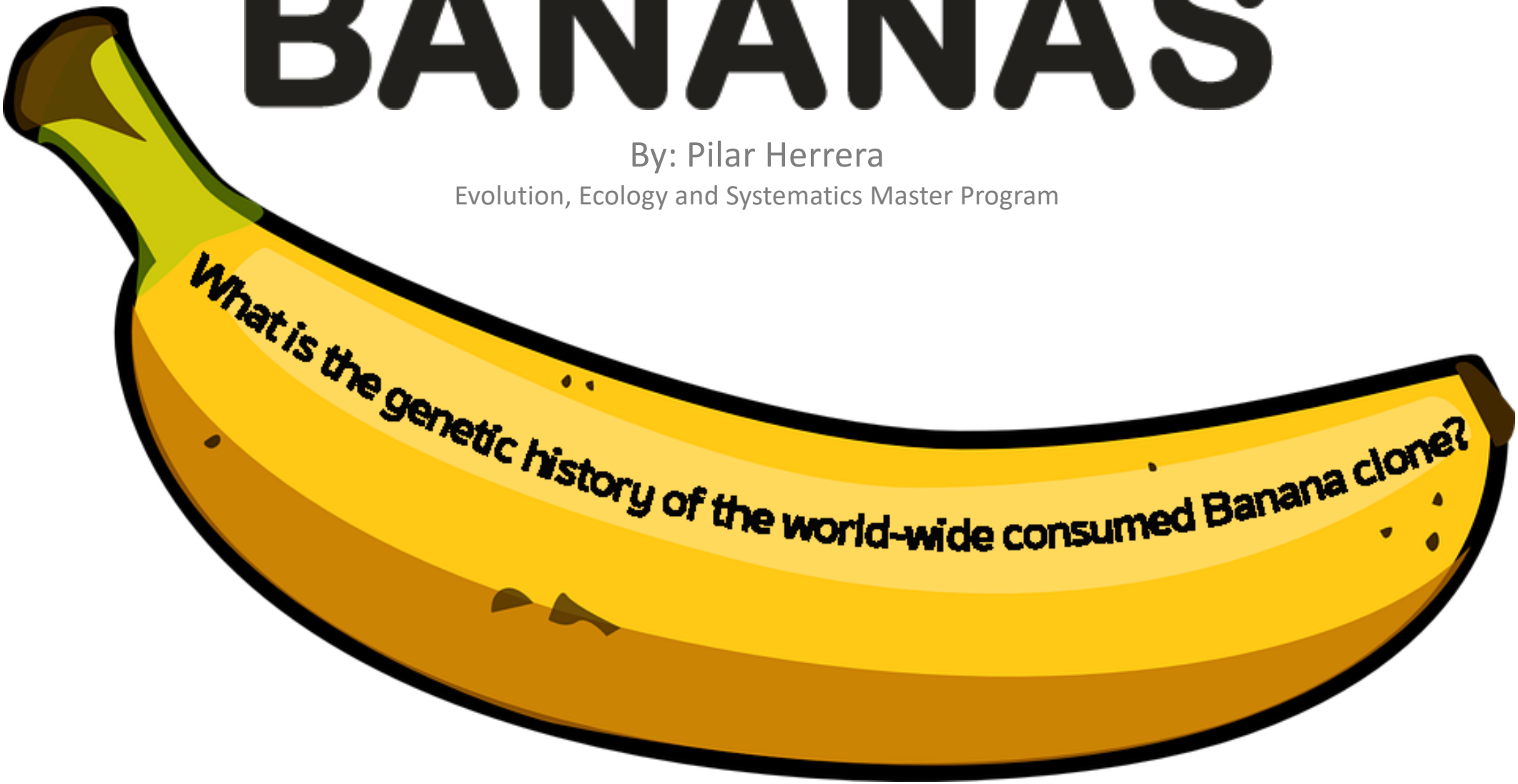
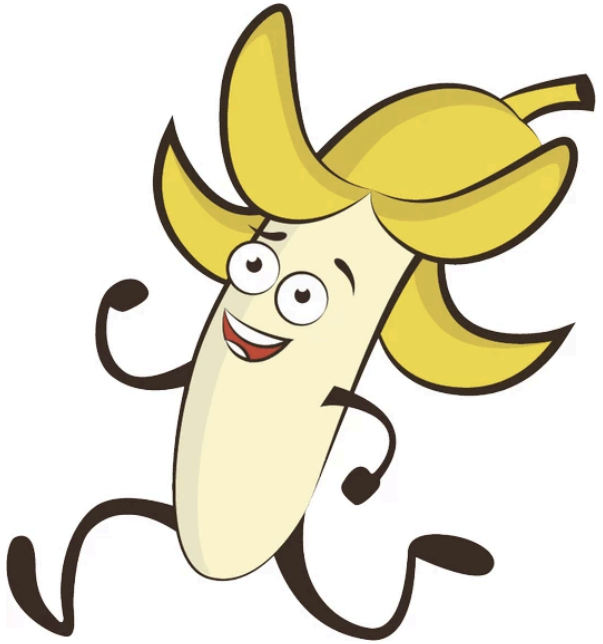
BANANAS

By: Pilar Herrera
Evolution, Ecology and Systematics Master Program



OUTLINE

- Introduction: biological background
- Why study bananas?
- Genetic evolutionary history
- Domestication
- Challenges and diseases



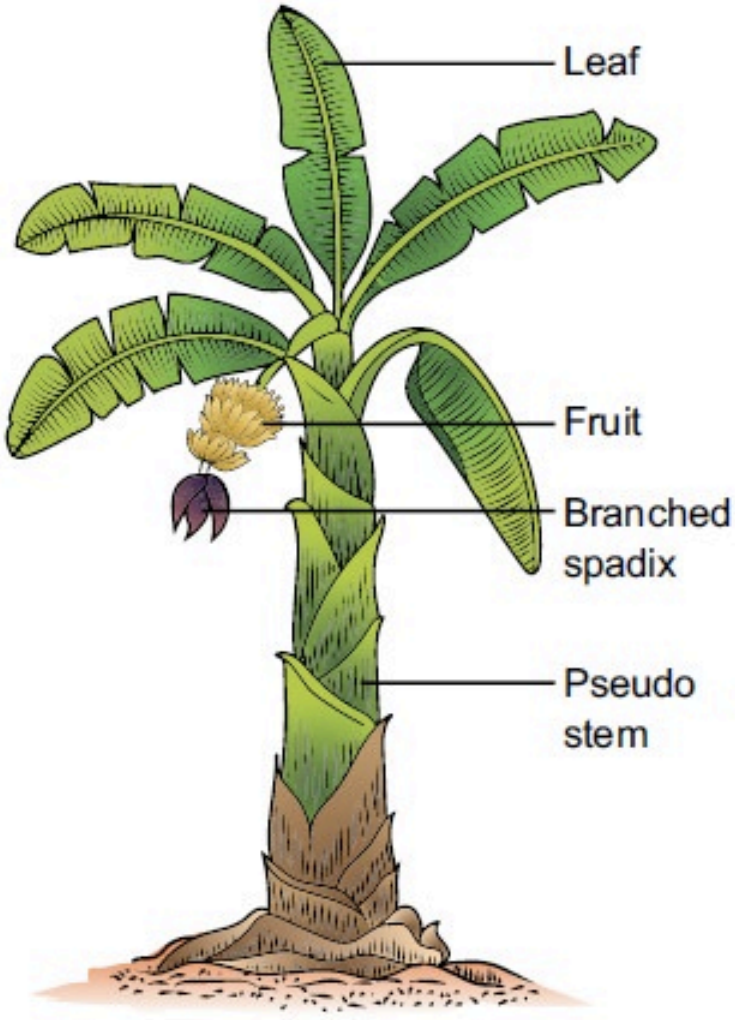
Introduction

Musa paradisiaca

M. acuminata x *M. balbisiana*



Source: www.wur.nl



Source: www.brainkart.com

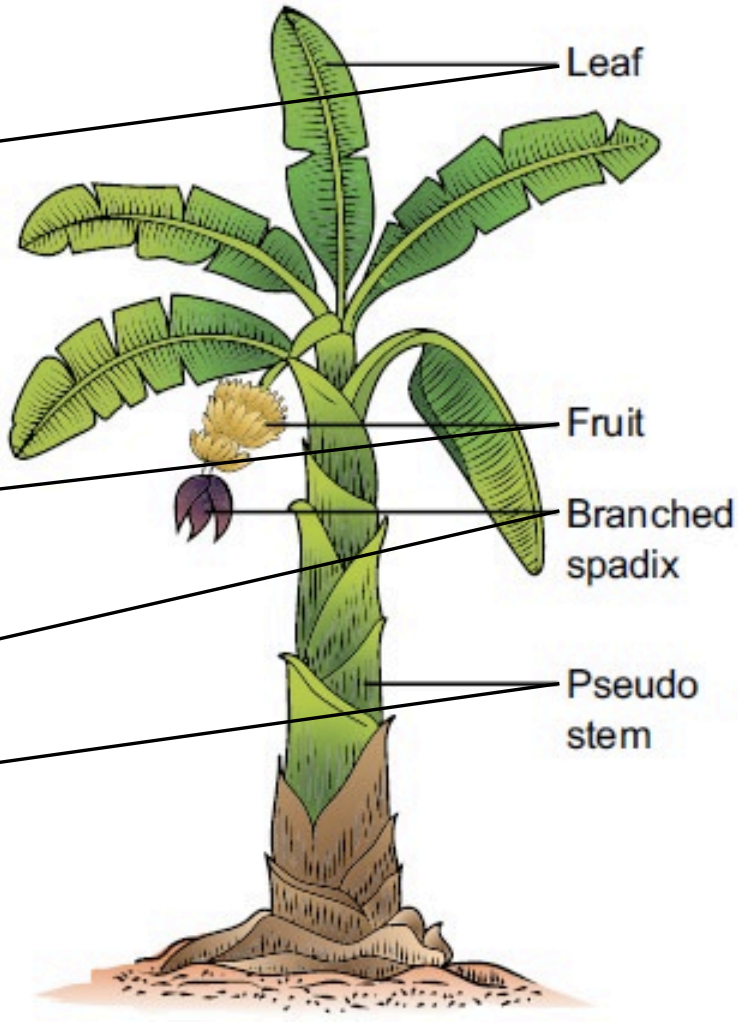
Musa paradisiaca

M. acuminata x *M. balbisiana*

- Perennial herb
- Pseudo-stem
- Rhizome
- ”Suckers”



Source: www.wur.nl

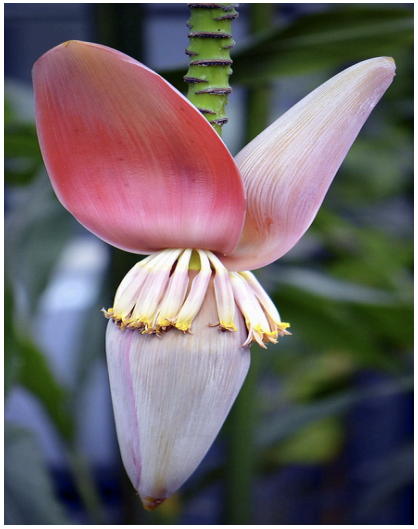


Source: www.brainkart.com

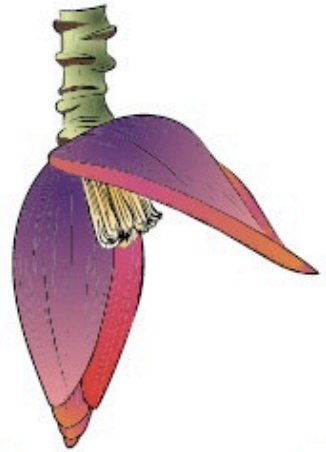
Introduction

Musa paradisiaca

M. acuminata x *M. balbisiana*

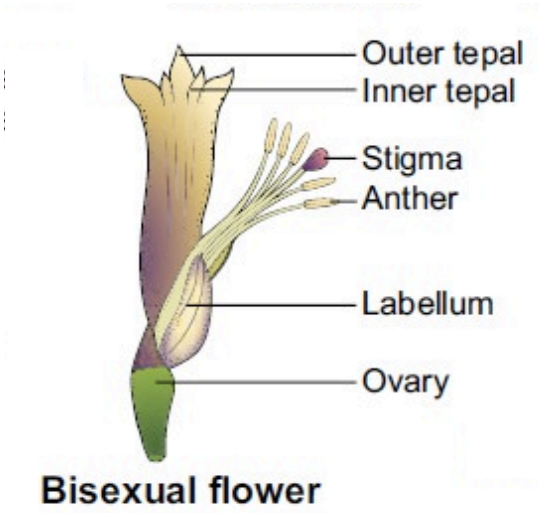


Source: www.farm6.staticflickr.com





Source: Sunandar & Kahar (2017)



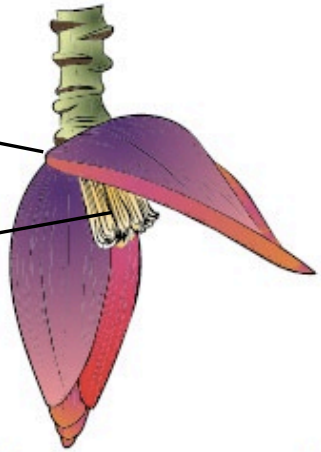
Source: www.brainkart.com

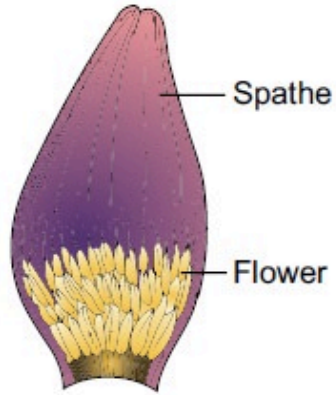
Musa paradisiaca

M. acuminata x *M. balbisiana*

- Unisexual and bisexual flowers
- Cultivars present parthenocarpy
- Wild plants: bat pollination
- Wild bananas: diploids





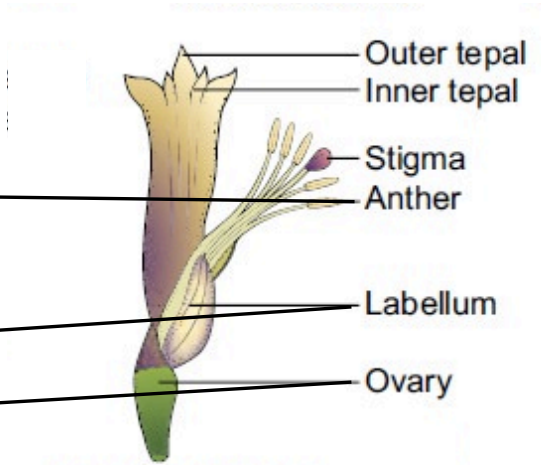


Inflorescence

Spathe with flowers

Source: www.farm6.staticflickr.com



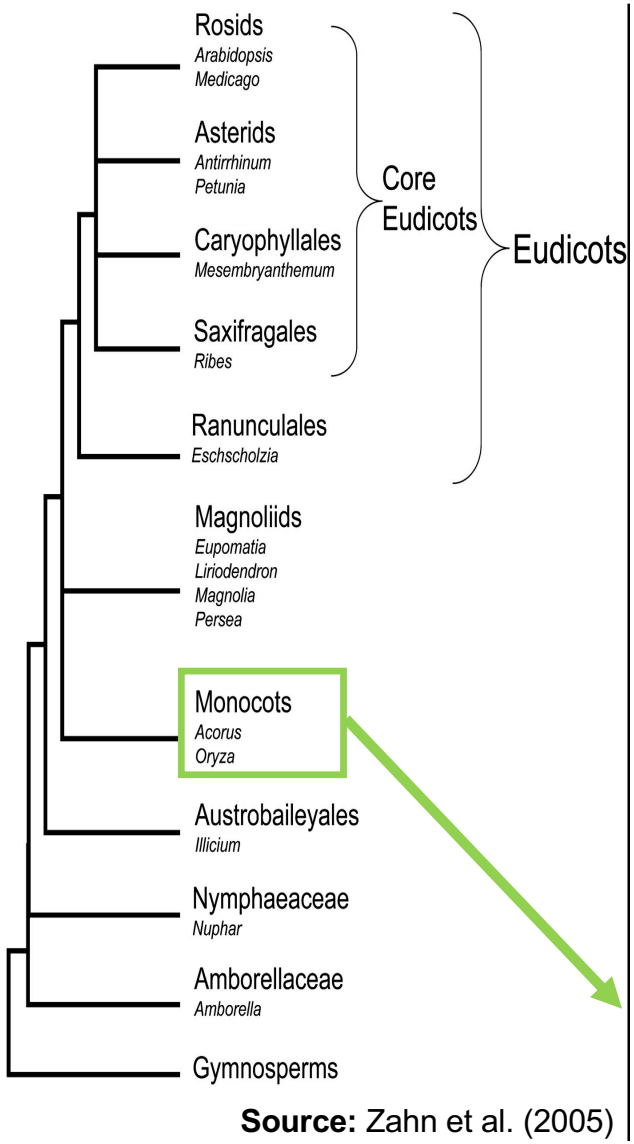


Bisexual flower

Source: Sunandar & Kahar (2017)

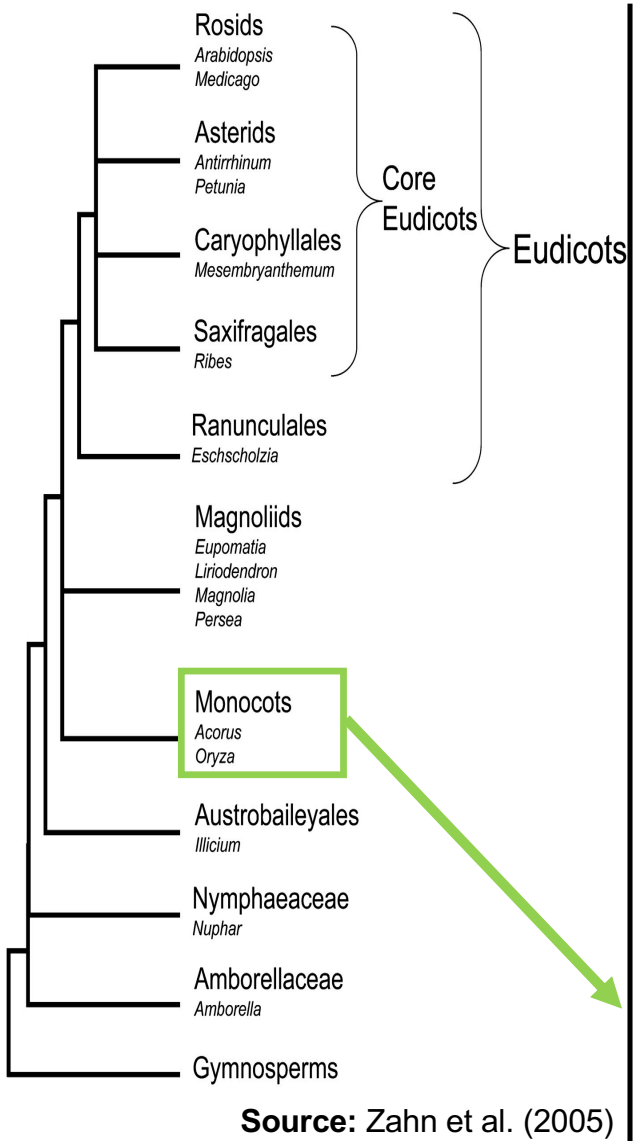
Source: www.brainkart.com

Introduction

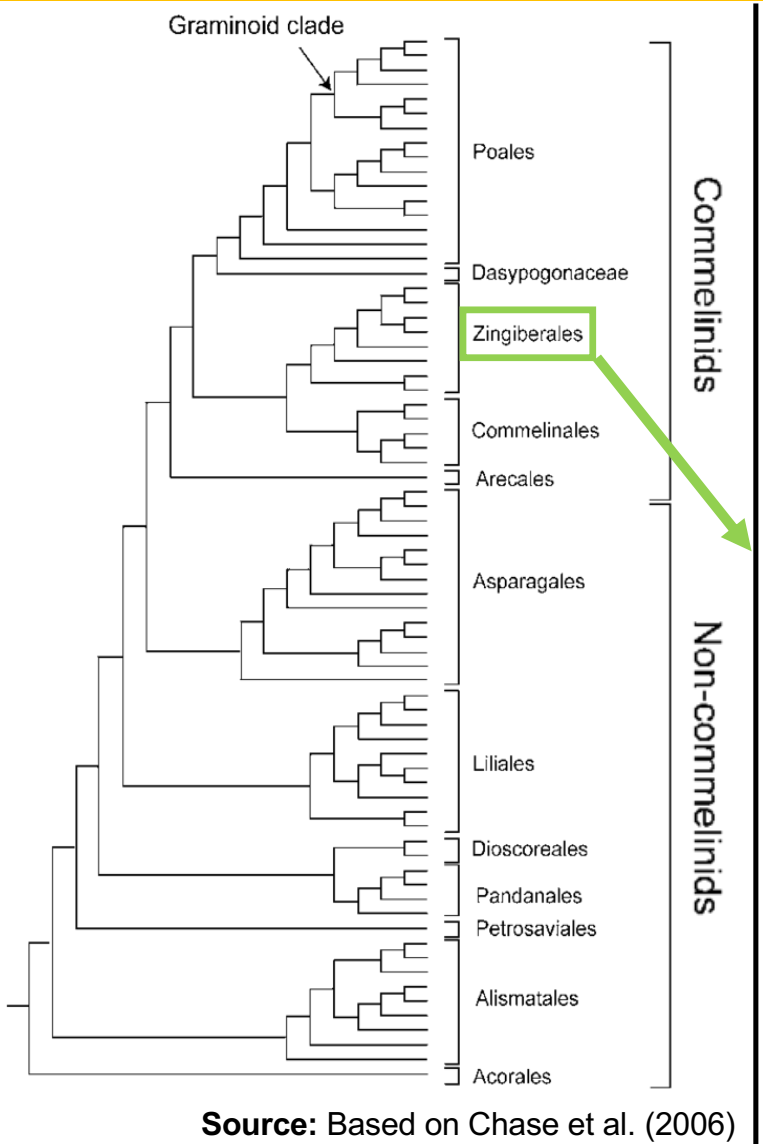


Source: Zahn et al. (2005)

