Bananas: past, present and future

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UNIVERSITY OF LEICESTER

South China Botanical Garden
Chinese Academy of Sciences

WINE
Luxembourg
79.5 litres
(17.5 gal)
By contrast, the smallest measurable wine consumer is Egypt, where the average yearly wine consumption amounts to about two tablespoons.

BREAKFAST CEREAL
Sweden
10.4 kg (22 lb 14 oz)

BAKED BEANS
United Kingdom
5.3 kg (11 lb 10 oz)
In contrast, the USA consumes just 1.3 kg (2 lb 13 oz) of baked beans per capita.

HONEY
Central African Republic
3 kg (6 lb 9.7 oz)

DID YOU KNOW?

*The **oldest cultivated plant for food** is the Abyssinian banana* (Ensete ventricosum). *Historians suggest that between 4,000 and 7,000 years ago, the hunter-gatherers of ancient Ethiopia learned to use this plant as food.*

ICE CREAM
Australia
16.6 litres
(3.6 gal)

TEA
Ireland
2.6 kg (5 lb 14 oz)
This equates to approximately 1,184 cups per person in one year.

CHOCOLATE
Switzerland
11.5 kg (25 lb 6 oz)
This is the equivalent of each person eating 230 bars weighing 50 g (1.75 oz) per year.

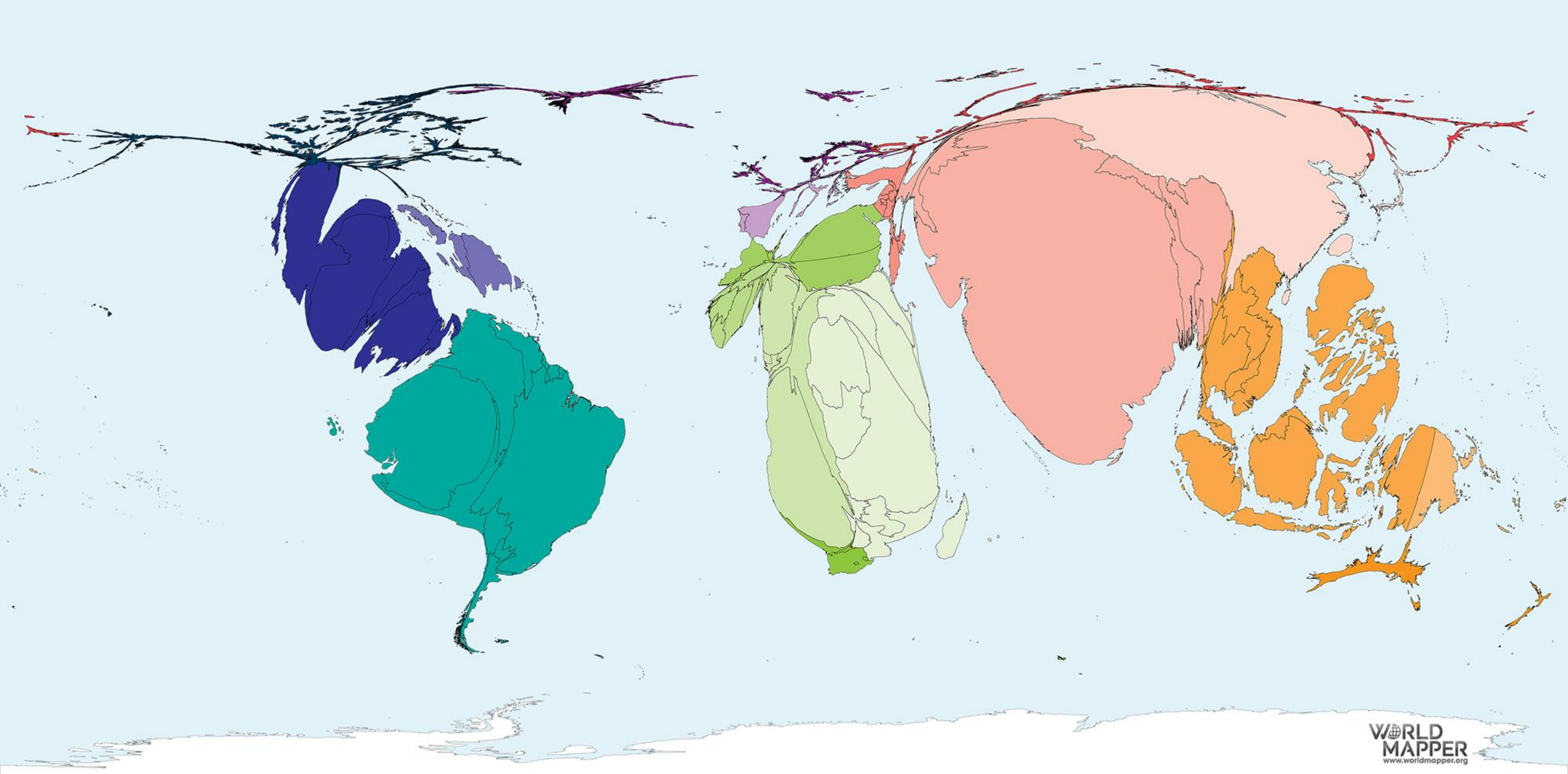
SPIRITS
Russia
6.2 litres
(1.3 gal)

the banana (musa sapientum) is the most consumed fruit in the world. It is the 4th most important staple food worldwide and the fifth most important agricultural product after cereal, sugar, coffee and cocoa. The Brits eat 140 million bananas every week!