Introduction

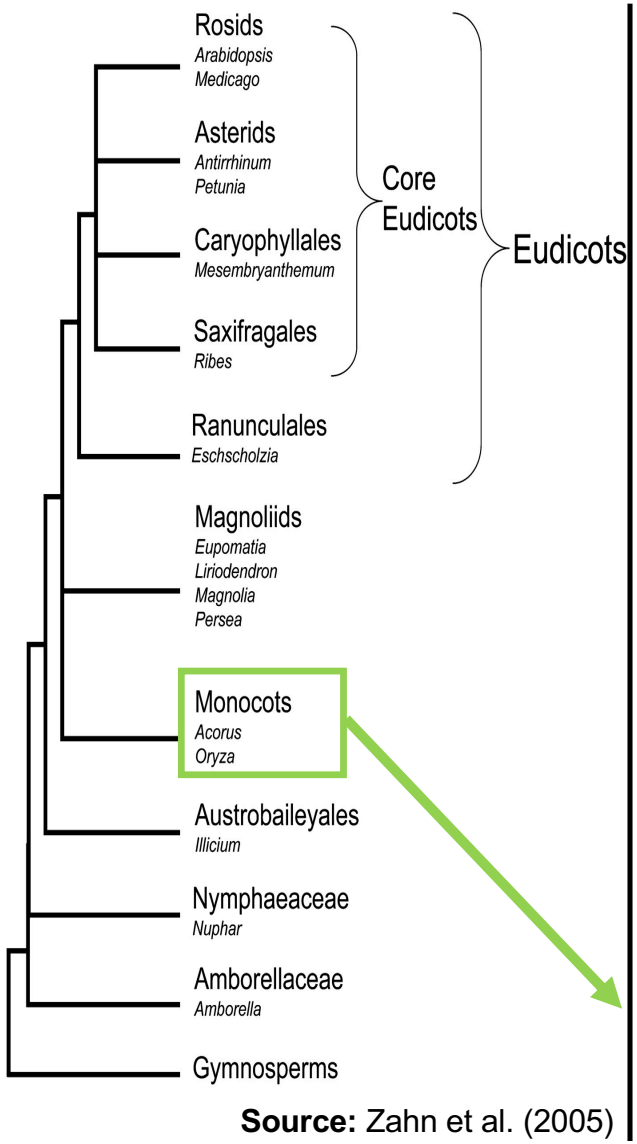


Source: Zahn et al. (2005)

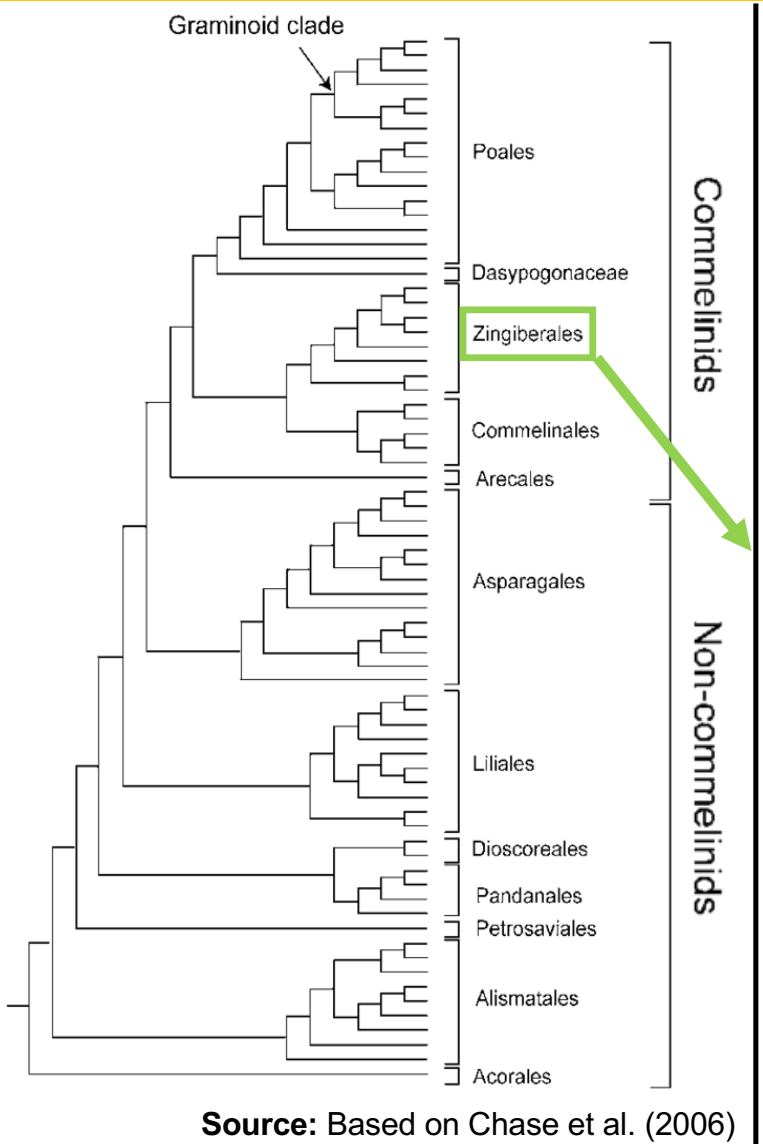


Source: Based on Chase et al. (2006)

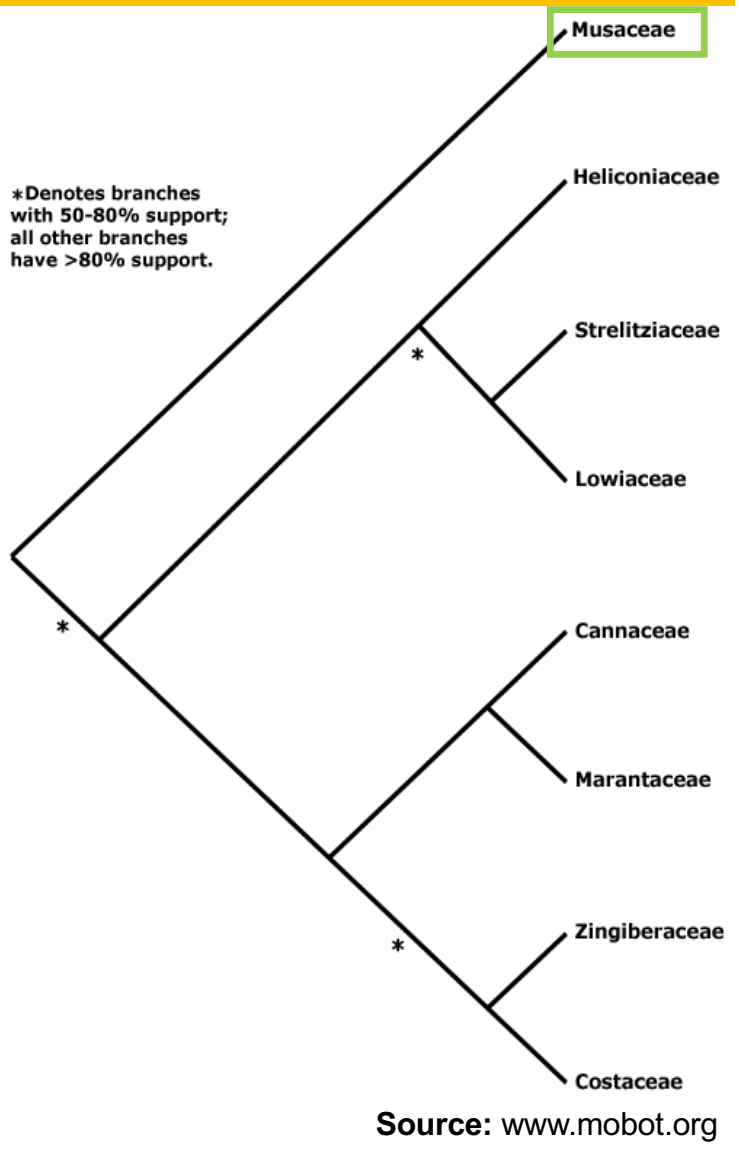
Introduction



Source: Zahn et al. (2005)



Source: Based on Chase et al. (2006)



Source: www.mobot.org

Importance

- 4th most important food crop in some countries



Importance

- 4th most important food crop in some countries
- Difficult genetic improvement: sterile cultivars



Source: www.b4fa.org

Importance

- 4th most important food crop in some countries
- Difficult genetic improvement: sterile cultivars
- Relatively small size genome (haploid genome of 500-600 Mbp)

Source: www. banana-genome-hub.southgreen.fr



Importance

- 4th most important food crop in some countries
- Difficult genetic improvement: sterile cultivars
- Relatively small size genome (haploid genome of 500-600 Mbp)
- Provide other type of sources (fiber, alcohol, etc)



Source: cdn.theculturetrip.com



Source: www.thegerberstore.com



Source: www.maliburumdrinks.com

The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants

D'Hont et al (2012)

- Description of draft sequence of 523 Mb genome of a *Musa acuminata* doubled-haploid genotype
  - **DH-Pahang**: *M. acuminata* ssp. *malaccensis* (2*n* = 22)



Source: www.promusa.org

The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants

D'Hont et al (2012)

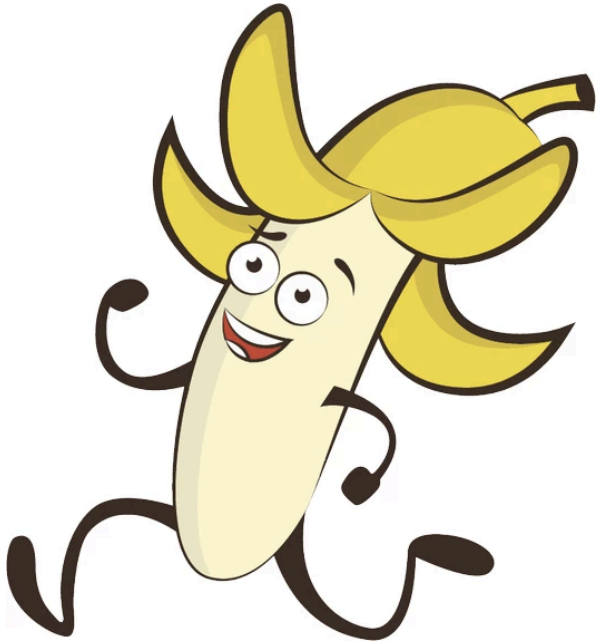
- Description of draft sequence of 523 Mb genome of a *Musa acuminata* doubled-haploid genotype
  - **DH-Pahang**: *M. acuminata* ssp. *malaccensis* (2*n* = 22)
  - 27.5 million Roche/454 single reads
  - 2.1 million Sanger reads

  ] 25X
  - Illumina data (50X) to correct sequence errors

The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants

D'Hont et al (2012)

Results I

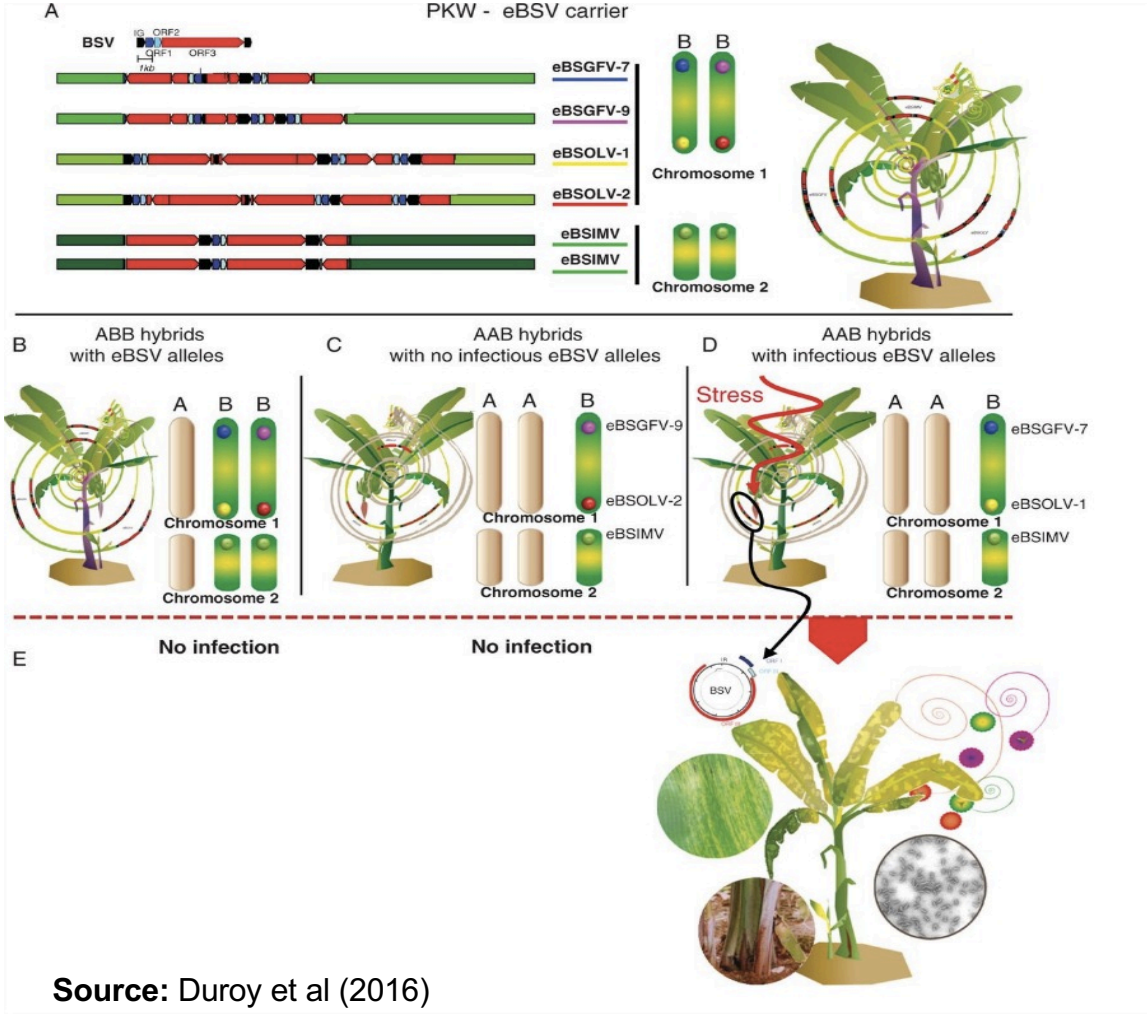


Gene identification

- 36,542 protein-coding gene models
- 235 microRNAs belonging to 37 microRNAs families
  - Only one *MIR* (exclusively in Poaceae) found

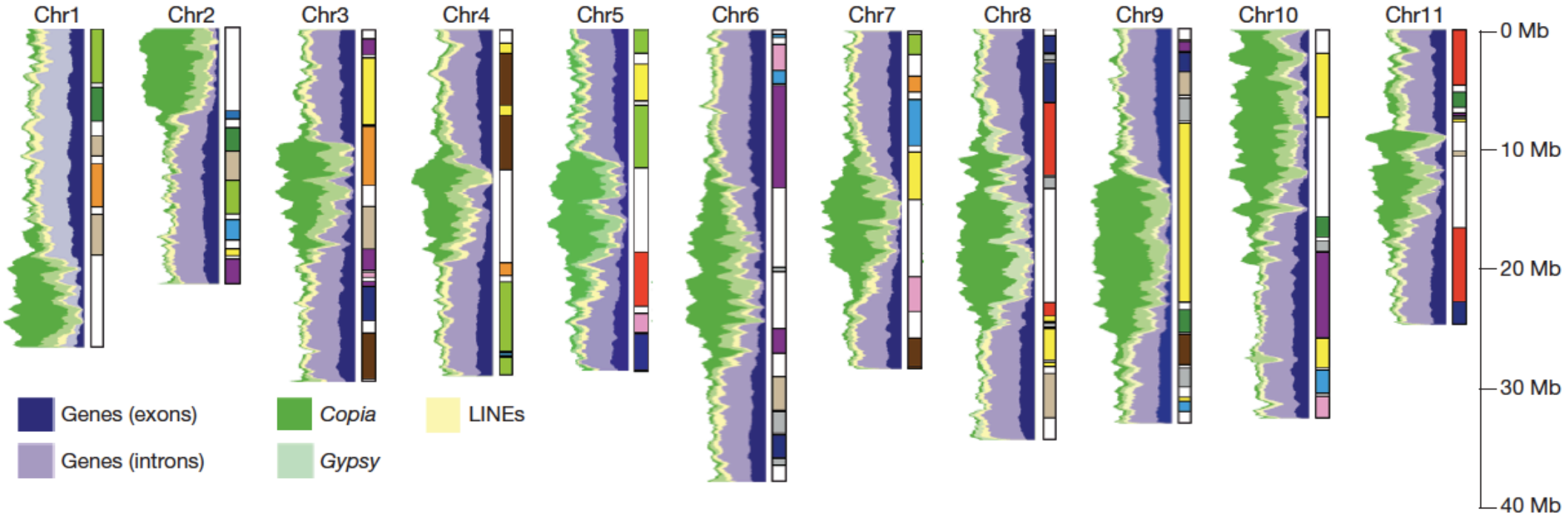
Gene identification

- 36,542 protein-coding gene models
- 235 microRNAs from 37 families
  - Only one *MIR* (exclusively in Poaceae) found
  - Viral sequences related to banana streak virus (BSV) dsDNA plant pararetovirus (24 loci in 10 chromosomes)



Source: Duroy et al (2016)

Chromosomal distribution



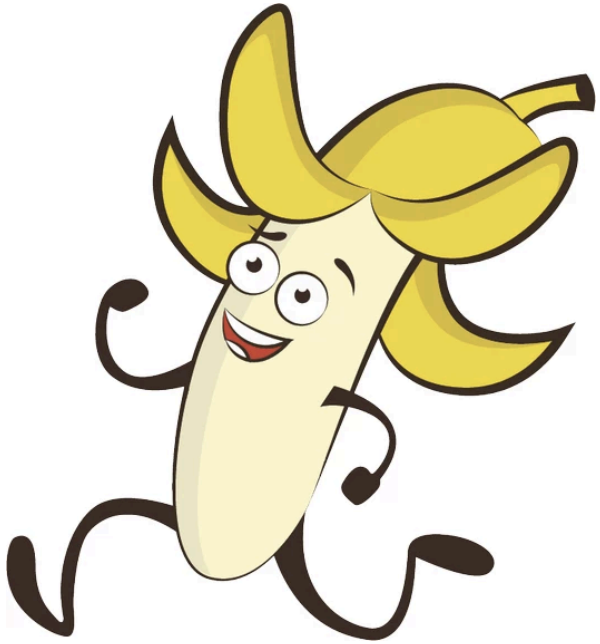
- TEs account around 50% (mostly in centromeres)
- LTR (largest parts): *Copia* > *Gypsy*
- LINEs represent 5,5% (centromeric and pericentromeric)
- Gene-rich regions on distal part of chromosomes

Source: D'Hont et al (2012)

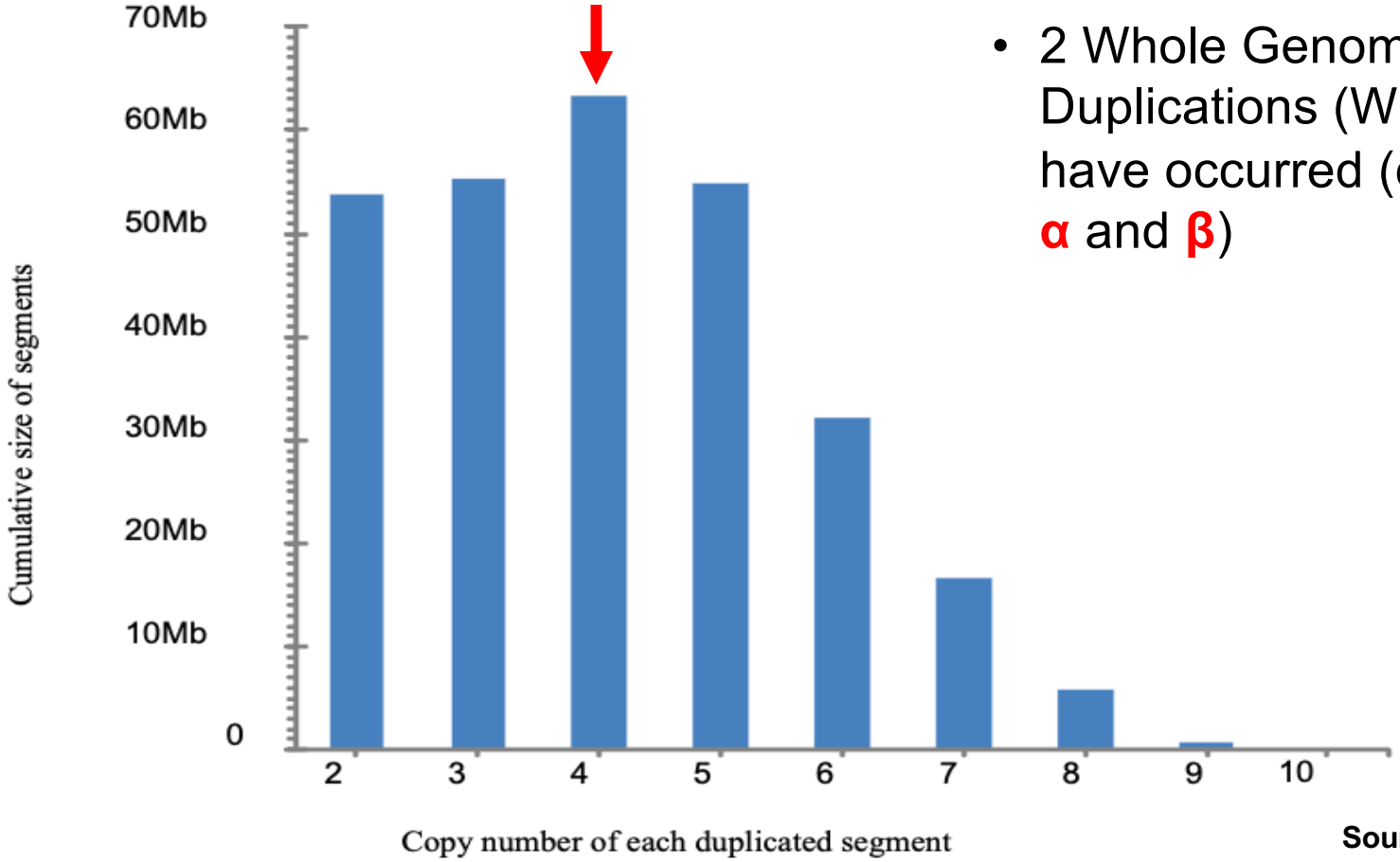
The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants

D'Hont et al (2012)

Results II



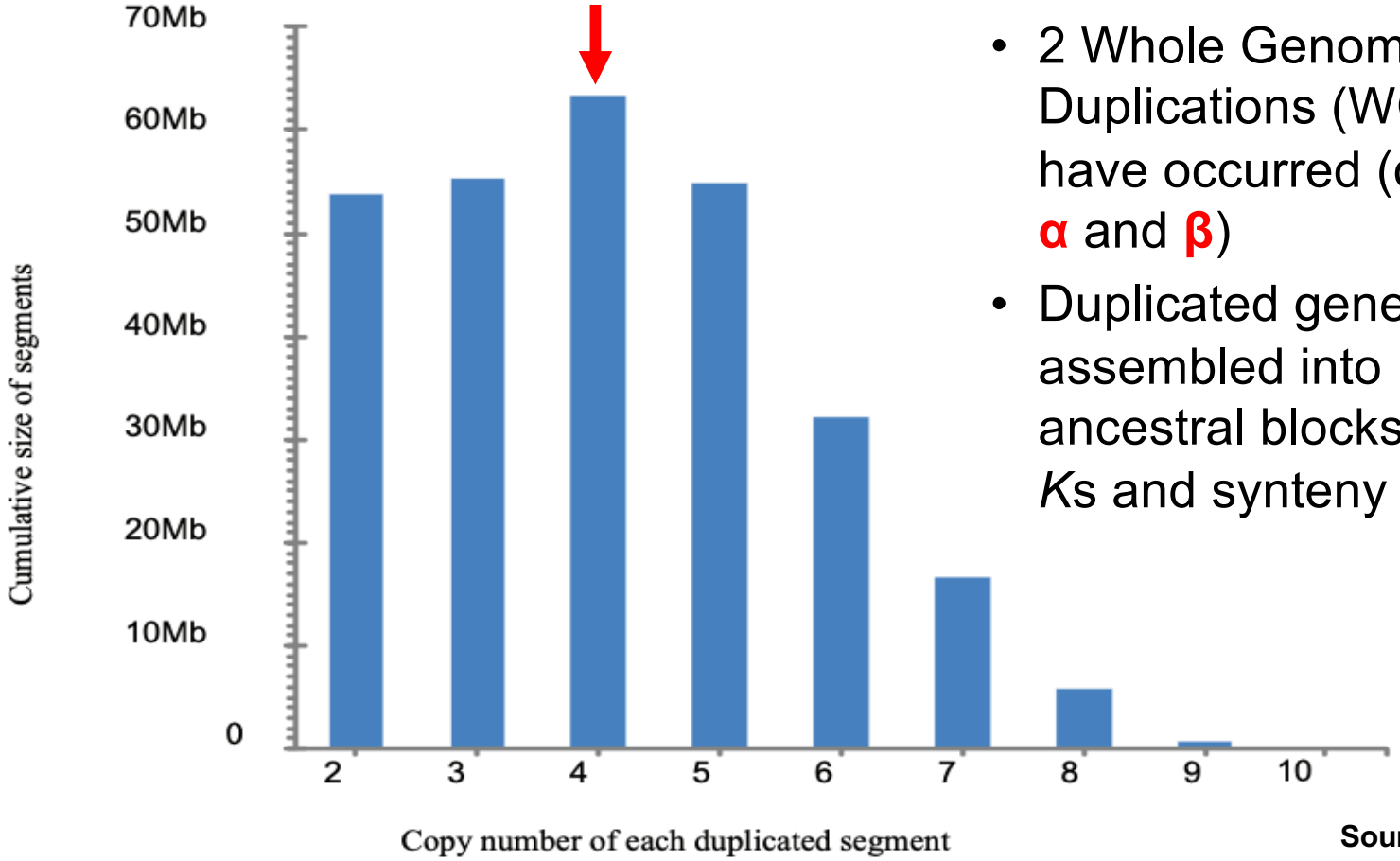
Distribution of duplicated chromosome segment copy number



- 2 Whole Genome Duplications (WGD) may have occurred (denominated **α** and **β**)

Source: D'Hont et al (2012)

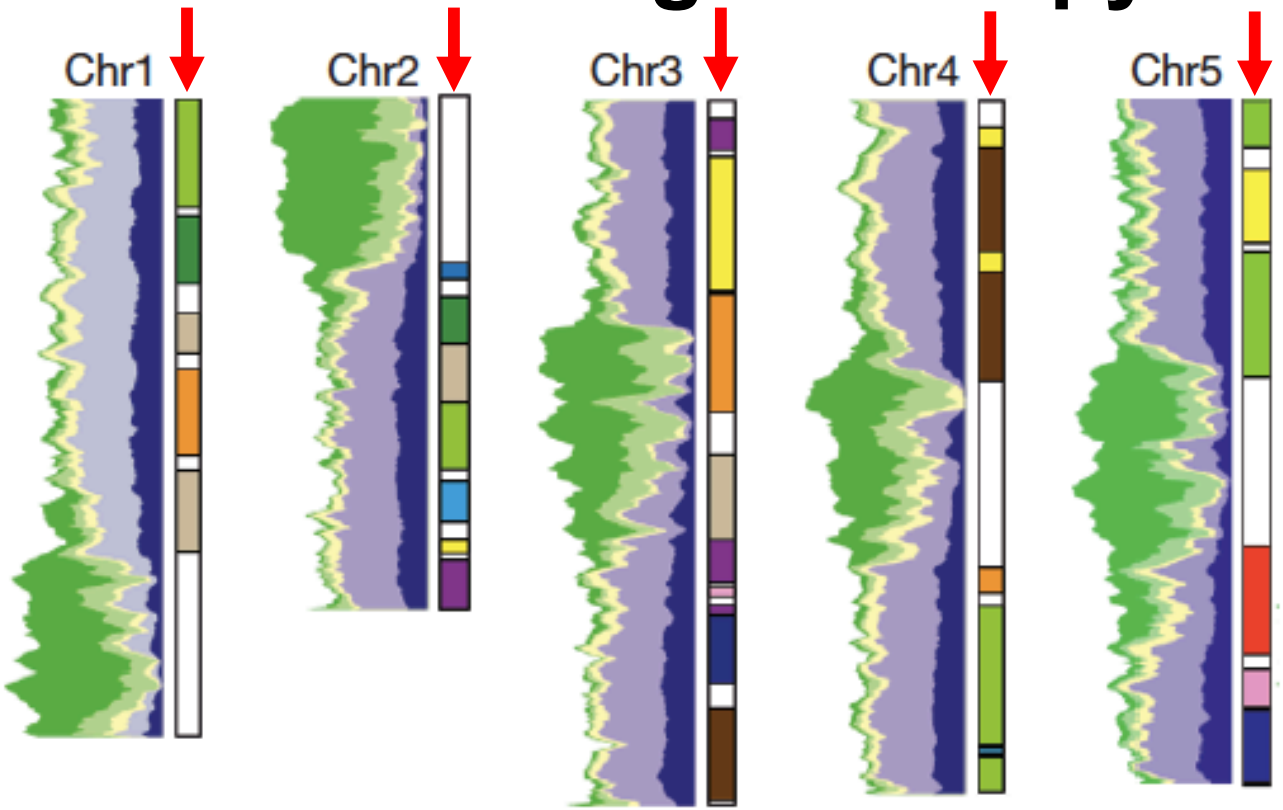
Distribution of duplicated chromosome segment copy number



- 2 Whole Genome Duplications (WGD) may have occurred (denominated **α** and **β**)
- Duplicated gene clusters assembled into 12 *Musa* ancestral blocks (based on *K*s and synteny relationships)

Source: D'Hont et al (2012)

Distribution of duplicated chromosome segment copy number

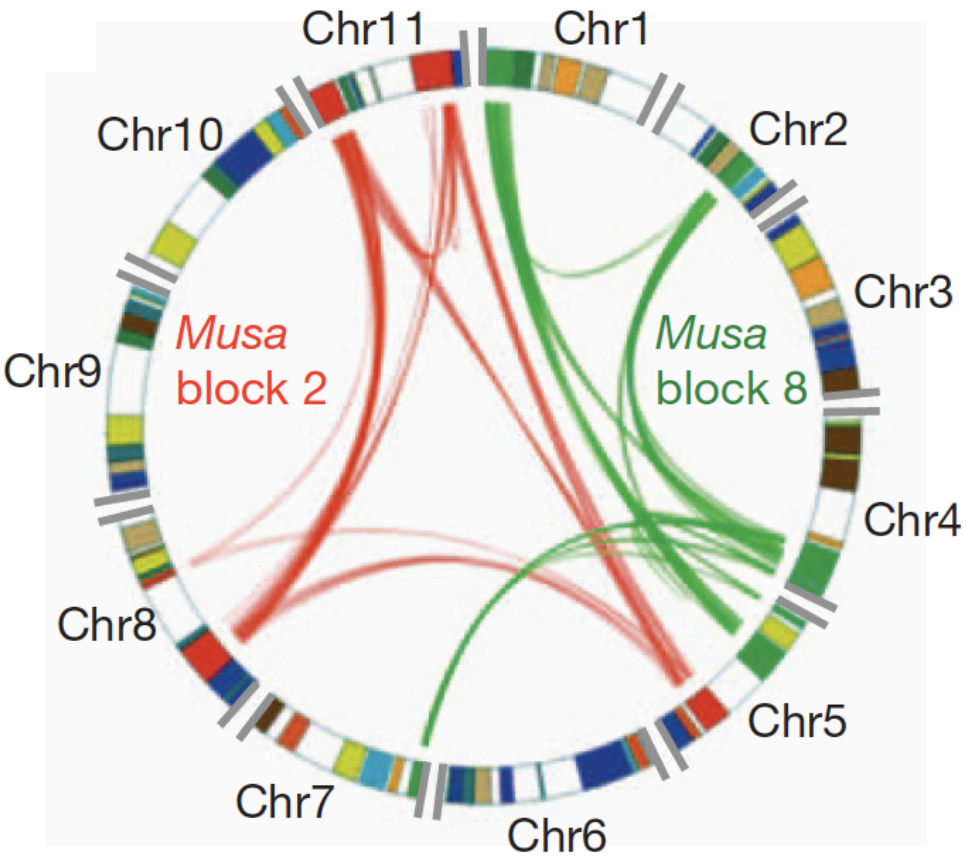


- 2 Whole Genome Duplications (WGD) may have occurred (denominated **α** and **β**)
- Duplicated gene clusters assembled into 12 *Musa* ancestral blocks (based on *K*s and synteny relationships)
- *Musa* ancestral blocks cover 222 Mb and contain 26,829 genes

Source: D'Hont et al (2012)

Paralogous and Orthologous relationships

Paralogous relationships between
Musa α/β ancestral blocks

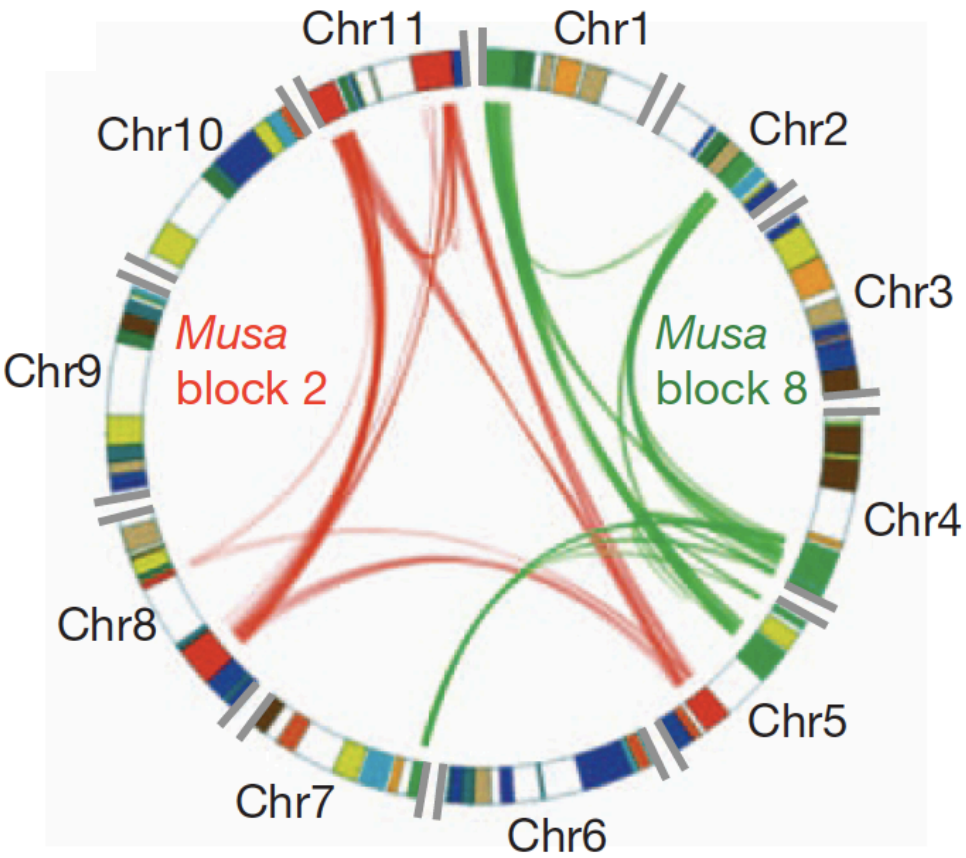


- 2 WGDs (**α** and **β**) dated at a similar period of 65 Myr ago.
- Higher *K*s values suggested a more ancient duplication event (denoted as **γ**) occurred ~100 Myr ago

Source: D'Hont et al (2012)

Paralogous and Orthologous relationships

Paralogous relationships between
Musa α/β ancestral blocks



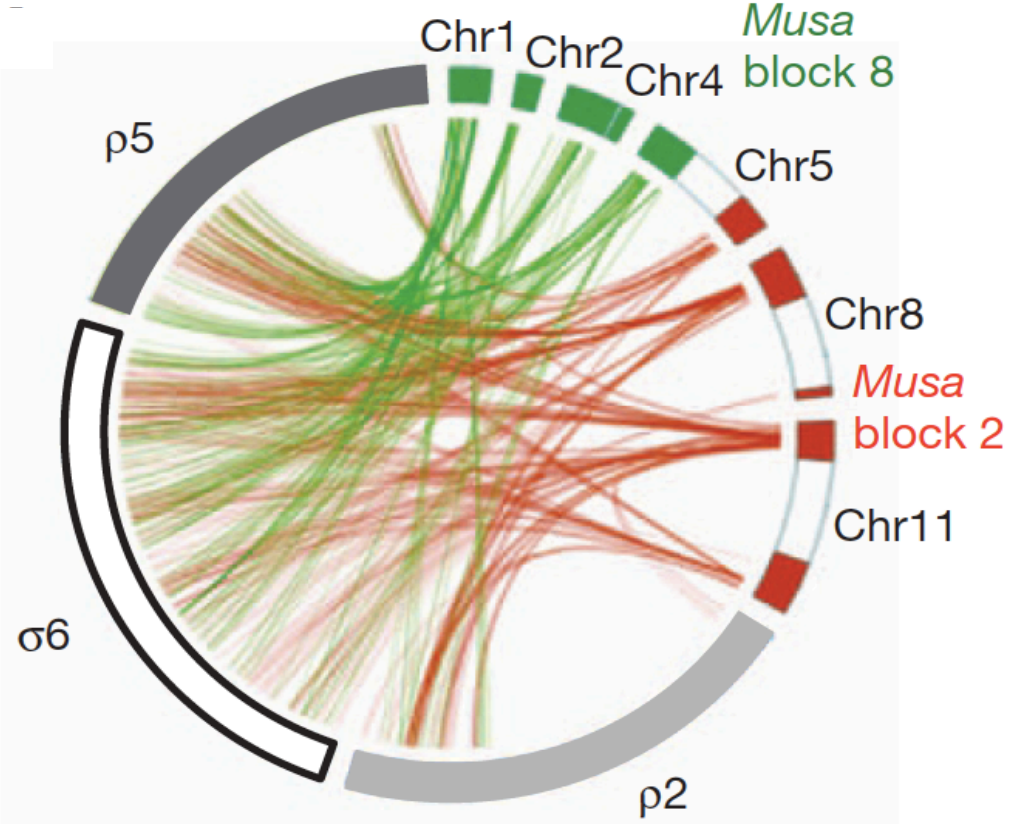
- 2 WGDs (**α** and **β**) dated at a similar period of 65 Myr ago.
- Higher *K*s values suggested a more ancient duplication event (denoted as **γ**) occurred ~100 Myr ago
- In grass lineage, one WGD occurred (denoted as **ρ**) around 50-70 Myr ago
- Earlier WGD (denoted as **σ**) in monocots, after divergence from eudicots.

Source: D'Hont et al (2012)

Paralogous and Orthologous relationships

- Genes from segments of different **ρ** blocks have orthologous relationships with the same *Musa* regions: the Poaceae event **σ** is not shared with *Musa*

Orthologous relationships between Musa α/β ancestral blocks with rice ancestral blocks

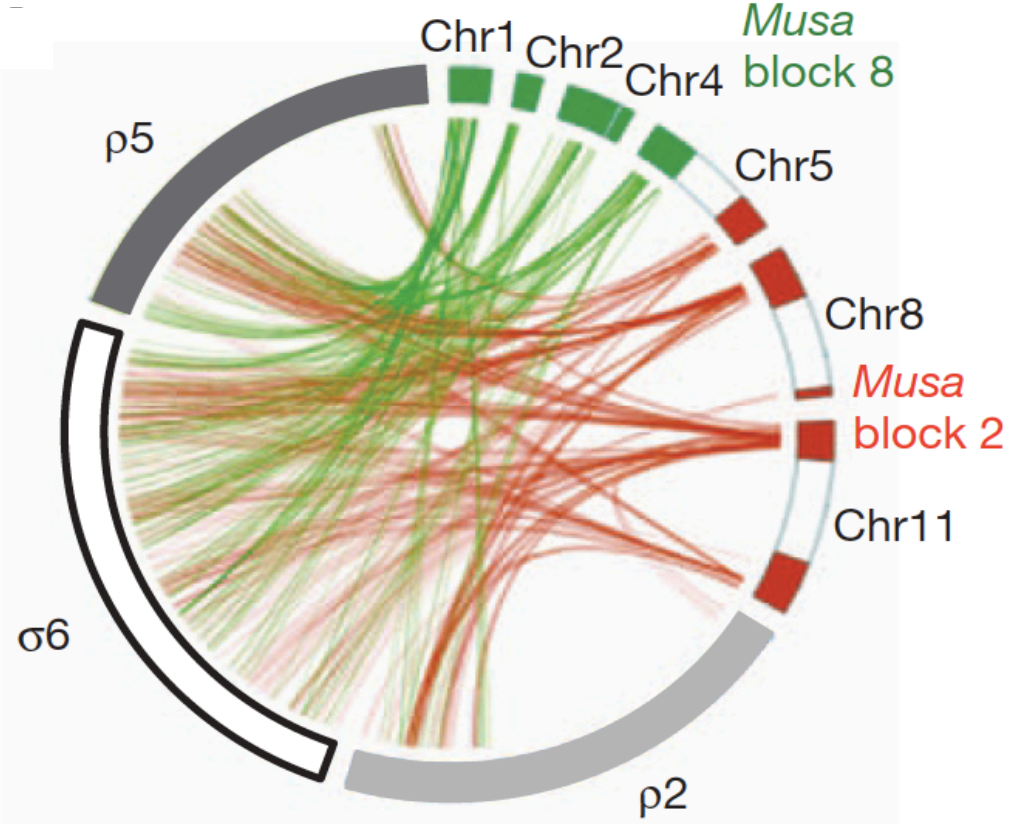


Source: D'Hont et al (2012)

Paralogous and Orthologous relationships

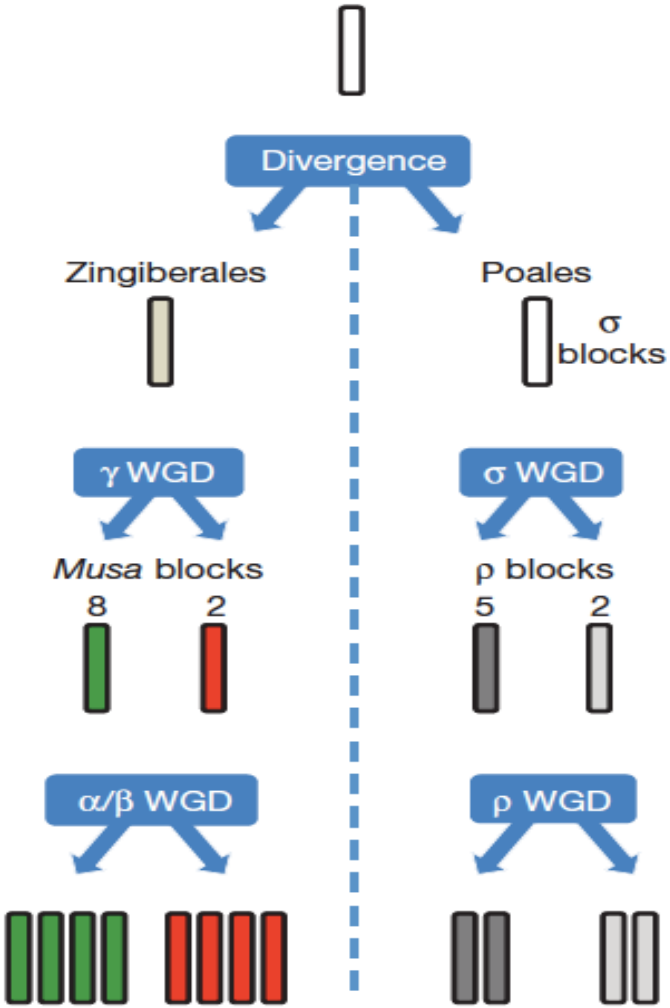
- Genes from segments of different **ρ** blocks have orthologous relationships with the same *Musa* regions: the Poaceae event **σ** is not shared with *Musa*
- *Musa* **α/β** paralogous segments have orthologous relationships with the same **ρ** and **σ**: **γ** is not shared with Poaceae