Uganda

- 400 kg/person/year annual consumption
- Matoke of steamed bananas then mashed

From www.synesthete.com

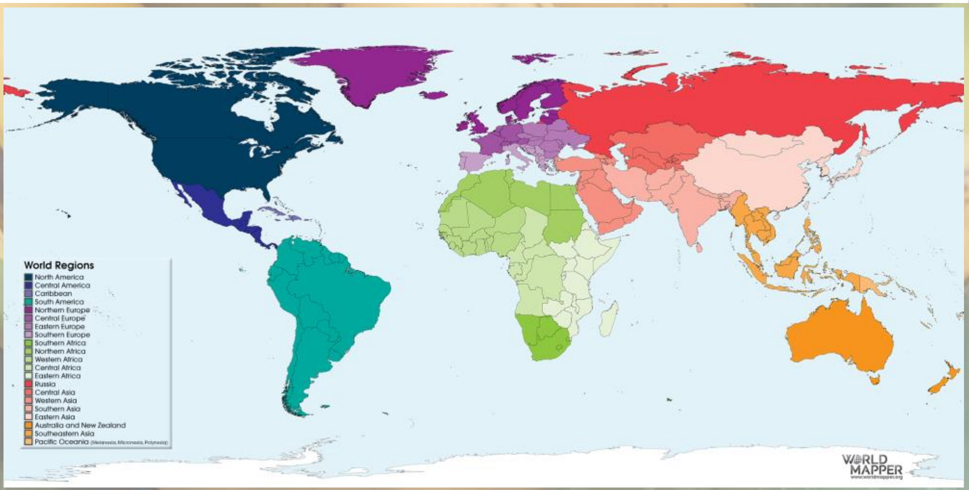


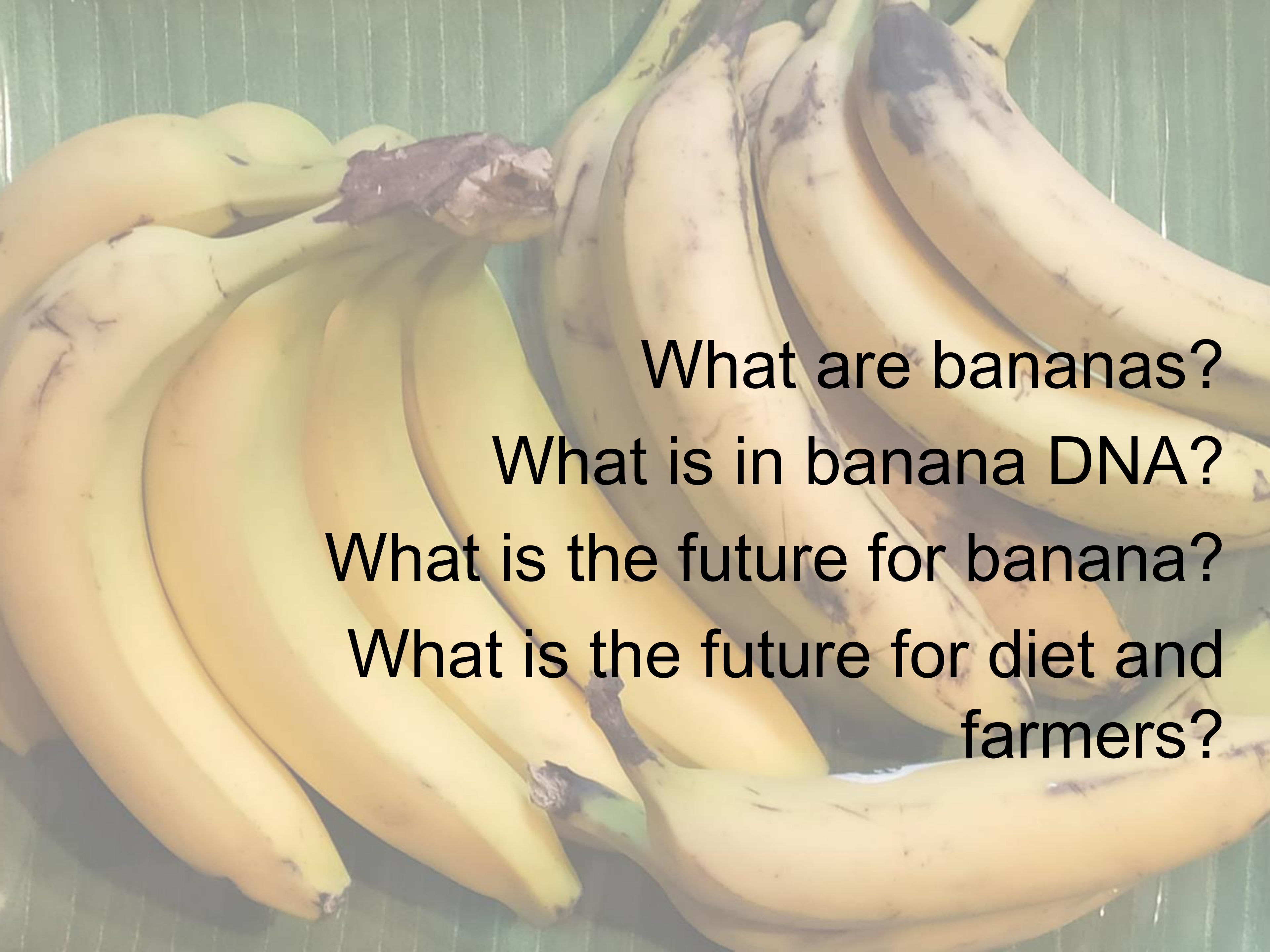
World Banana Production

Almost all tropical

India: 30Mt but no export

“Banana economy” is praise





What are bananas?

What is in banana DNA?

What is the future for banana?

What is the future for diet and farmers?

Zingiberales Order Bed, National Botanic Garden of Wales, 2006

Ensete ventricosum 2nd genus in Musaceae

enset, ensete, false banana

Staple food in Ethiopia

What is a banana?

Monocotyledon – giant herb not a tree!

Banana Evolution

- Cultivars: sterile, parthenocarpic clones
- In the wild, all fruits have a seed (only in last decade for lemons, limes, watermelon; not olive yet)
- Bananas introduced with farming: domesticated, along with other major crops and animals, 8000-10000 years ago


PRATT'S
BANANAS
Importers & Ripeners
BES
Dole
DOLE CA

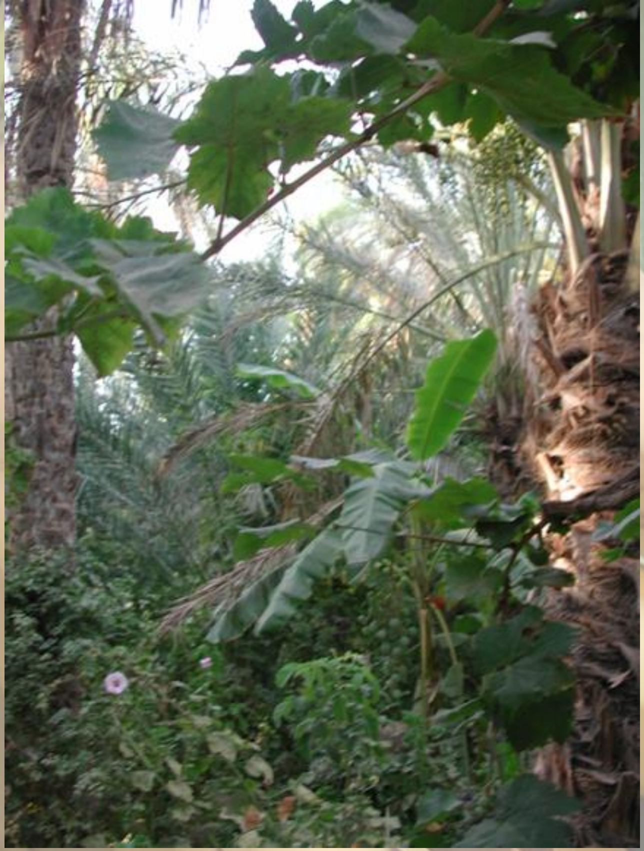
Banana Plantains *Musa*

1-7 year plantation
Vegetatively propagated
(exclusively)

85% used as local staple

20-30kg fruit bunch
>120Mt /yr

Sterile



- Subsistence agriculture
- Smallholder farms
- Cash crop
- Commercial
- Year-round production
- Eaten by all ages of people

Cultivated banana

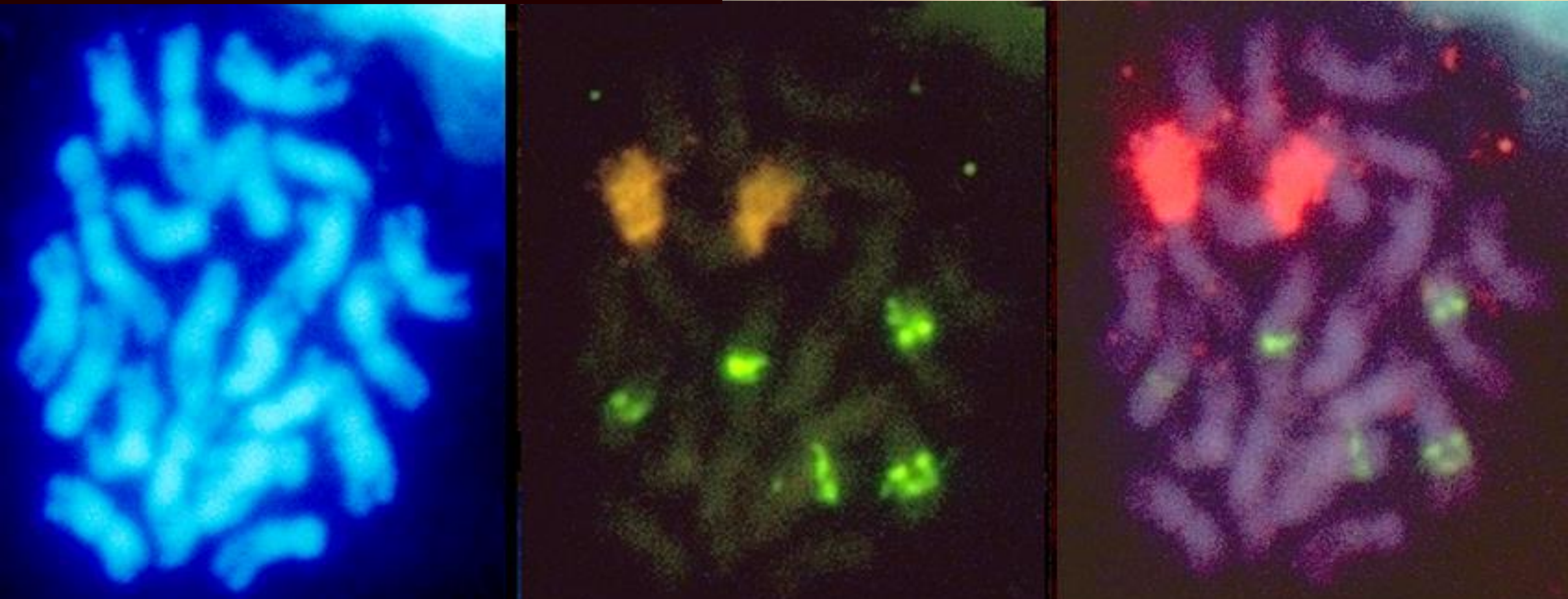
- Origin from two species in Asia:
- *Musa acuminata* (the A genome) and *Musa balbisiana* (B genome)

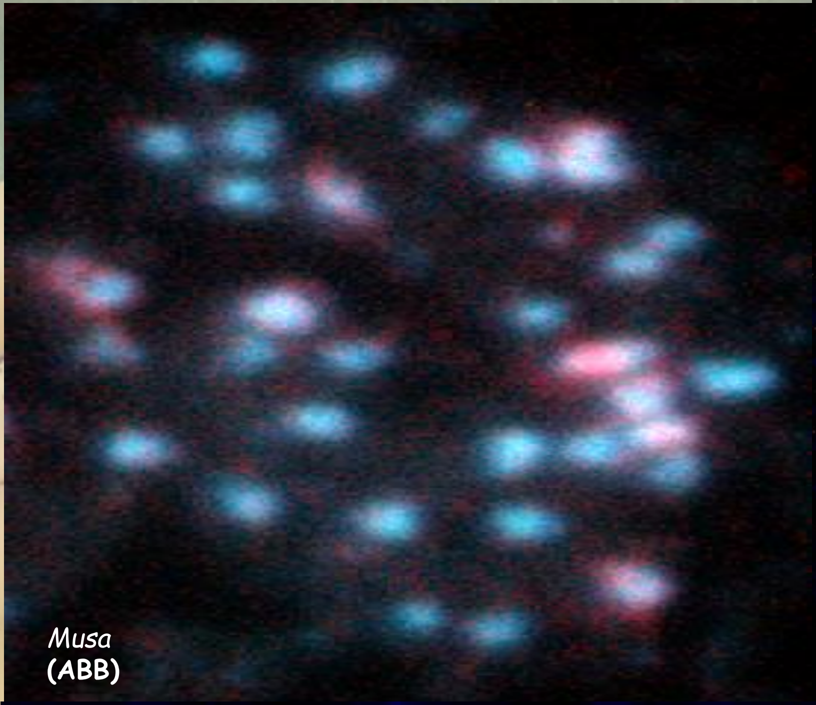

NSK
NSK
NSK

L to R:
Red - AAA
Palayam codan AAB (two bunch yellow, one green)
Peyan ABB (green cooking banana),
Njalipoovan AB (yellow)
Robusta AAA (green ripe)
Nendran AAB
Poovan AAB (one yellow bunch)
Red AAA
Peyan