Orthologous relationships between Musa α/β ancestral blocks with rice ancestral blocks



Source: D'Hont et al (2012)

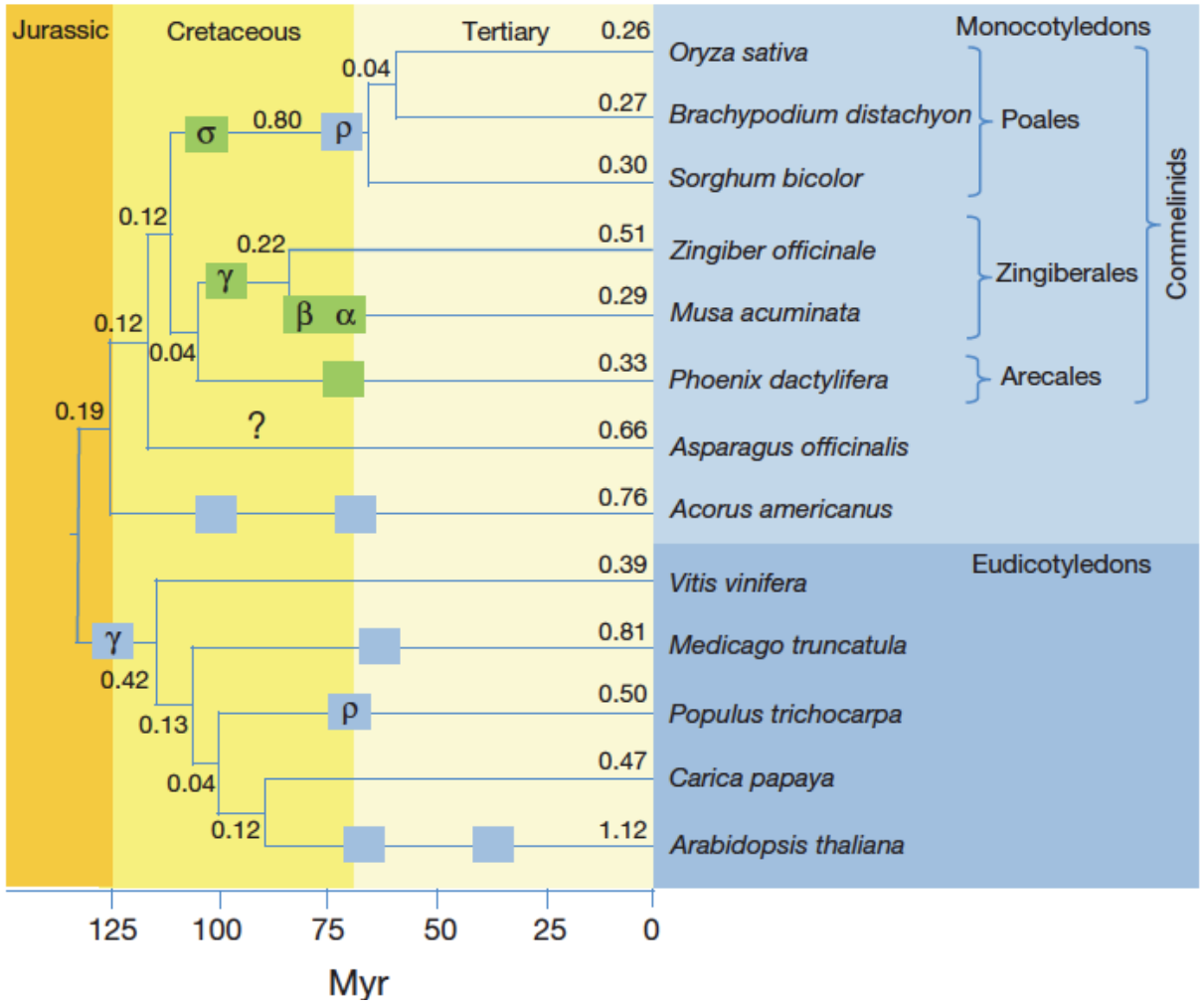
Paralogous and Orthologous relationships



- **α** and **β** dated at a similar period of 65 Myr ago.
- **γ** ancient duplication event occurred ~100 Myr ago
- In grass lineage, **ρ** WGD occurred ~50-70 Myr ago
- Earlier **σ** in monocots, after divergence from eudicots.
- **σ** is not shared with *Musa*
- **γ** is not shared with Poaceae.

Source: D'Hont et al (2012)

Timing of WGDs relative to speciation events



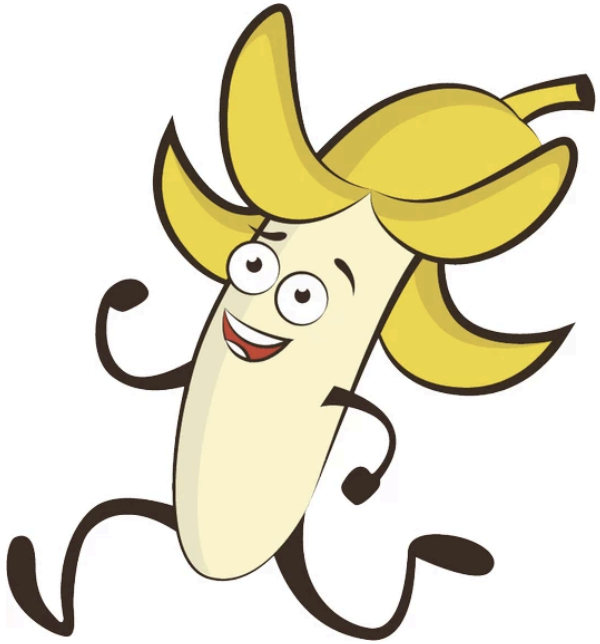
- The three rounds of paleopolyploidization reported in *Musa* and two in Poaceae are indepent events.

Source: D'Hont et al (2012)

The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants

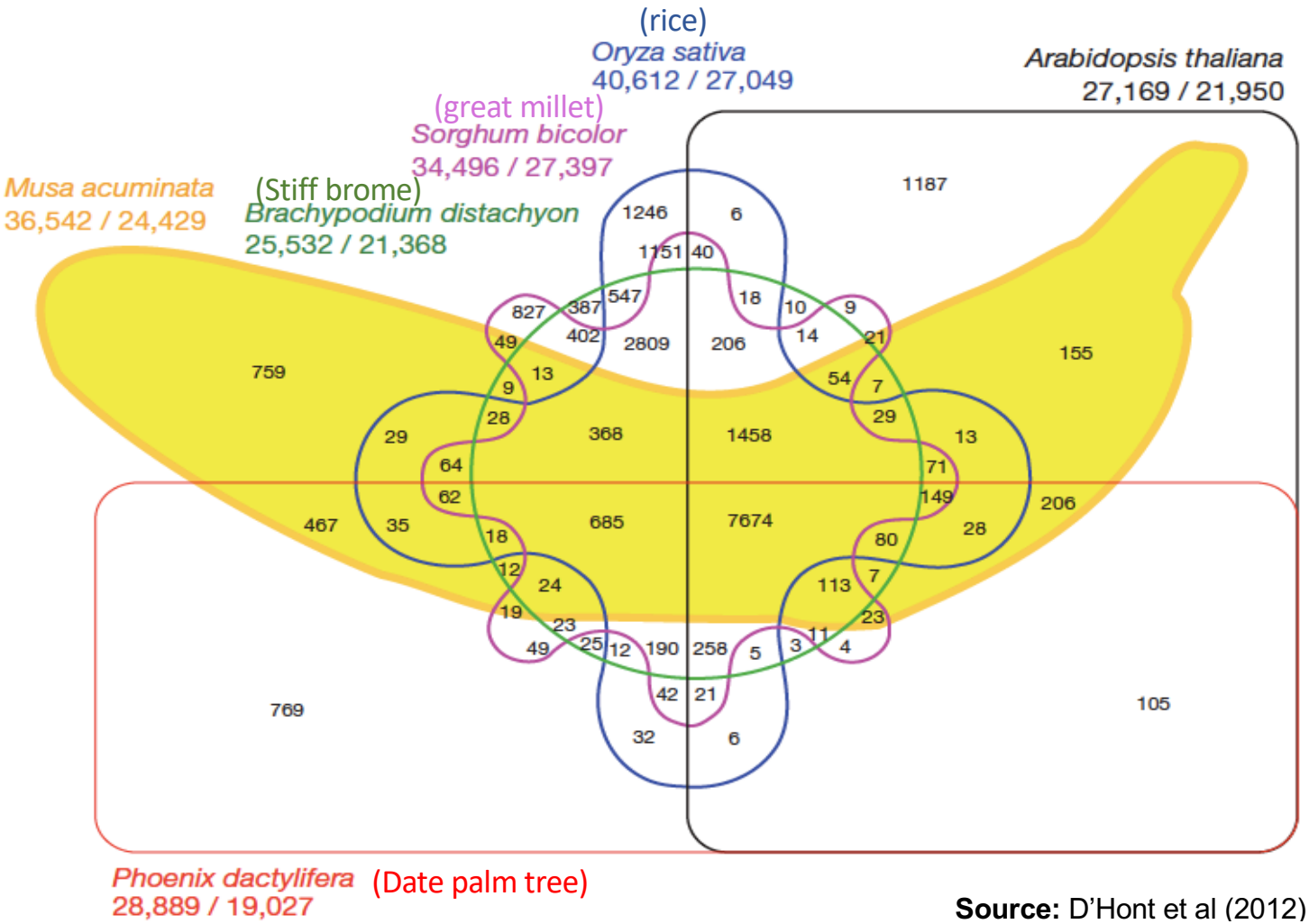
D'Hont et al (2012)

Results III



Shared genes families

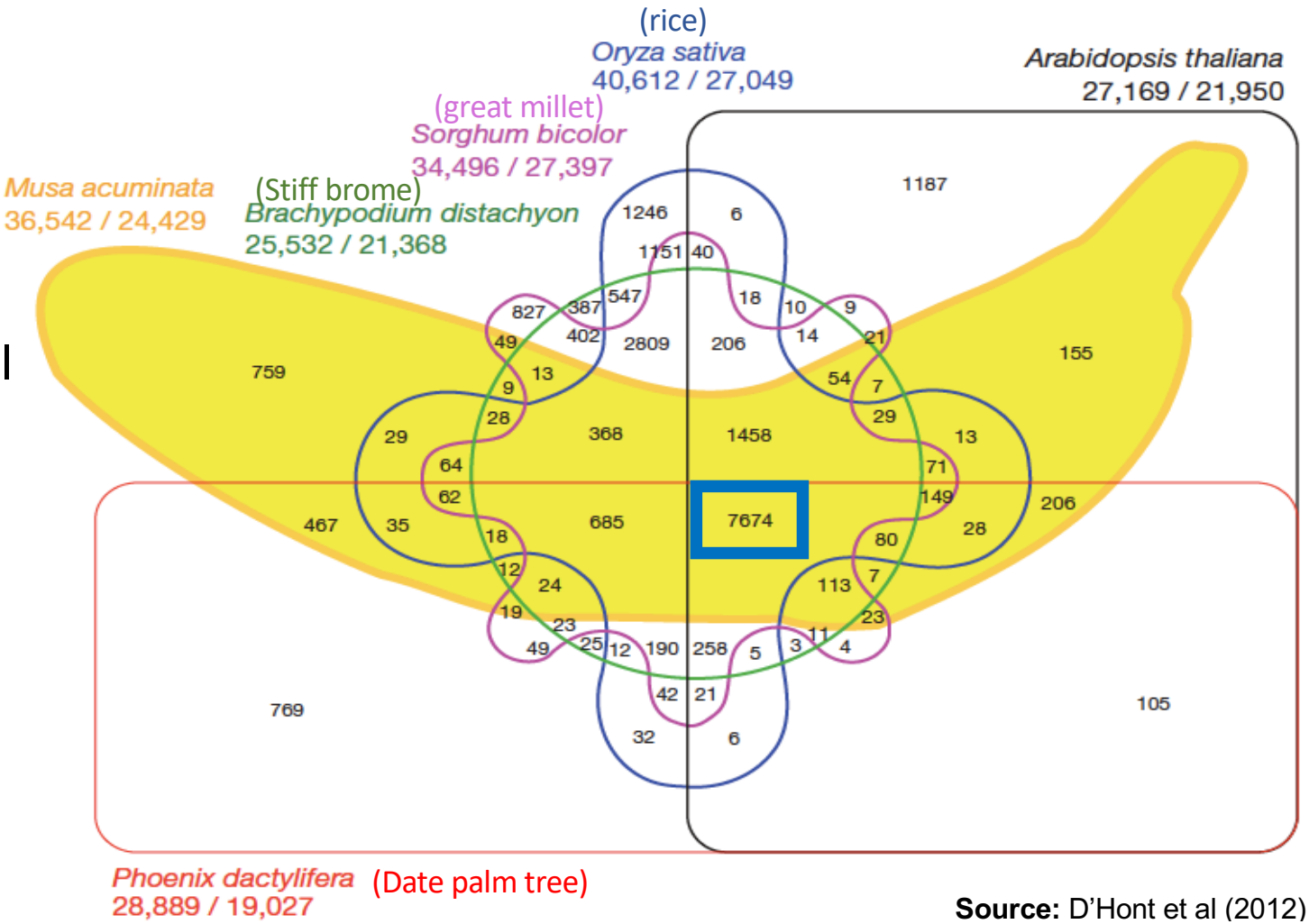
- *Musa,* date palm, *Brachypodium* (grass), rice, sorghum and *Arabidopsis* proteomes



Source: D'Hont et al (2012)

Shared genes families

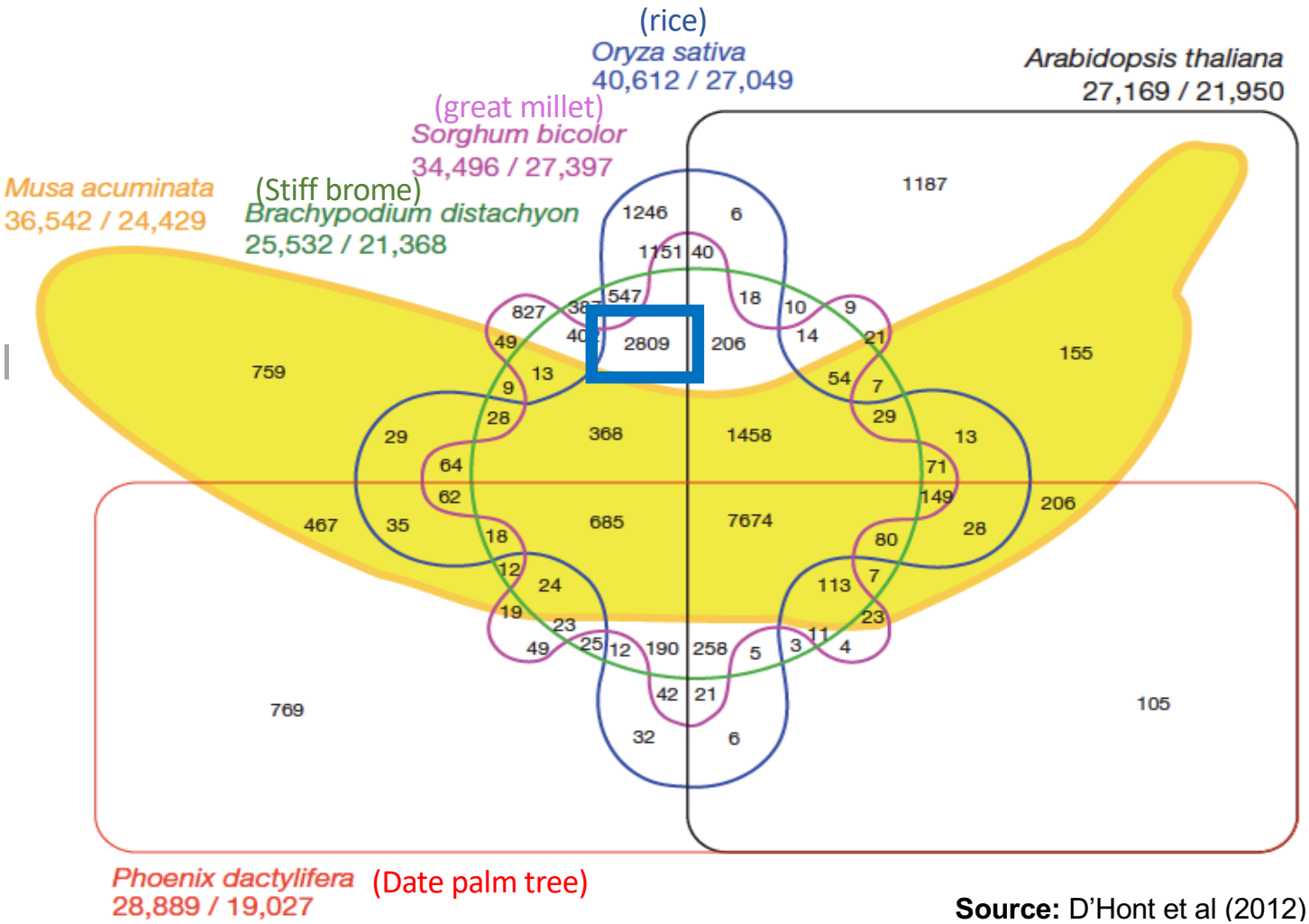
- *Musa,* date palm, *Brachypodium* (grass), rice, sorghum and *Arabidopsis* proteomes
- 7,674 represent ancestral gene families



Source: D'Hont et al (2012)

Shared genes families

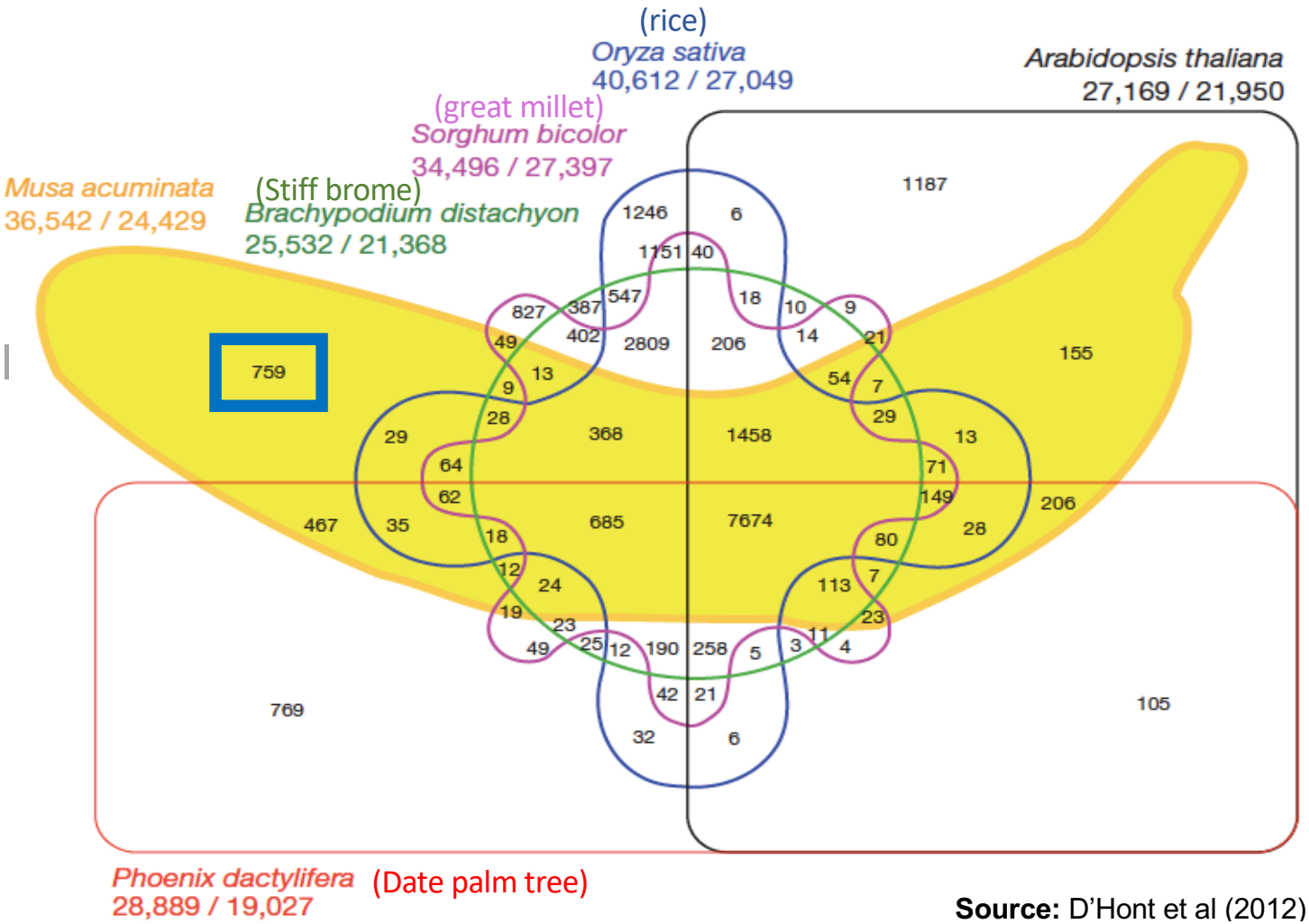
- *Musa,* date palm, *Brachypodium* (grass), rice, sorghum and *Arabidopsis* proteomes
- 7,674 represent ancestral gene families
- High level of gene divergence and diversification in grasses.



Source: D'Hont et al (2012)

Shared genes families

- *Musa,* date palm, *Brachypodium* (grass), rice, sorghum and *Arabidopsis* proteomes
- 7,674 represent ancestral gene families
- High level of gene divergence and diversification in grasses.
- Genes enriched in genes coding transcription factors, etc.



Source: D'Hont et al (2012)

Evolution of the Banana Genome (*Musa acuminata*) is impacted by Large Chromosomal Translocations

Martin et al (2017)

- Search and characterize large chromosomal rearrangements and its impact in chromosome segregation
- *M. acuminata* ssp. *malaccensis* accession (PT-BA-00267)



Source: www.promusa.org

Evolution of the Banana Genome (*Musa acuminata*) is impacted by Large Chromosomal Translocations

Martin et al (2017)

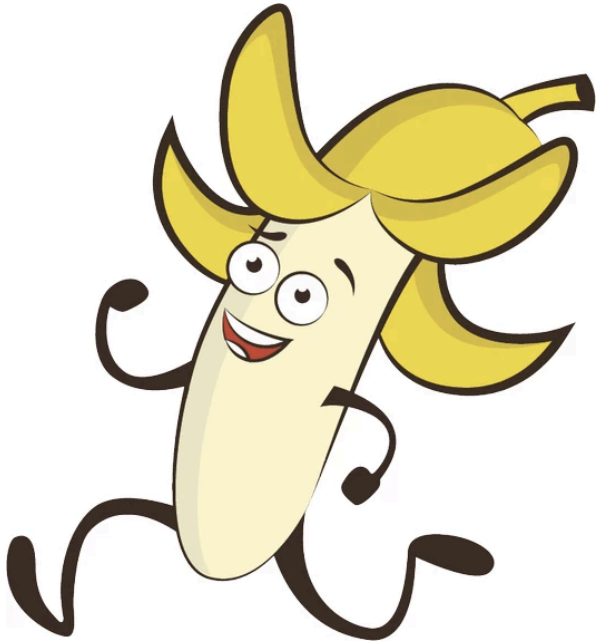
- Search and characterize large chromosomal rearrangements and its impact in chromosome segregation
- *M. acuminata* ssp. *malaccensis* accession (PT-BA-00267)
  - Mate-pair sequencing
  - BAC-FISH
  - Targeted PCR
  - DArTseq marker segregation

Evolution of the Banana Genome (*Musa acuminata*) is impacted by Large Chromosomal Translocations

Martin et al (2017)

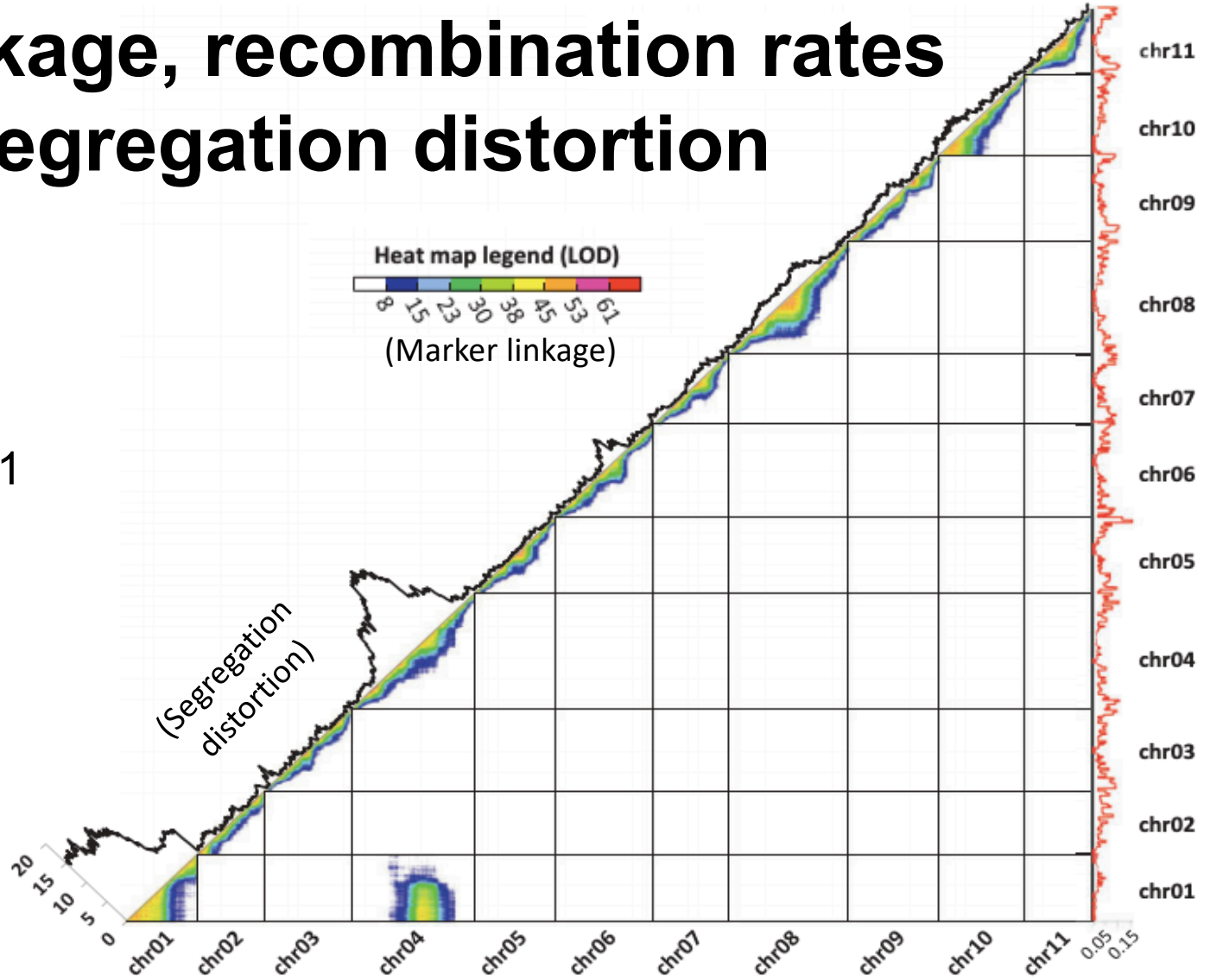
Results I

- 180 self-progeny individuals of the PT-AB-00267 accession were genotyped



Marker linkage, recombination rates and segregation distortion

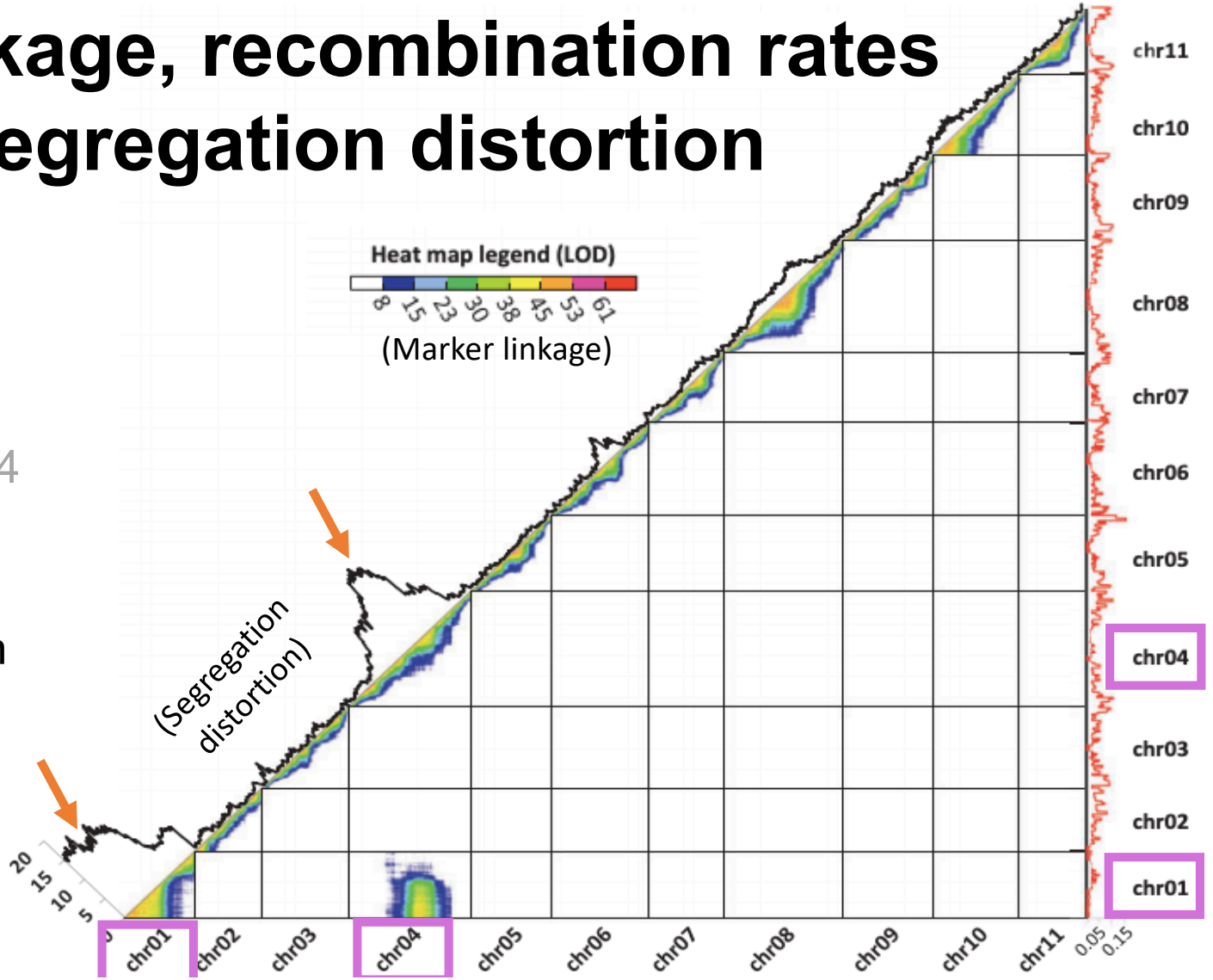
- Recombination rate was positively correlated with gene density
  - Except two gene-rich regions: chromosome 01 and 04



Source: Martin et al. (2017)

Marker linkage, recombination rates and segregation distortion

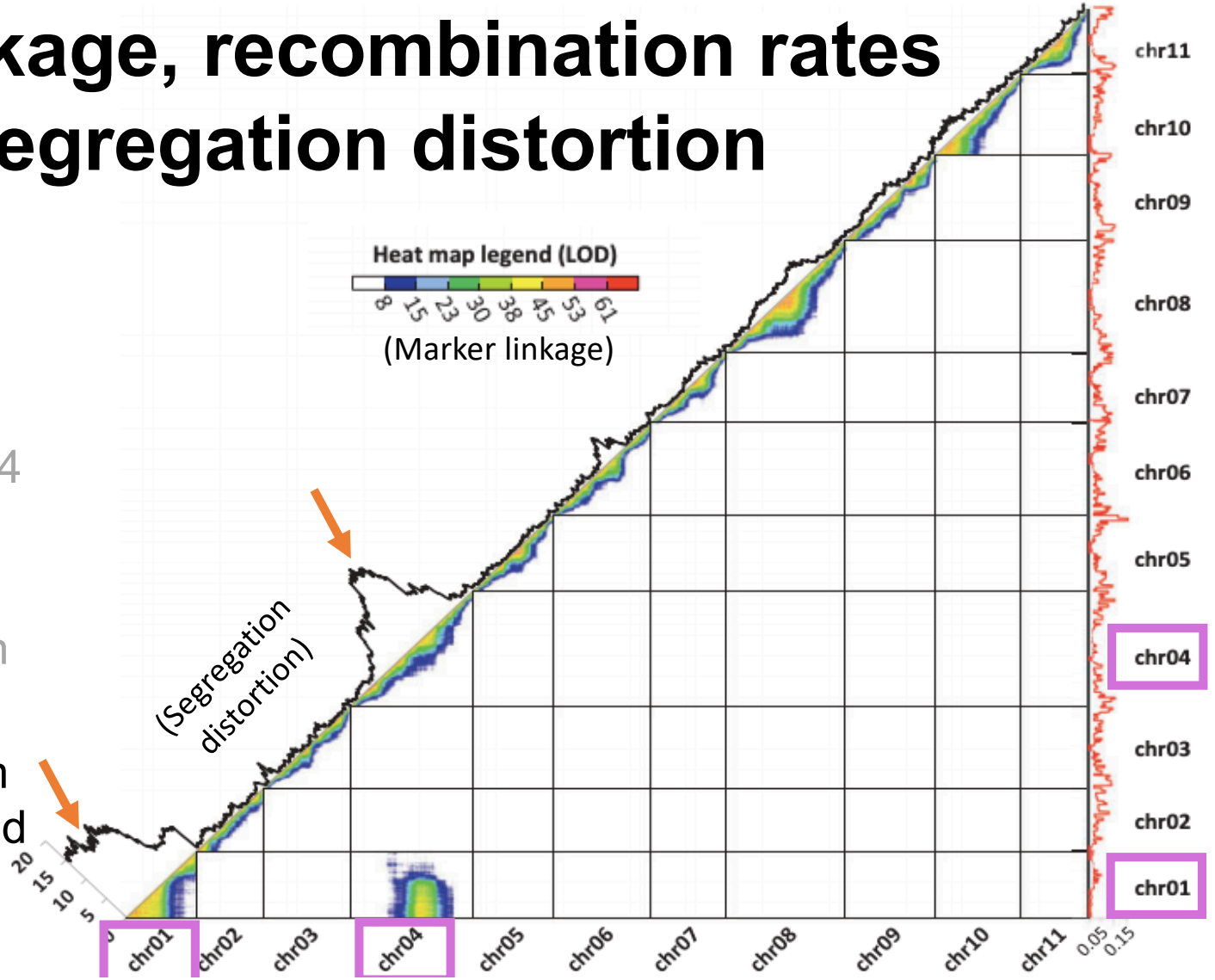
- Recombination rate was in positively correlated with gene density
  - Except two gene-rich regions: chromosome 04 and 01
- Regions of Chr. 01 and 04 with reduced recombination showed highest distortion



Source: Martin et al. (2017)

Marker linkage, recombination rates and segregation distortion

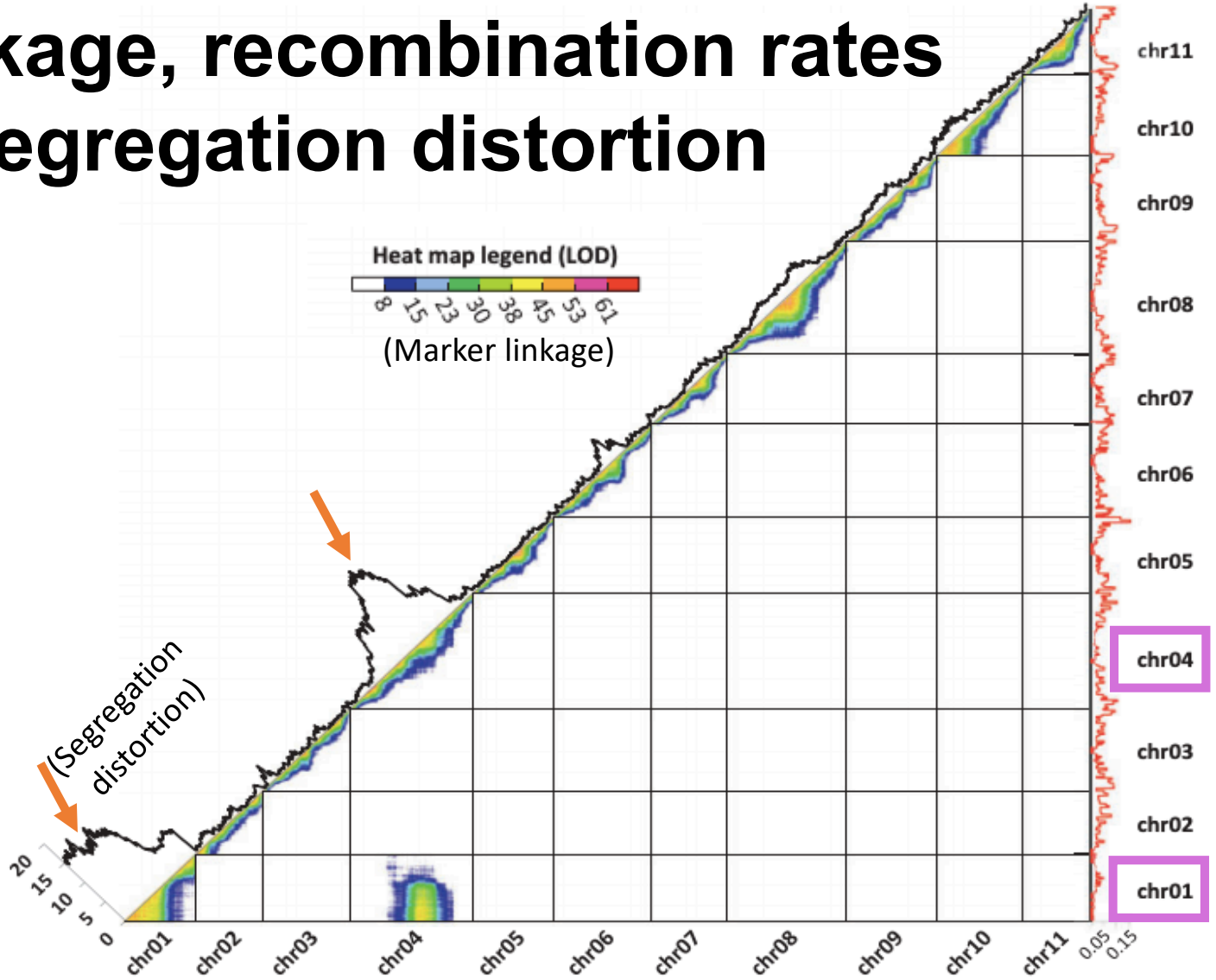
- Recombination rate was in positively correlated with gene density
  - Except two gene-rich regions: chromosome 04 and 01
- Regions of Chr. 01 and 04 with reduced recombination showed highest distortion
- 24% markers deviated from Mendelian ratio (Chr. 01 and 04)



Source: Martin et al. (2017)

Marker linkage, recombination rates and segregation distortion

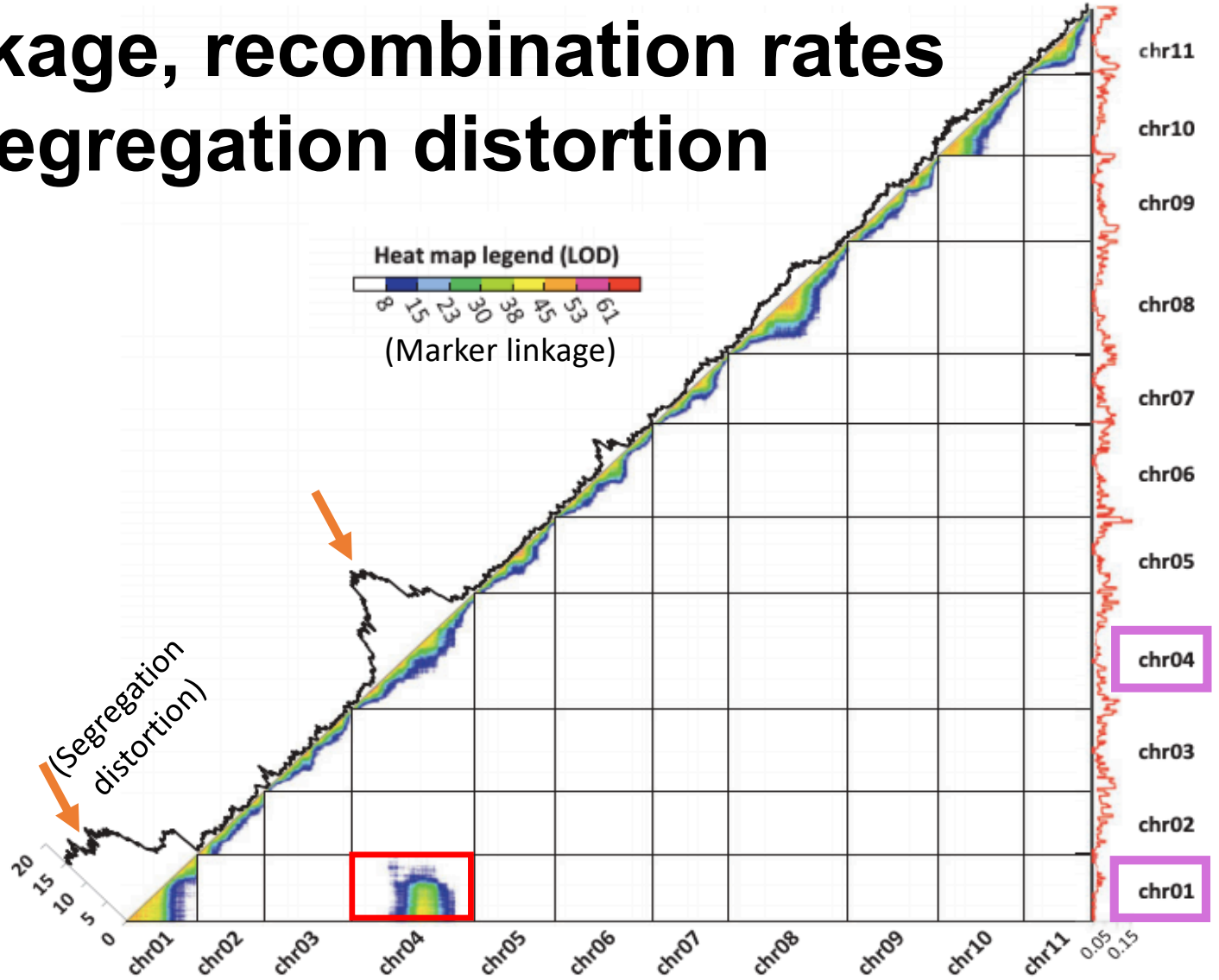
- Segregation bias consisted in an excess of one genotype: AA, 53% vs 25% expected (Aa, 39% vs 50%; aa, 8% vs 25%



Source: Martin et al. (2017)

Marker linkage, recombination rates and segregation distortion

- Segregation bias consisted in an excess of one genotype: AA, 53% vs 25% expected (Aa, 39% vs 50%; aa, 8% vs 25%
- Markers highly linked: distal region of acrocentric Chr.01 and pericentromeric region of Chr. 04.