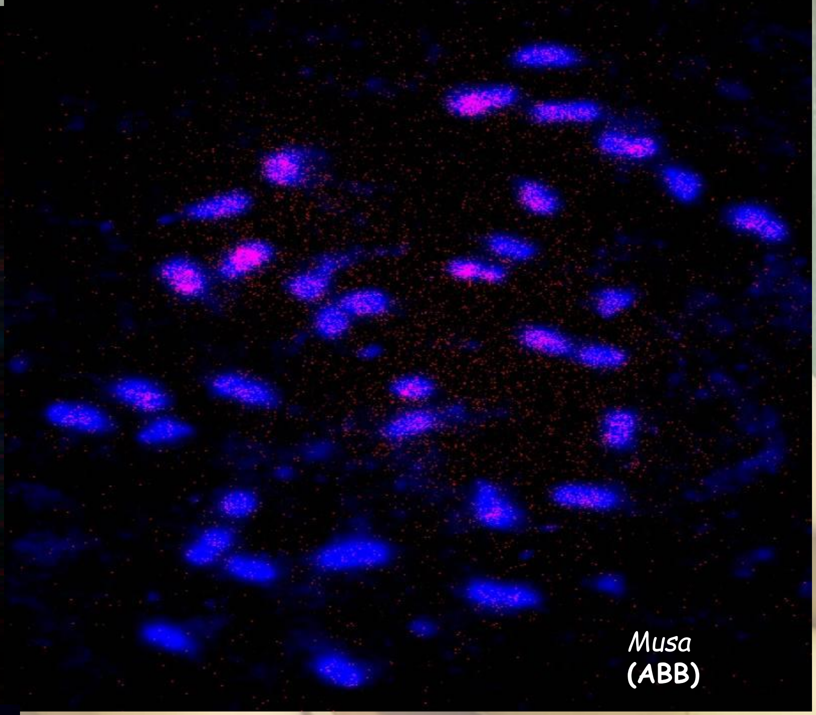
Varkala, Kerala, India

Wild banana
Musa acuminata ‘Calcutta 4’
AA genomes, 2n=2x=22
One genome and 11 chromosomes from mother
Other genome and 11 chromosomes from father

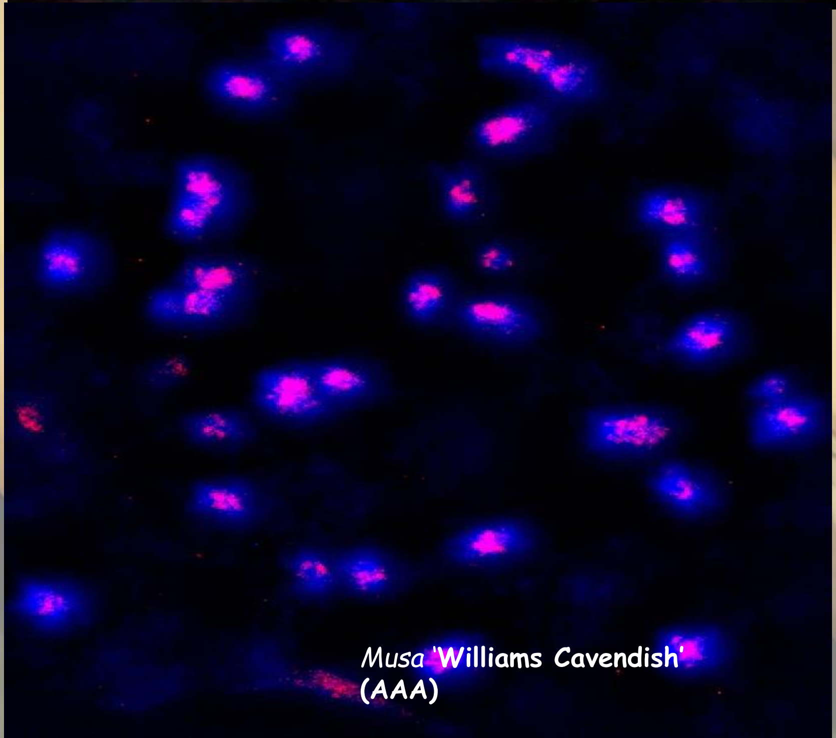




Musa
(ABB)



Musa
(ABB)