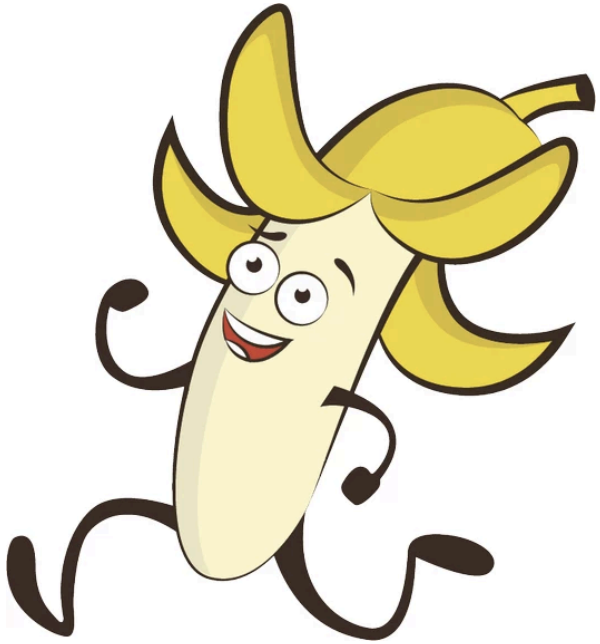


Source: Martin et al. (2017)

Evolution of the Banana Genome (*Musa acuminata*) is impacted by Large Chromosomal Translocations

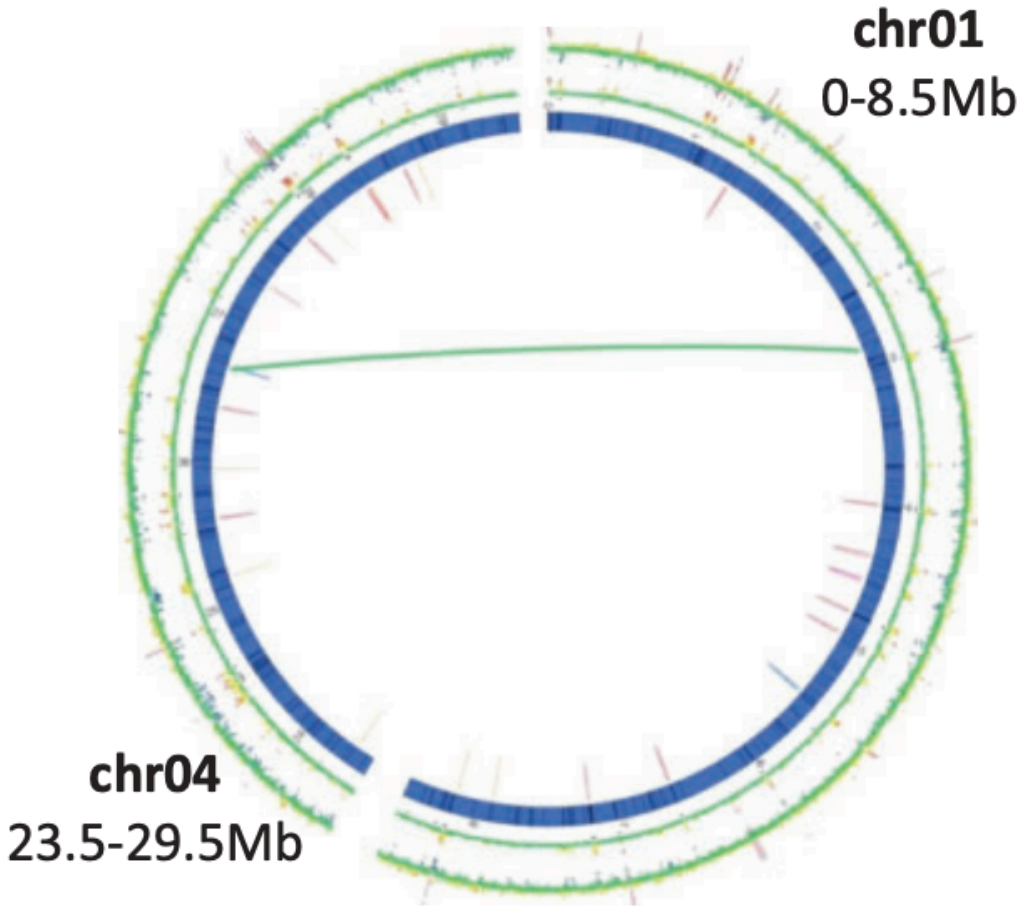
Martin et al (2017)

Results II



Paired read evidence for reciprocal translocation

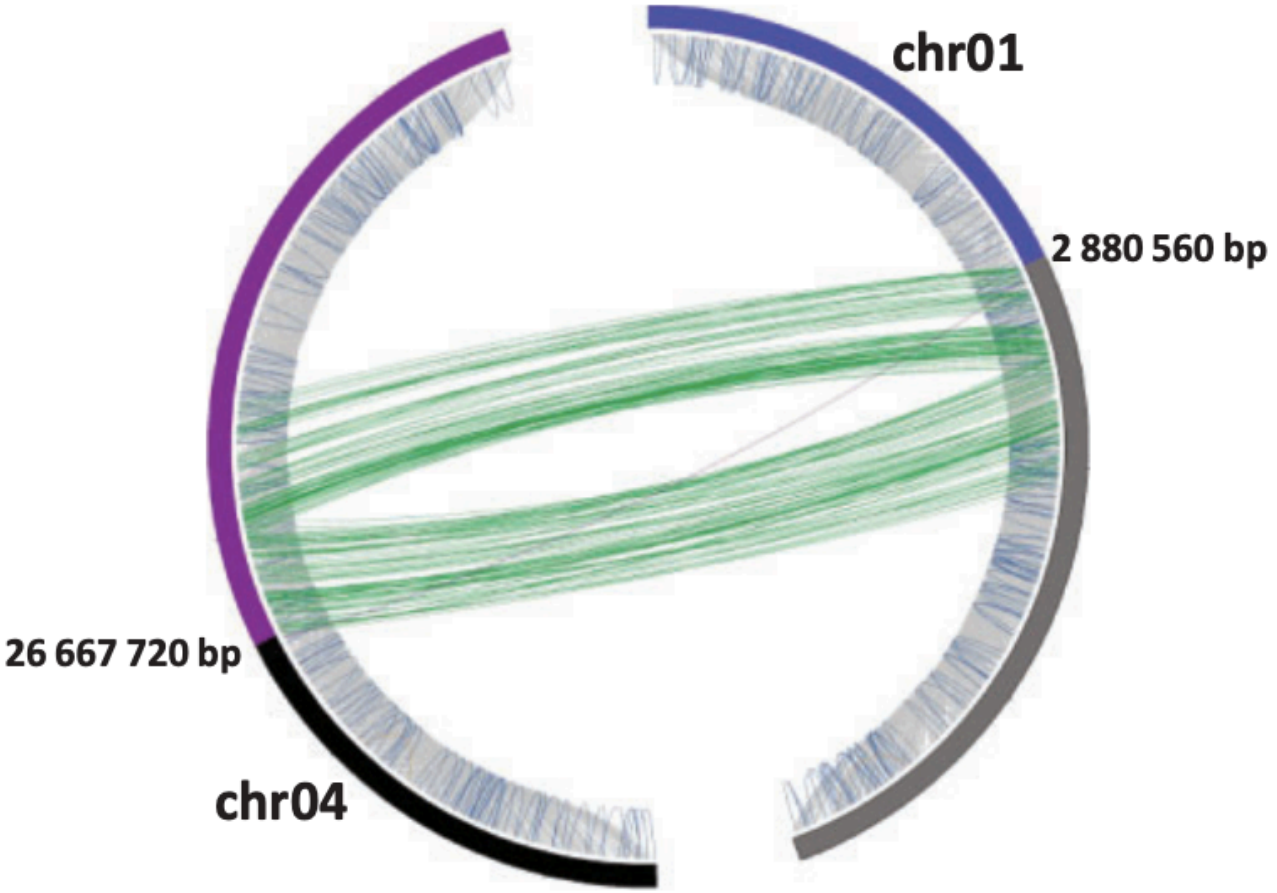
- Significant cluster of discordant paired reads was found linking the regions of reference genome 01 and 04
- Only one discordant cluster linking Chr. 01 and 04 (expected at least 2)



Source: Martin et al. (2017)

Paired read evidence for reciprocal translocation

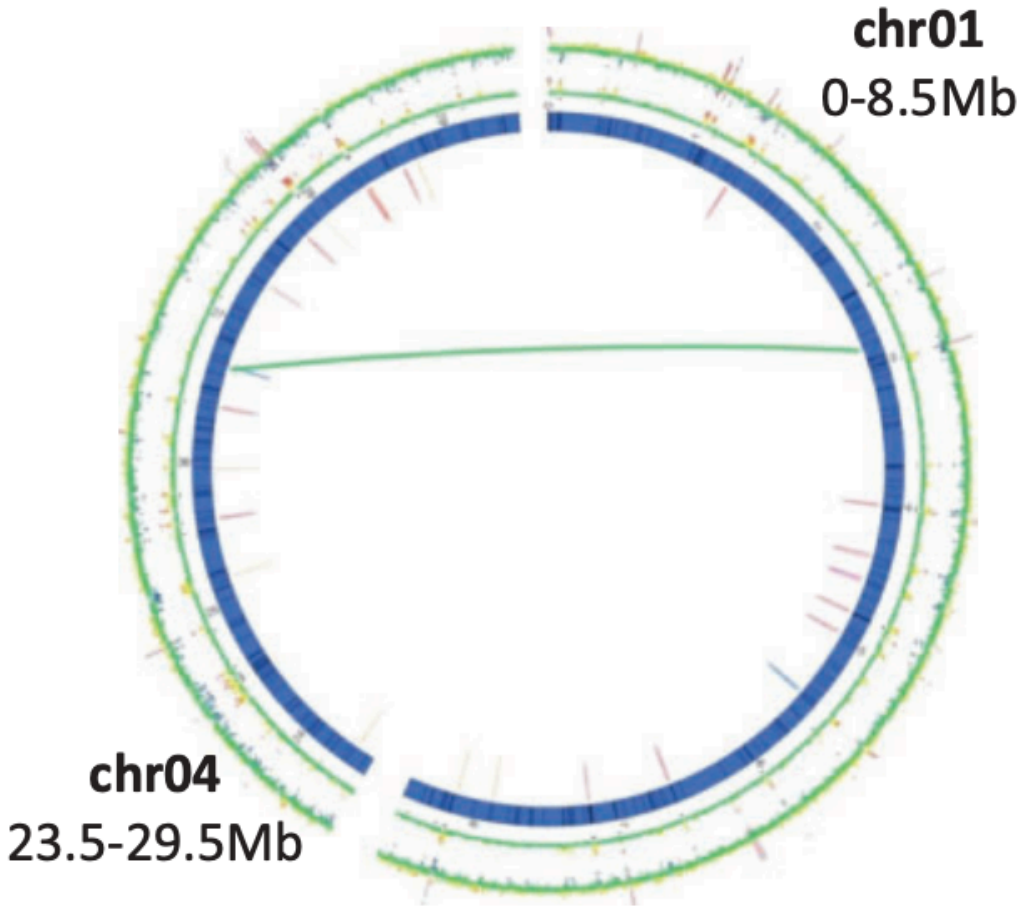
- Concordant mapped paired reads overlapping the two translocation breakpoints
- Structural variation was at a heterozygous state



Source: Martin et al. (2017)

Paired read evidence for reciprocal translocation

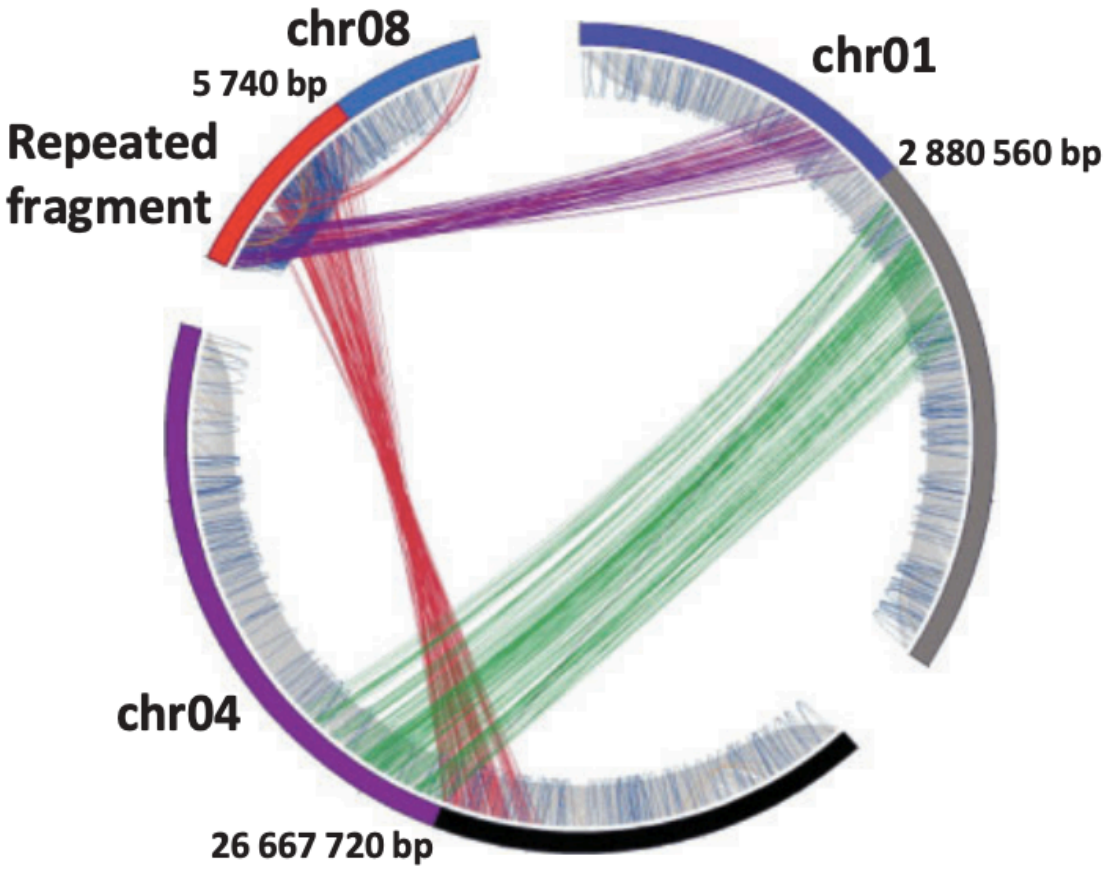
- Significant cluster of discordant paired reads was found linking the regions of reference genome 01 and 04
- Only one discordant cluster linking Chr. 01 and 04 (expected at least 2)



Source: Martin et al. (2017)

Paired read evidence for reciprocal translocation

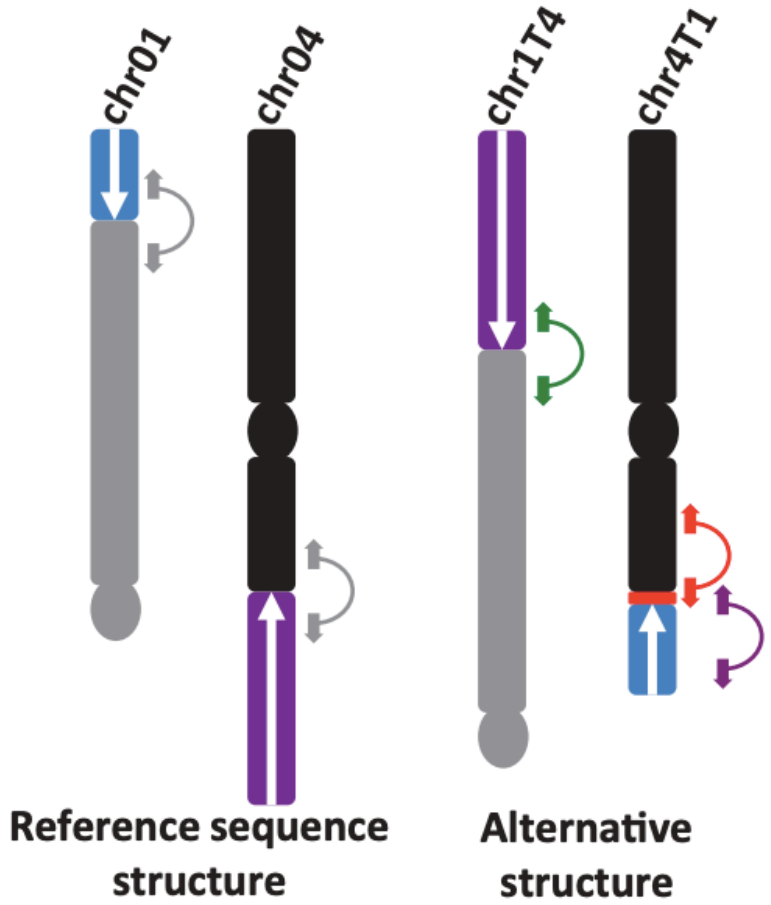
- A cluster (64 paired reads) links Chr. 01 to the extremity of Chr. 08.
- A second cluster (104 paired reads) that linked same region of Chr. 08 to reference Chr.04
- Presence of reciprocal translocation in a heterozygous state involving both chromosomes



Source: Martin et al. (2017)

Paired read evidence for reciprocal translocation

- Reciprocal translocation in a heterozygous state involving Chr. 01 and 04
- Chr. 01 and 04: reference genome sequence
- Chr. 1T4 and 4T1: chromosomal structures from reciprocal translocation
- Repeat sequence only present in Chr.08: indirect link between Chr.01 and 04 through Chr.08

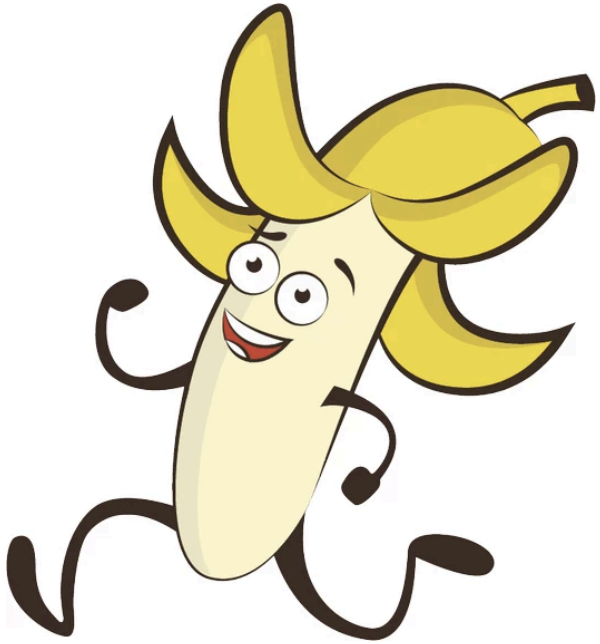


Source: Martin et al. (2017)

Evolution of the Banana Genome (*Musa acuminata*) is impacted by Large Chromosomal Translocations

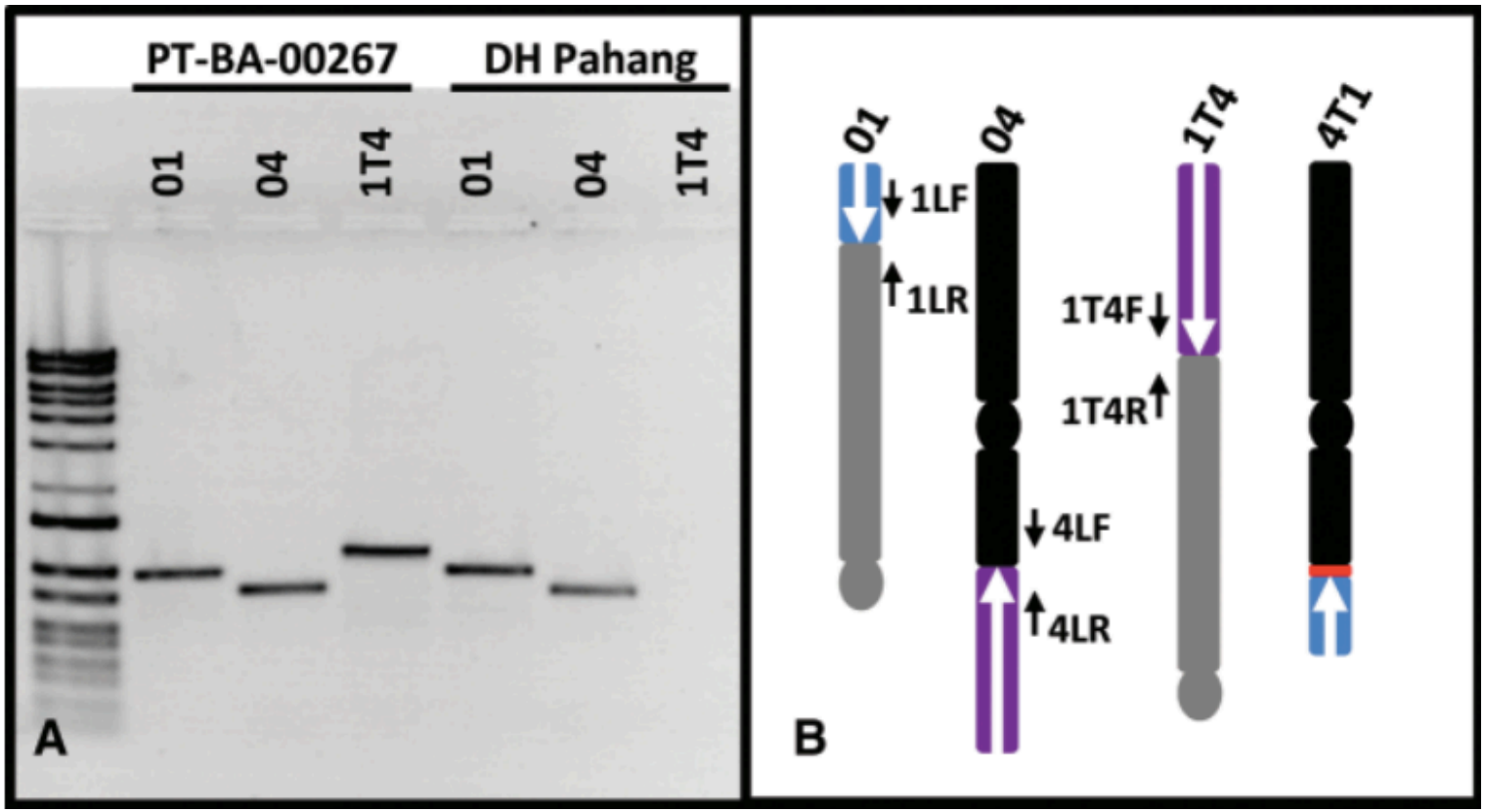
Martin et al (2017)

Results III



Validation of PT-BA-00267 structural heterozygosity

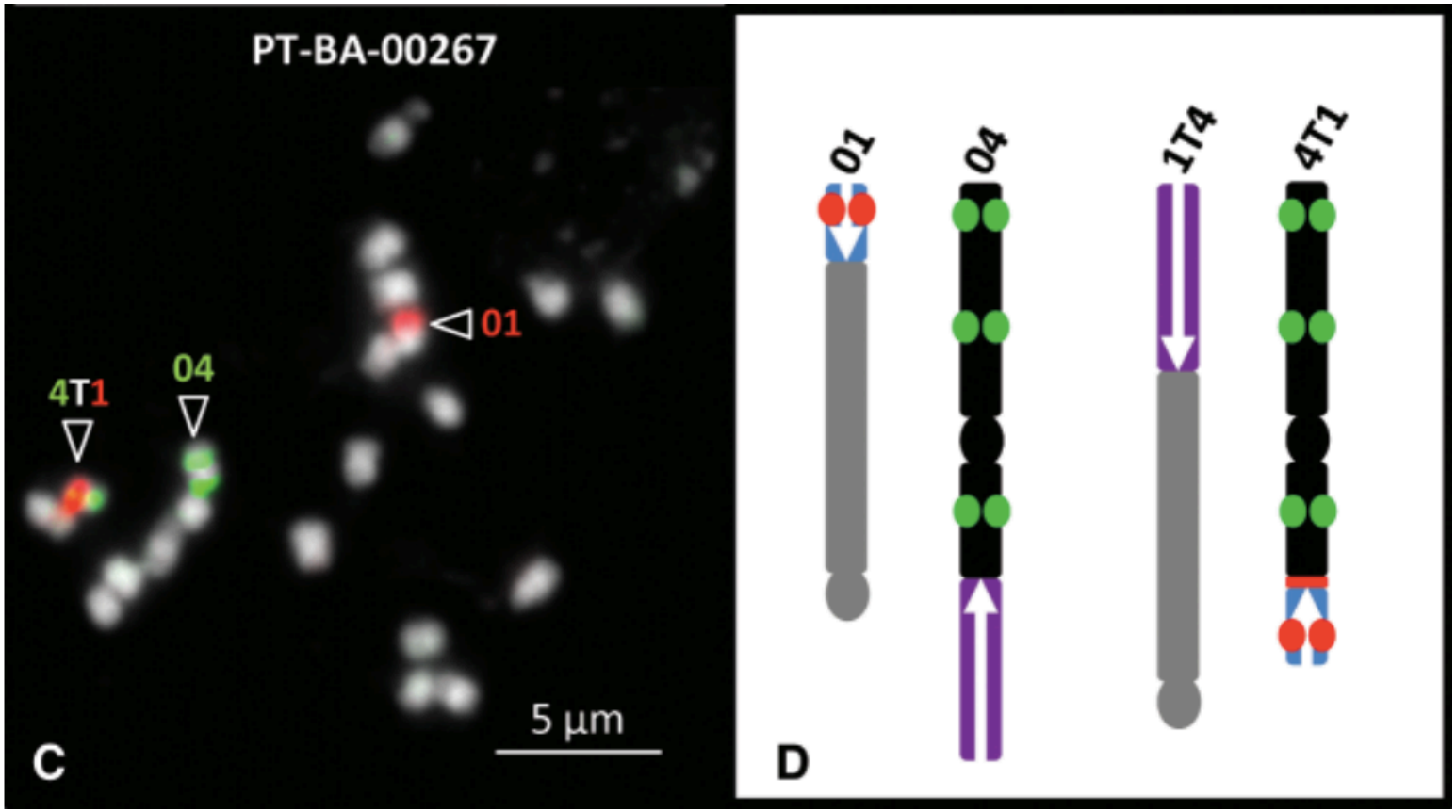
- PCR primer to asses the presence of a breakpoint on Chr. 01, 04 and 1T4
- PCR confirmed presence of breakpoints



Source: Martin et al. (2017)

BAC-FISH for presence of reciprocal translocation

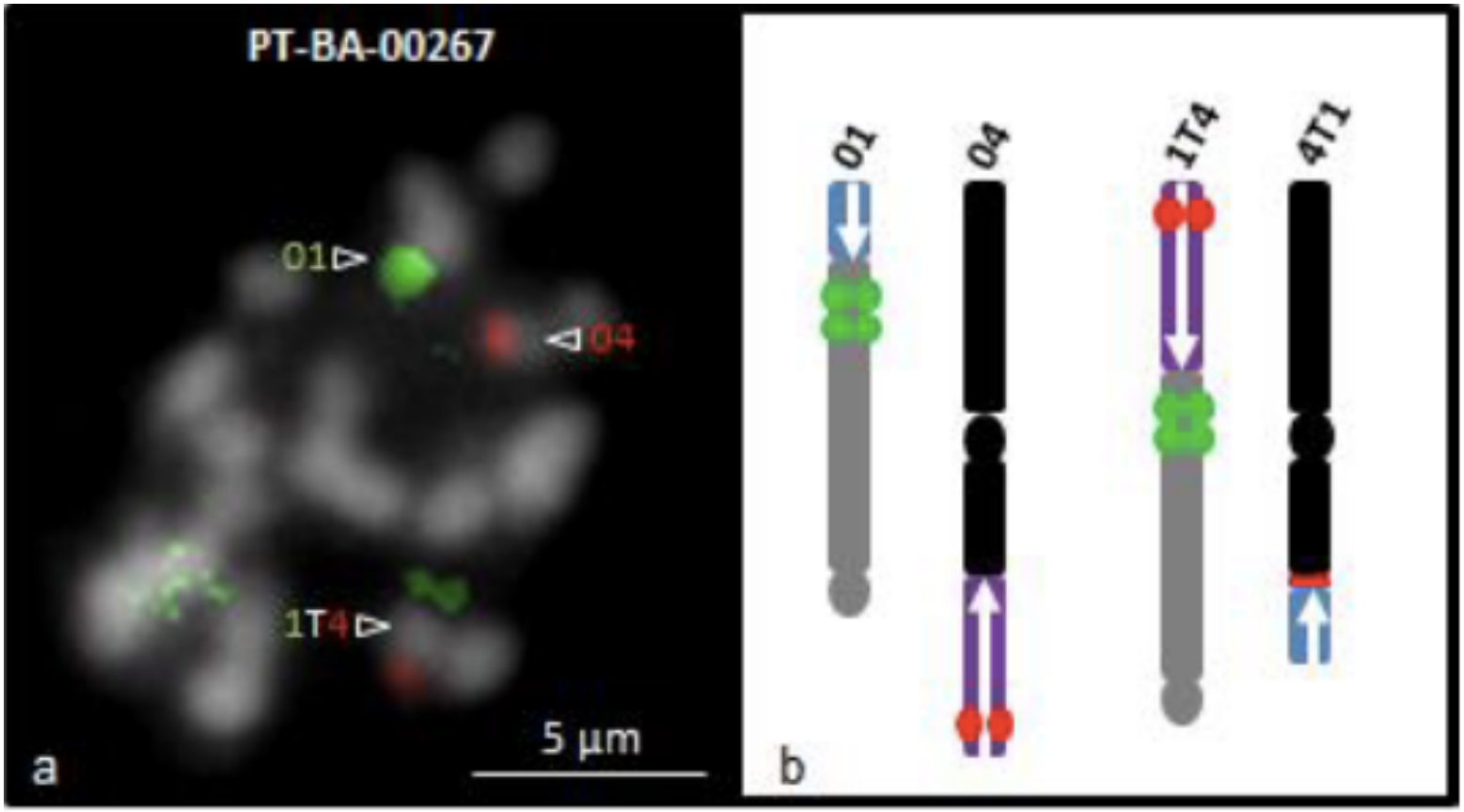
- Presence of four breakpoints, reference Chr. 01 and 04, and Chr. 1T4 and 4T1.



Source: Martin et al. (2017)

BAC-FISH for presence of reciprocal translocation

- Presence of four breakpoints, reference Chr. 01 and 04, and Chr. 1T4 and 4T1.

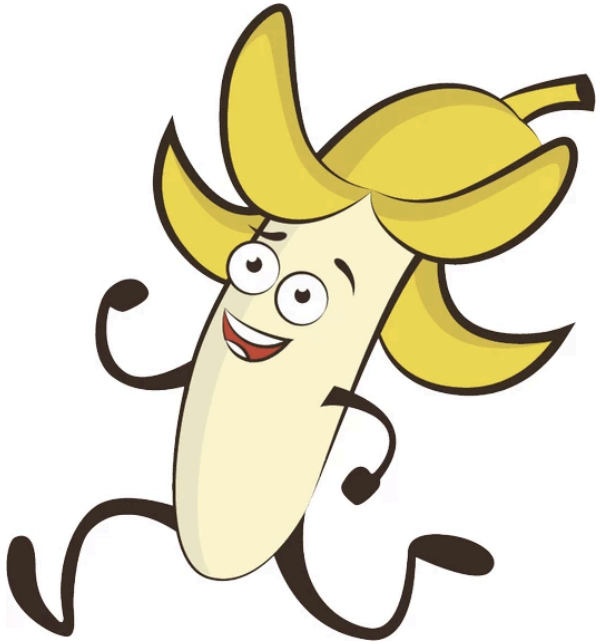


Source: Martin et al. (2017)

Evolution of the Banana Genome (*Musa acuminata*) is impacted by Large Chromosomal Translocations

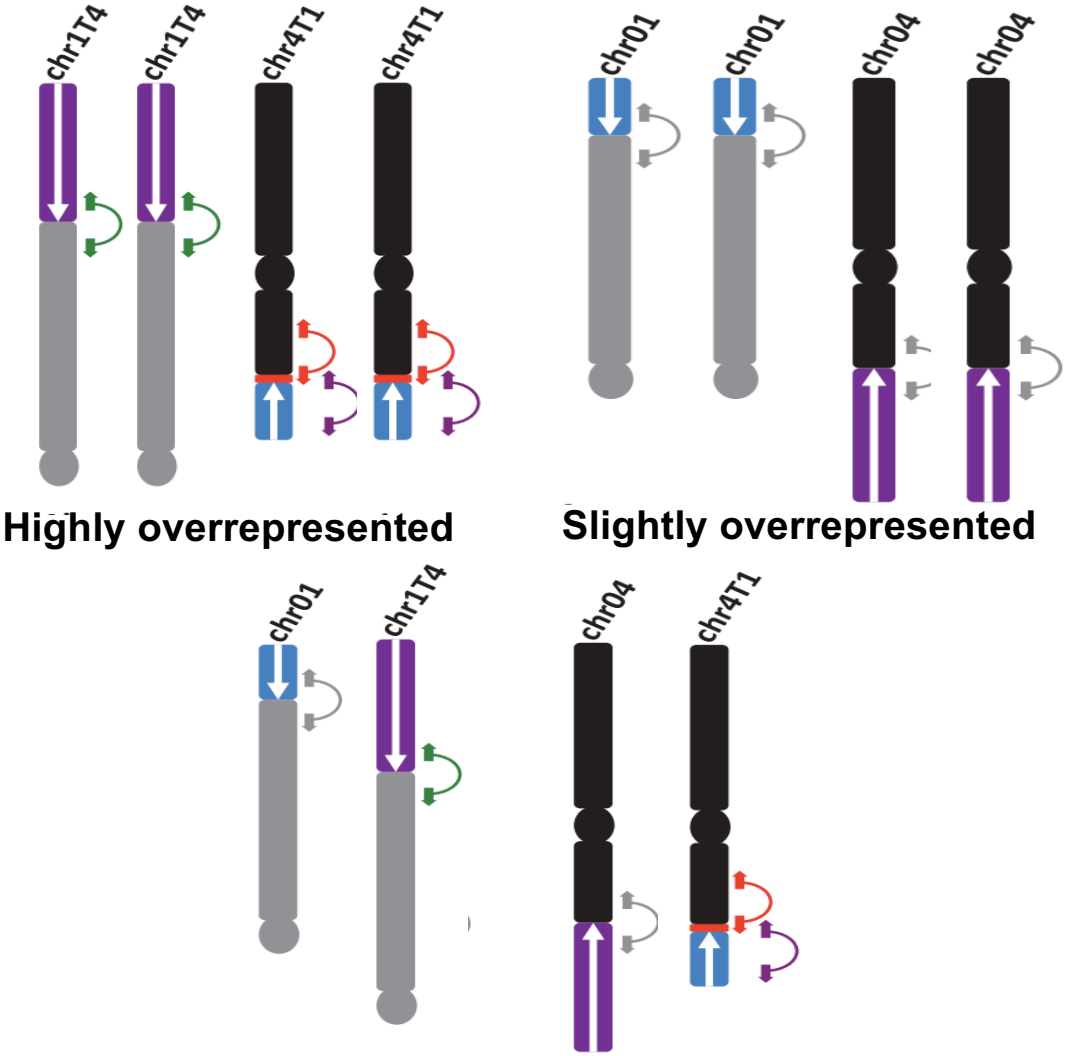
Martin et al (2017)

Results IV



Structural heterozygosity consequences

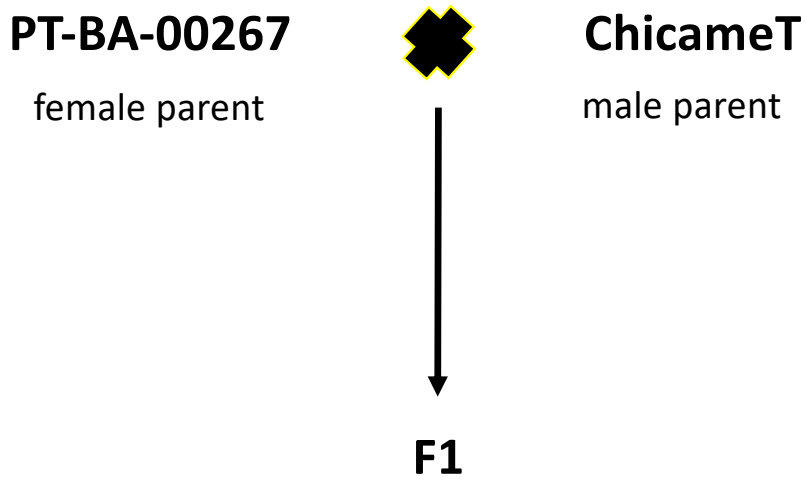
- Marker segregation biased in favor of an excess of one homozygous genotype
  - Overrepresented homozygous for Chr. 1T4 and 4T1
- 4 possible genotype combinations, 3 exhibited in higher than expected Mendelian segregation frequency and 1 lower.
- Gametic or zygotic selection?



Source: Martin et al. (2017)

Structural heterozygosity consequences

- F1 showed high segregation distortion and linkage involving Chr. 01 and 04
- Gametic selection: only maternal gametes having 1T4 and 4T1 (100% viability) or 01 and 04 (28% viability) were transmitted.

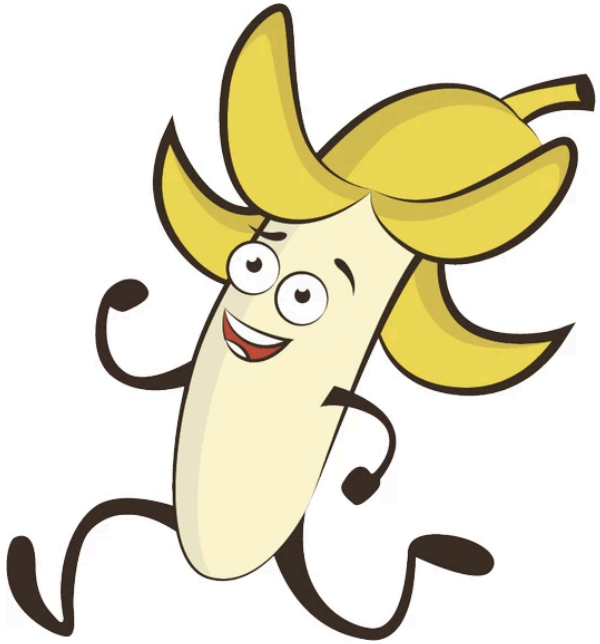


Source: Martin et al. (2017)

Evolution of the Banana Genome (*Musa acuminata*) is impacted by Large Chromosomal Translocations

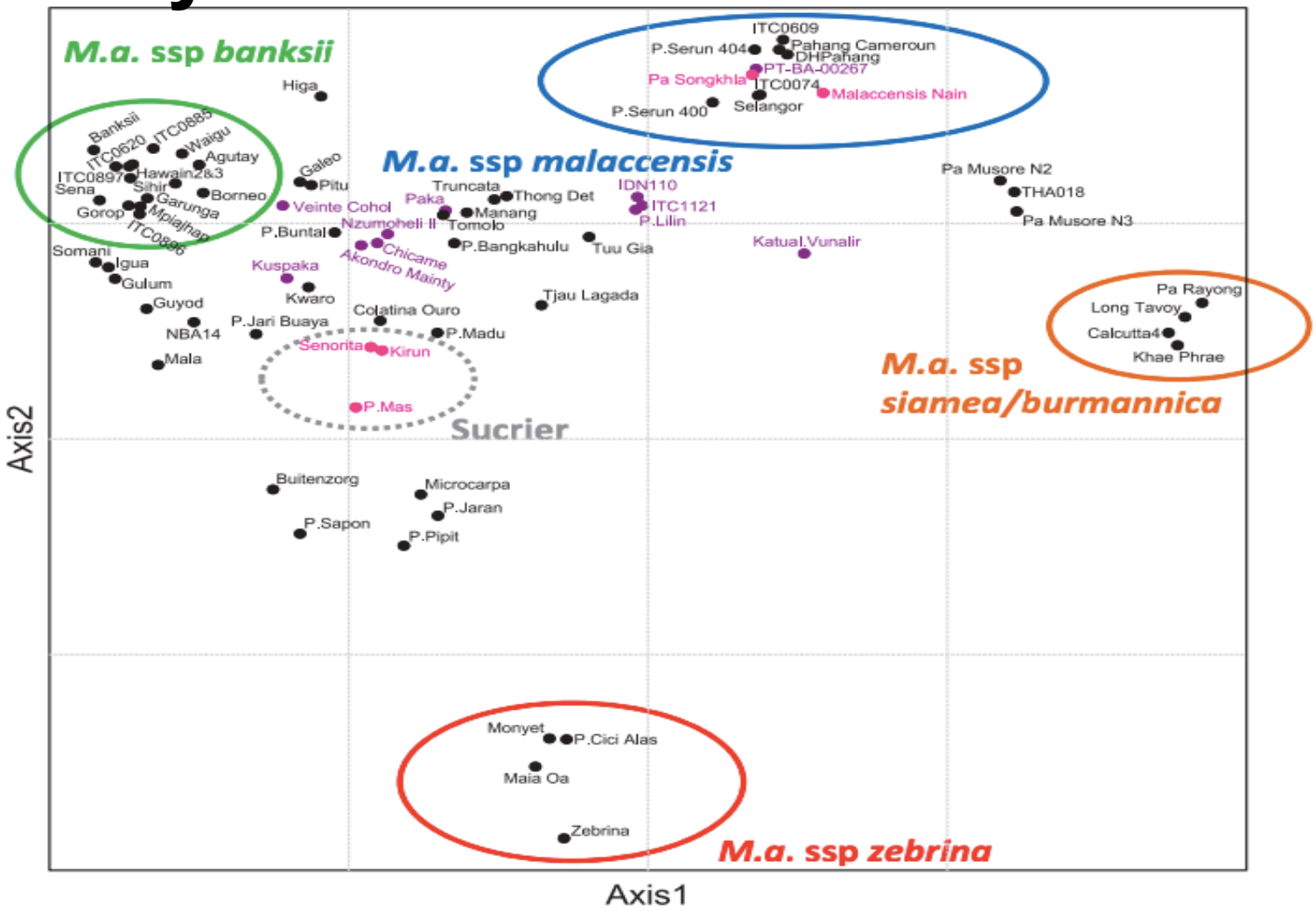
Martin et al (2017)

Results V



Factorial analysis in *Musa* accessions

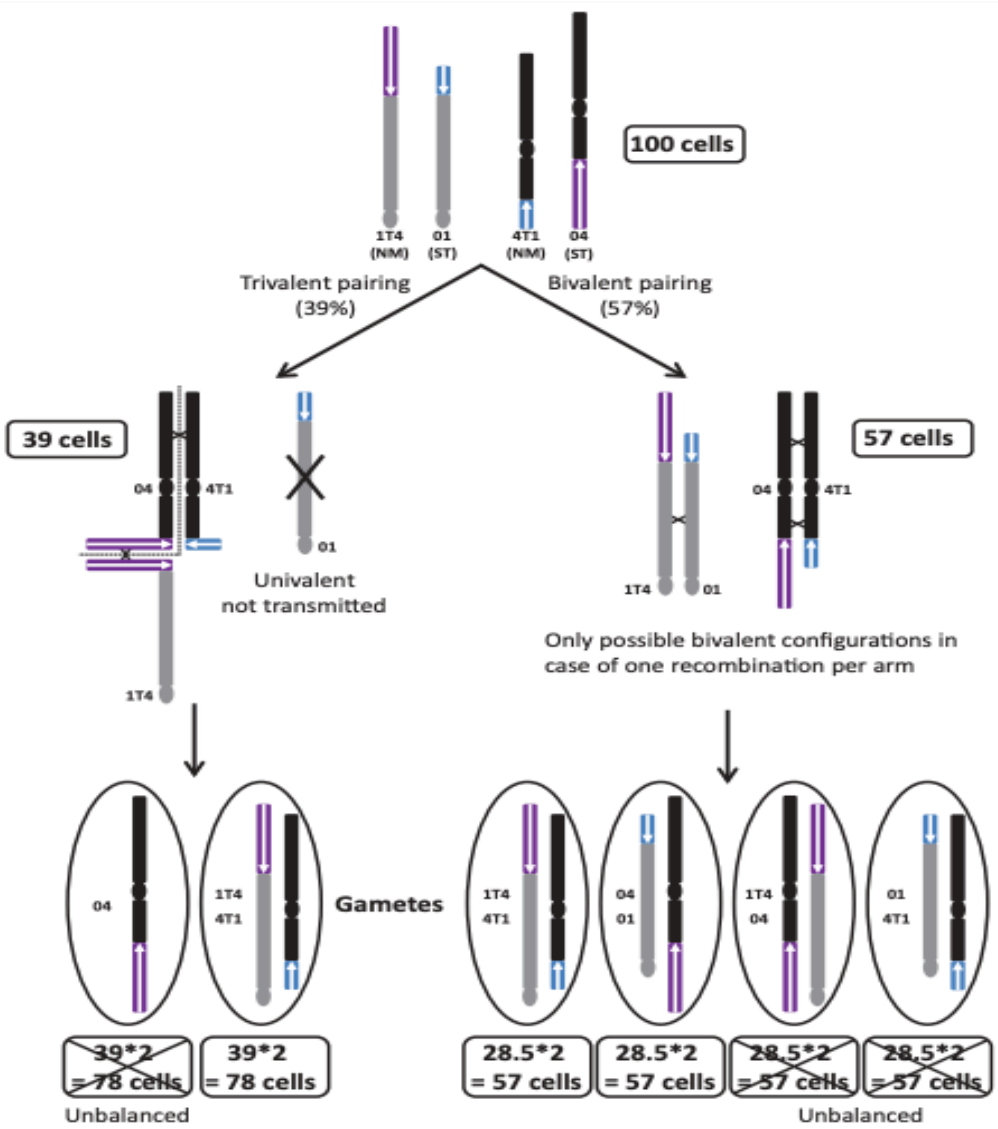
- Homozygous for Chr. 1T4 and 4T1 present in two genetic groups (pink)
- Heterozygous accessions located in triangle (purple).