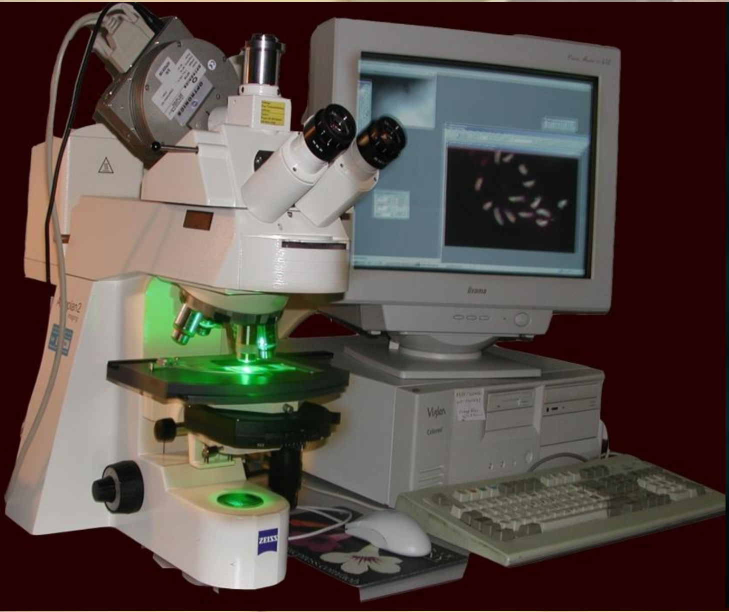


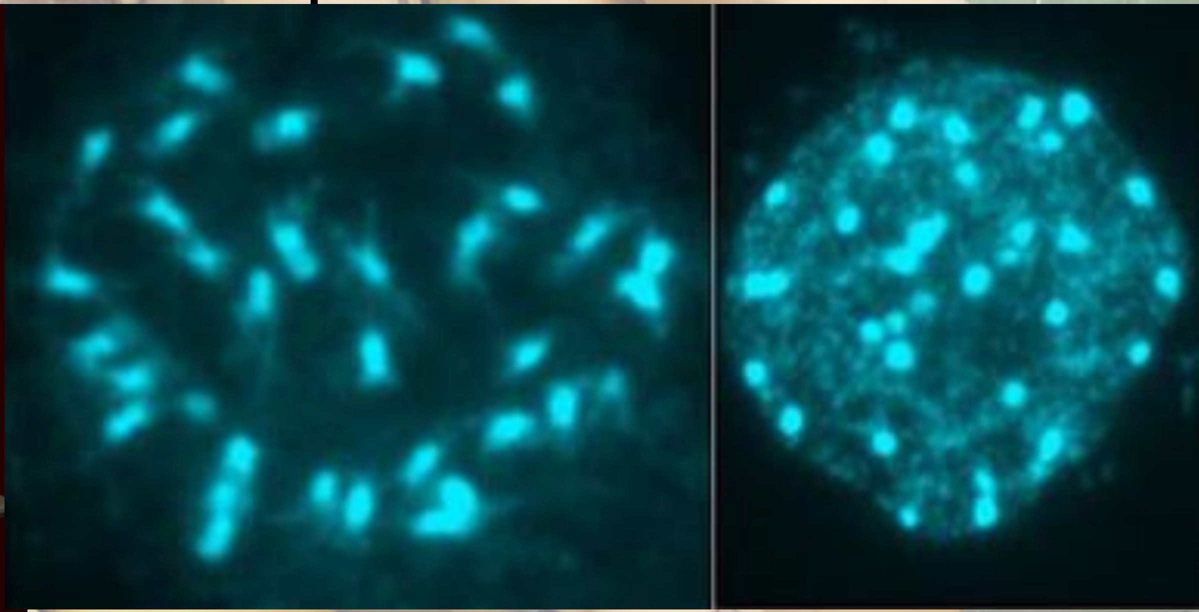
Musa 'Williams Cavendish'
(AAA)

Florescent in situ hybridization: An A-genome specific hAT in three *Musa* hybrids (2n=3x=33) located on A-genome chromosomes.

What is a genome?

- In bananas and plantains, about 500 million base pairs of DNA





```
ta clone MuG9, genomic, 73268bp
aaatccaatcaatccagatcaatattgatcg
gacgaagcagtcaaactgatcactaaaattc
gagtgctgatttcagaaacttaatcccttct
caacttacactaattagtcttaaaactcatt
ataaatgtcatattacccttccaggtcataa
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aaatgacattttttgaactctgcagaatta
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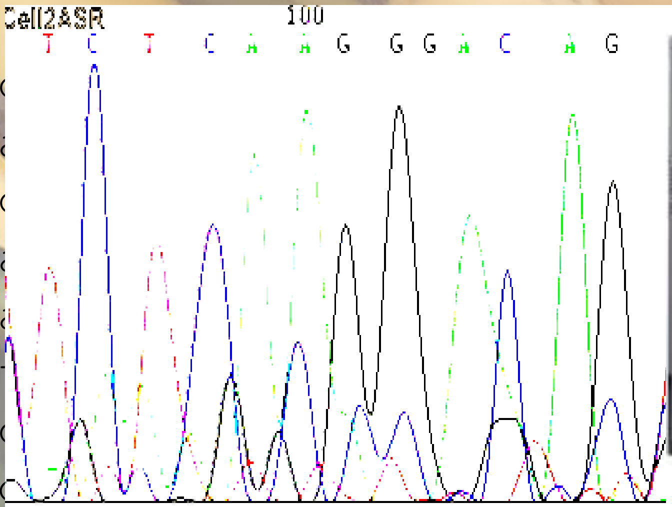
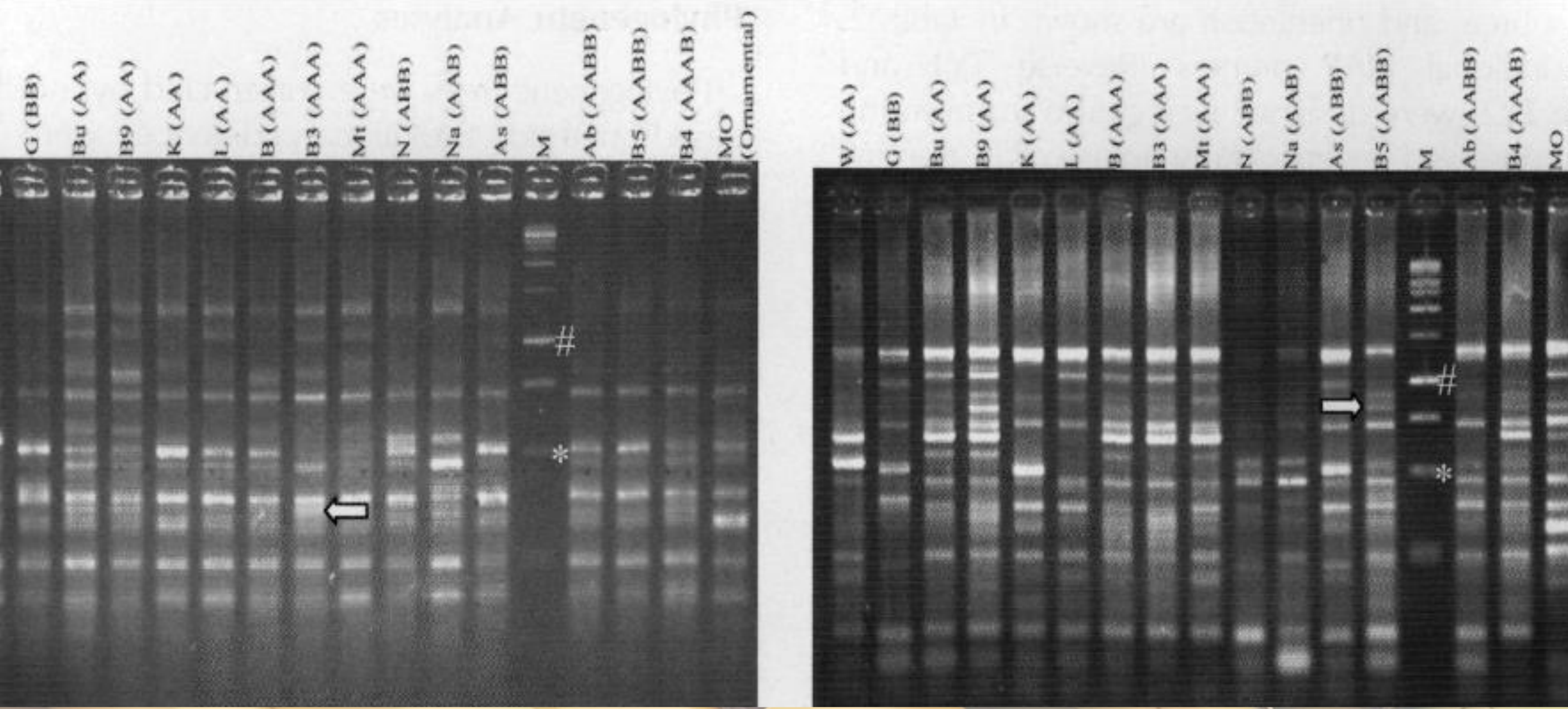
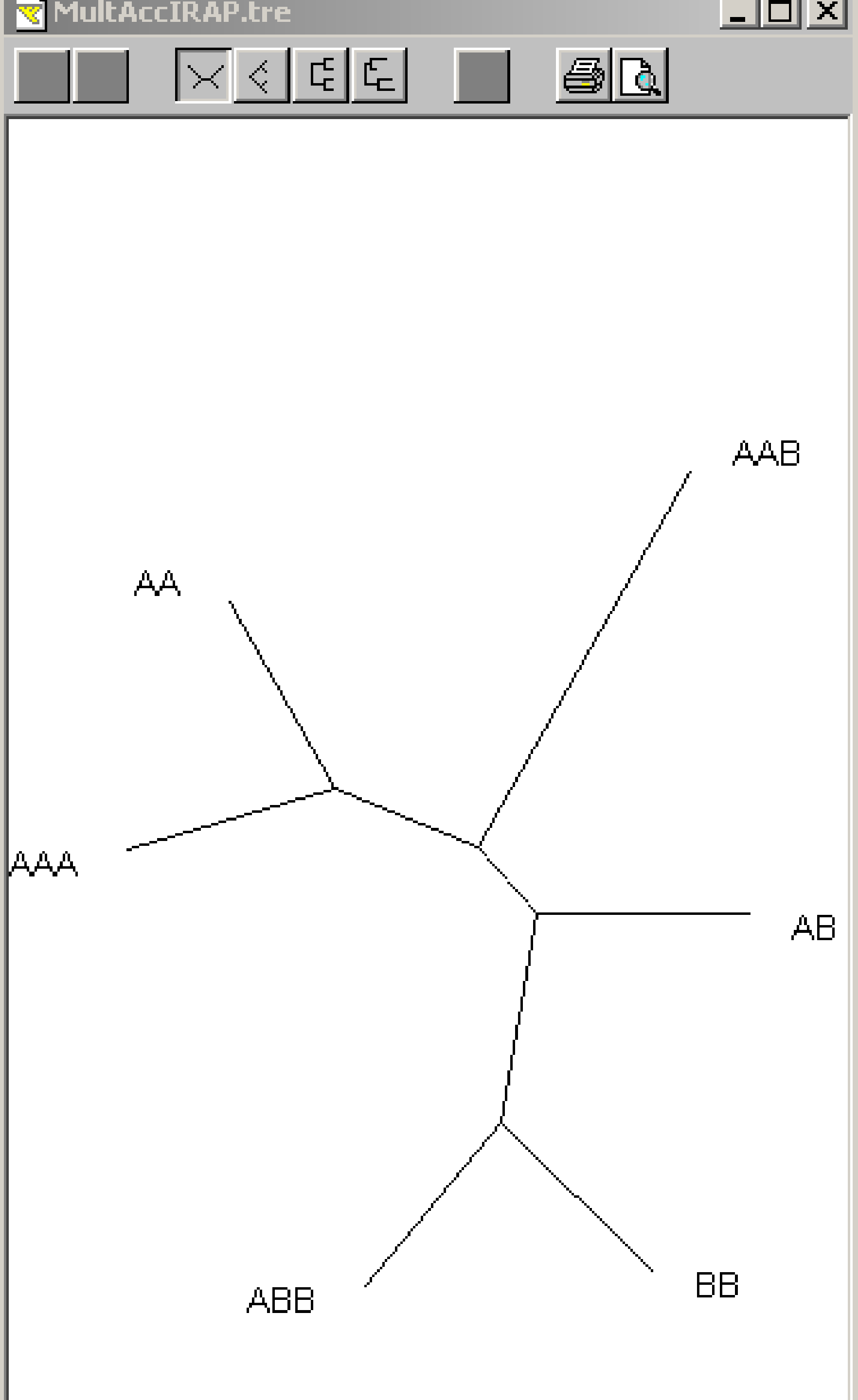


DNA diversity in Musa

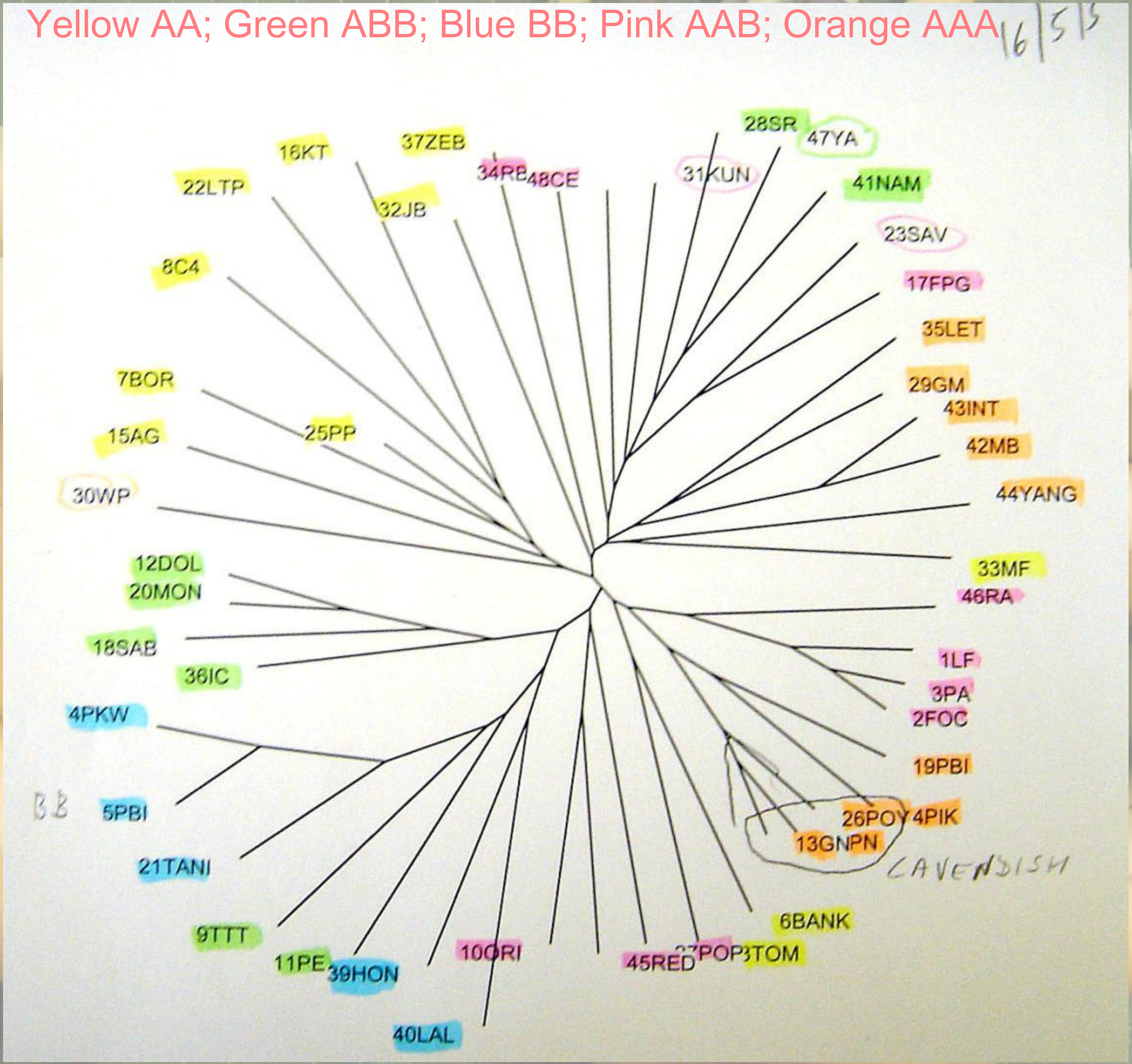


Teo, Tan, Ho, Faridah, Othman, HH, Kalendar, Schulman 2005 *J Plant Biol*

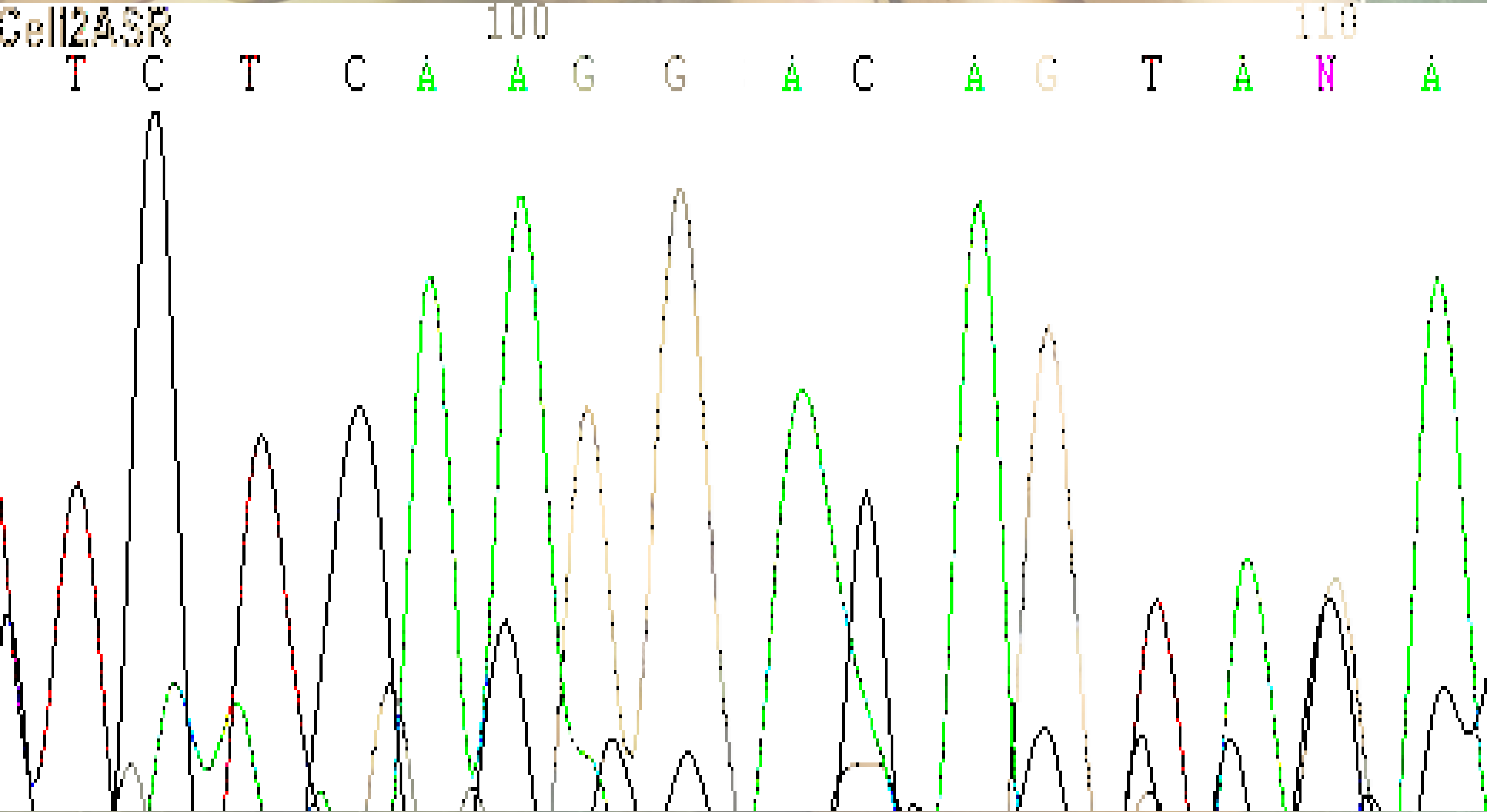
Nair, Teo, Schwarzacher, HH 2006 Euphytica

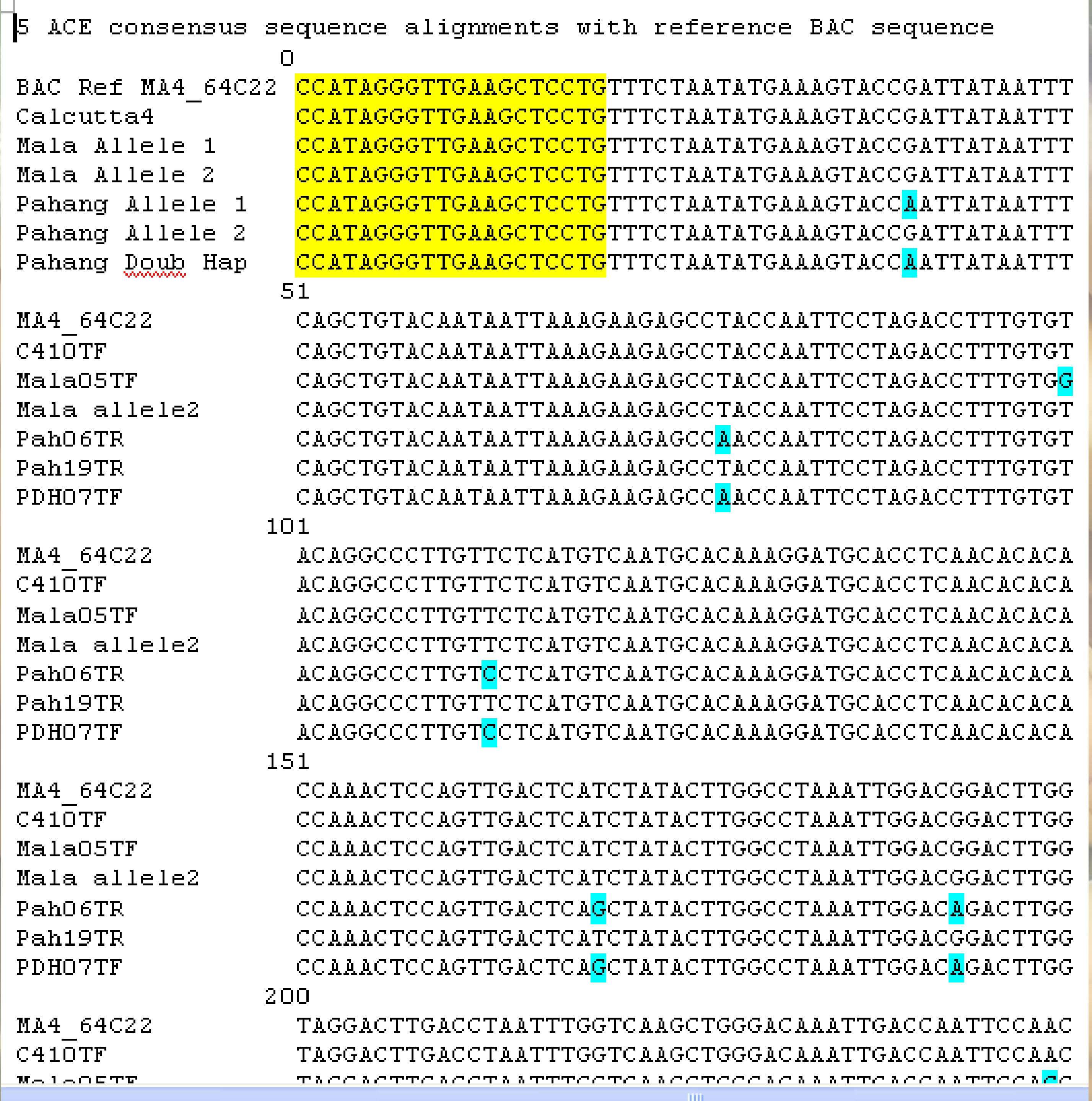