Source: Martin et al. (2017)

Chromosomal pairing within heterozygous accession

- Differential gamete transmission: biased proportion in favor of Chr. 1T4 and 4T1
- NM structure was found in 39% of tested banana cultivars



Source: Martin et al. (2017)

Becoming seedless

- Domestication process: form full of seeds to seedless
- Earliest archeological evidence: Papua New Guinea ~7000 years ago



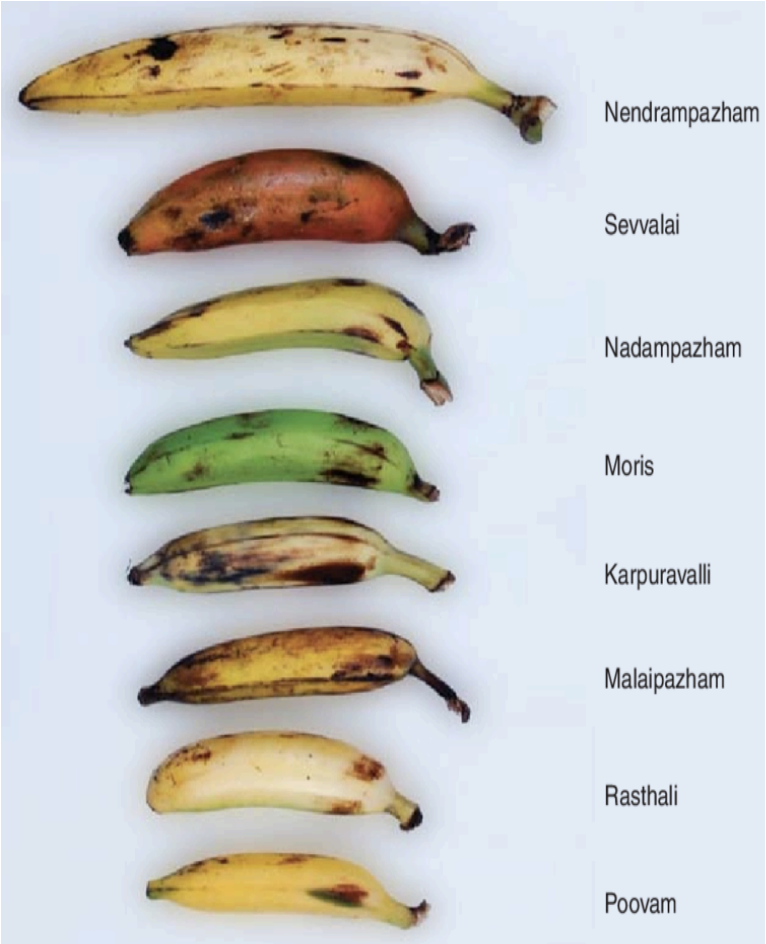
Source: Slesak et al. (2011)



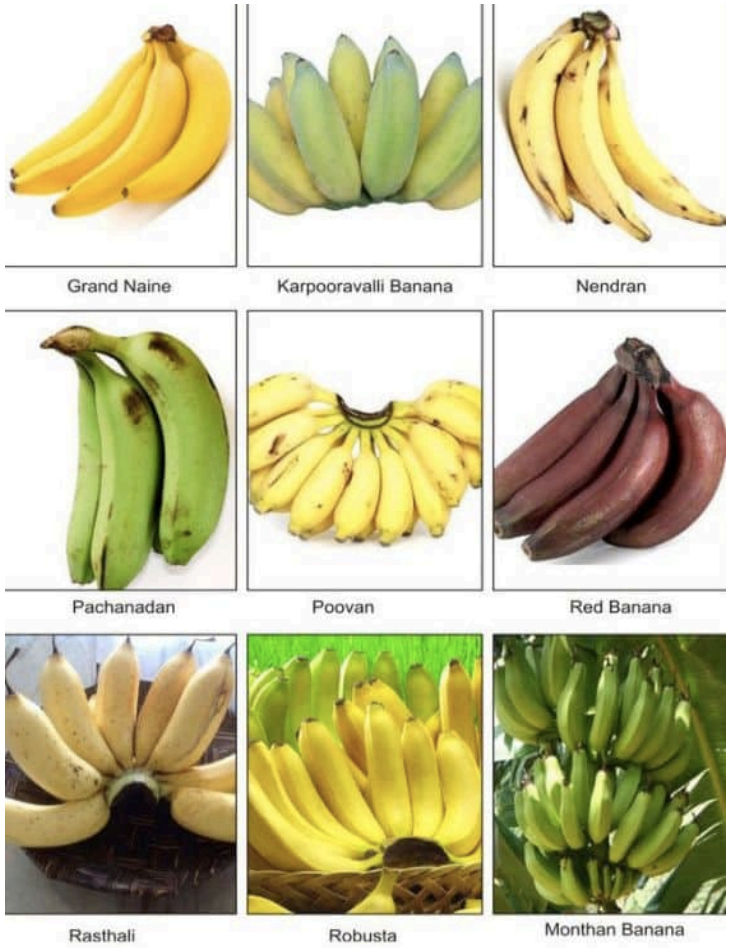
Source: www.musarama.org

Becoming seedless

- Domestication process: form full of seeds to seedless
- Earliest archeological evidence: Papua New Guinea ~7000 years ago
- Ancestor of bananas domesticated in Pacific regions has not been identified (Fei bananas)
- 1000 cultivar varieties



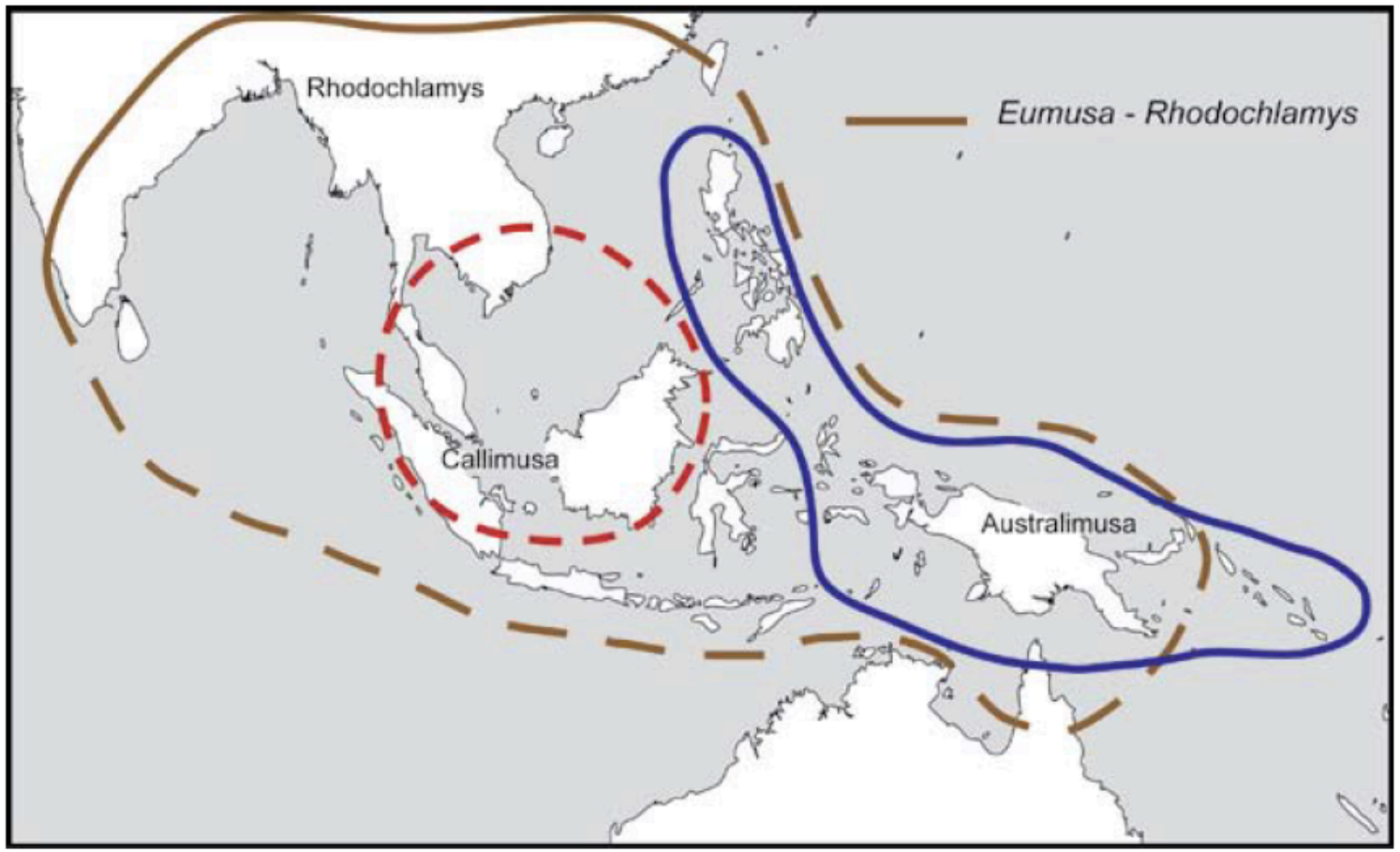
Source: Akilanathan et al. 2010



Source: www.agrifarming.in

Geographical distribution: Section *Musa*

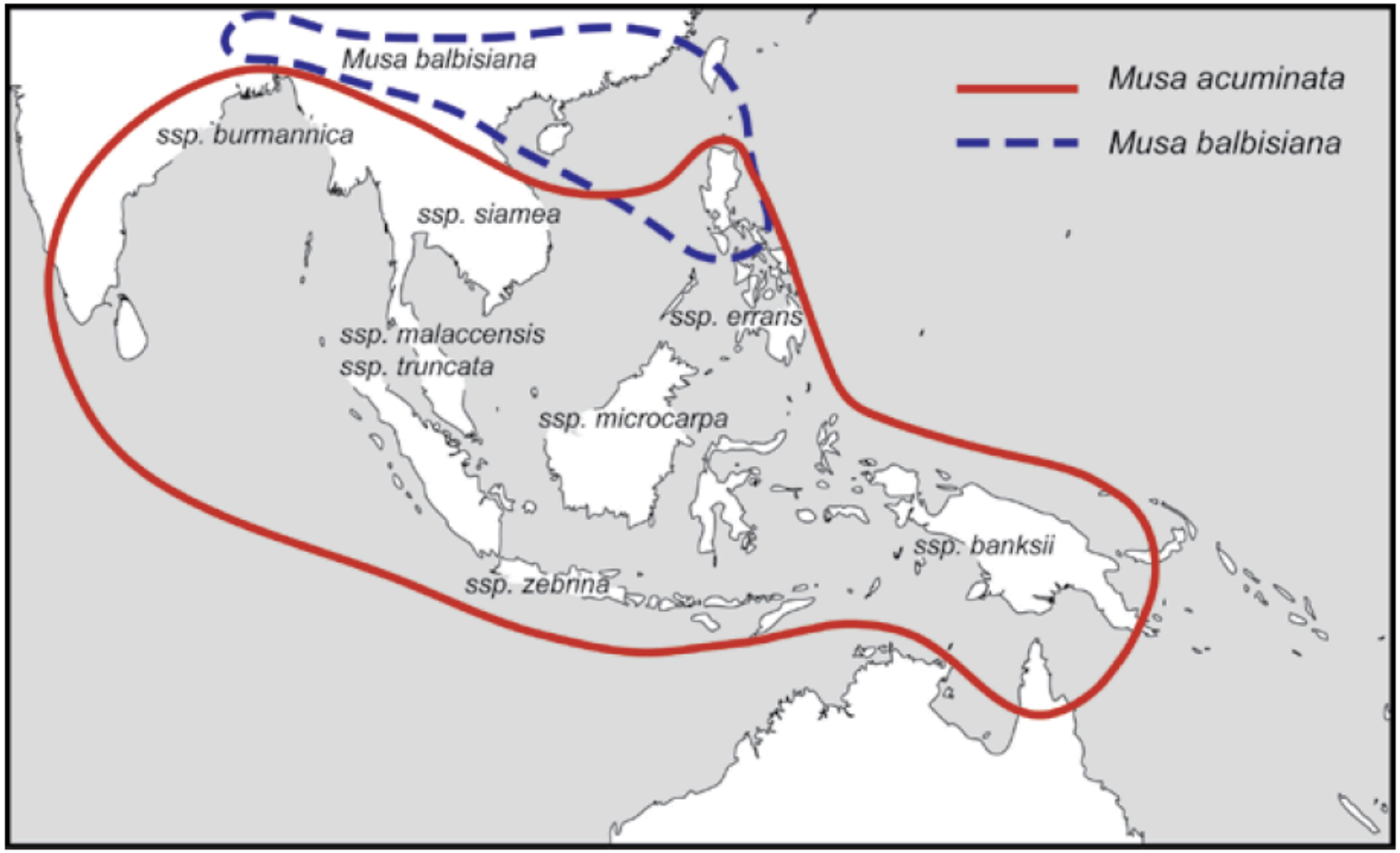
- North from Nepal and southern mountainous China
- South to the southern islands of Indonesia and New Guinea, with an outlier in the wet tropical rainforests of Queensland
- Western: India
- East: Melanesia



Source: De Langhe et al. (2009)

Ancestors of edible bananas

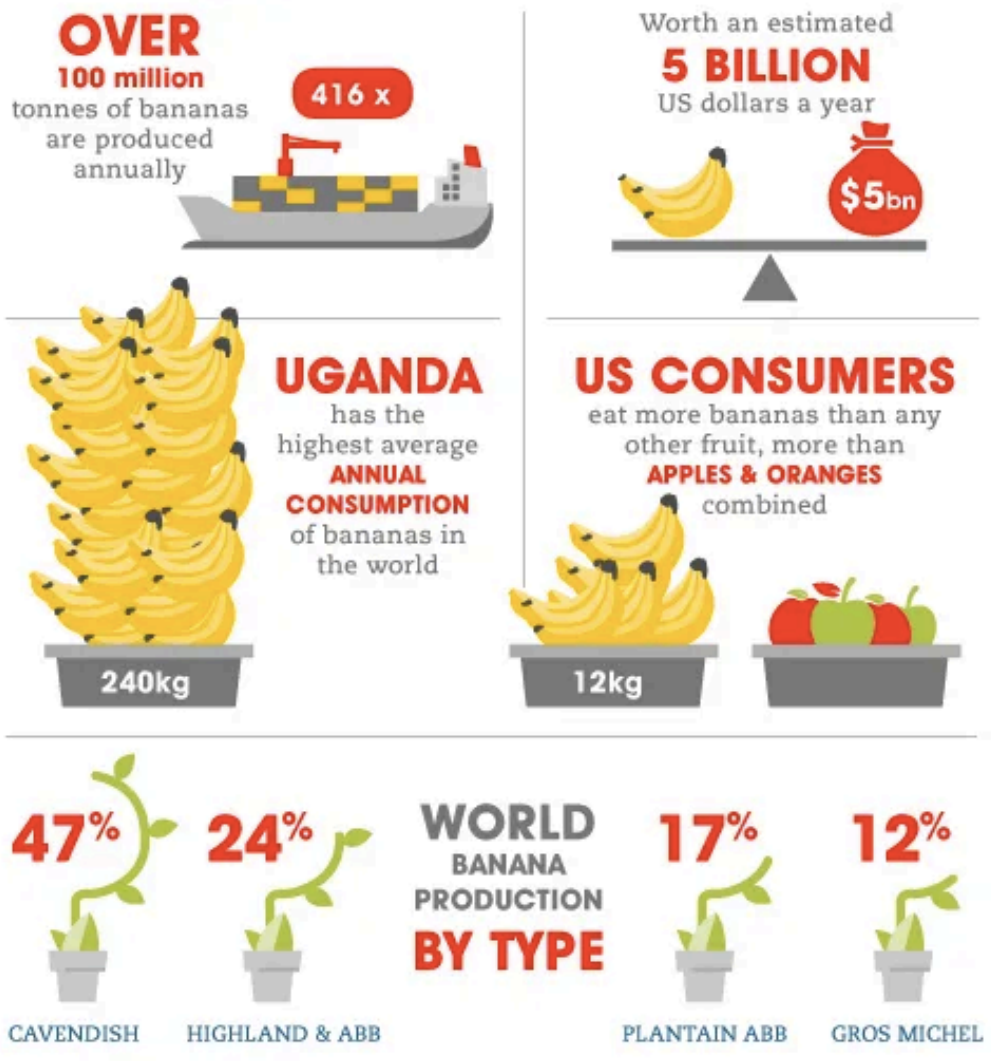
- Presence of *M. balbisiana* in lowlands may be due to anthopogenic effects
- Human migration during Holocene transporte plant material



Source: De Langhe et al. (2009)

Banana production

- Production exceeds 100 millions tons
- Staple food for more than 400 million people
- Current 45% world consumption relies on a single genotype (cv. Cavendish)
- Susceptible to *Musa* diseases



Source: www.innovationtoronto.com

Pest and diseases

- Bananas are host to a wide range of pests and diseases.
  - Panama disease – *Fusarium* wilt
  - Cordana leaf spot
  - Bunchy top
  - Bract mosaic
  - Black leaf streak
  - Xanthomonas wilt



Source: Scot Nelson/flickr



Source: www.foodsafety.com.au

An extinct variety of bananas

- Gros Michel bananas were even sweeter than current Cavendish bananas.
- A fungus, *Fusarium oxysporum,* caused a disease called “Panama disease” that exterminated entire plantations of this banana
- Disease was reported in 1890s



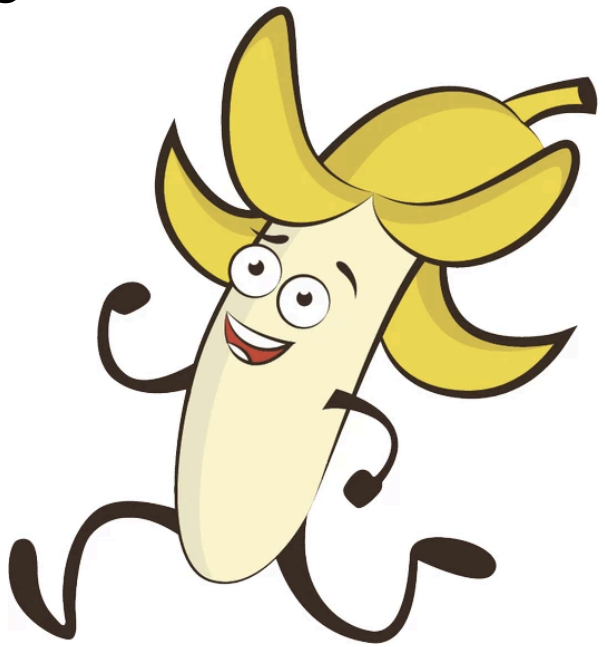
Source: www.ferrebeekeeper.files.wordpress.com



Source: www.ferrebeekeeper.files.wordpress.com

CONCLUSIONS

- Most bananas cultivars genomes come from *M. acuminata* and *M. balbisiana* genomes
- Musa genome have had two recent WGDs are independent of WGDs in Poaceae
- There are two reciprocal translocations in Chromosome 01 and Chromosome 04 in Musa genome



QUESTIONS?

Thanks for your attention!