MultAccIRAP.tre
AAB
AA
AAA
AB
ABB
BB

- Yellow AA; Green ABB; Blue BB; Pink AAB; Orange AAA



Cellulose Synthase
Single Nucleotide Polymorphism SNP





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5 ACE consensus sequence alignments with reference BAC sequence
                  0
BAC Ref MA4_64C22  CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCGATTATAATTT
Calcutta4          CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCGATTATAATTT
Mala Allele 1      CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCGATTATAATTT
Mala Allele 2      CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCGATTATAATTT
Pahang Allele 1    CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCAATTATAATTT
Pahang Allele 2    CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCGATTATAATTT
Pahang Doub Hap    CCATAGGGTTGAAGCTCCTGTTTCTAATATGAAAGTACCAATTATAATTT
                  51
MA4_64C22          CAGCTGTACAATAATTAAAGAAGAGCCTACCAATTCCTAGACCTTTGTGT
C410TF             CAGCTGTACAATAATTAAAGAAGAGCCTACCAATTCCTAGACCTTTGTGT
Mala05TF           CAGCTGTACAATAATTAAAGAAGAGCCTACCAATTCCTAGACCTTTGTGG
Mala allele2       CAGCTGTACAATAATTAAAGAAGAGCCTACCAATTCCTAGACCTTTGTGT
Pah06TR            CAGCTGTACAATAATTAAAGAAGAGCCAACCAATTCCTAGACCTTTGTGT
Pah19TR            CAGCTGTACAATAATTAAAGAAGAGCCTACCAATTCCTAGACCTTTGTGT
PDH07TF            CAGCTGTACAATAATTAAAGAAGAGCCAACCAATTCCTAGACCTTTGTGT
                 101
MA4_64C22          ACAGGCCCTTGTTCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
C410TF             ACAGGCCCTTGTTCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
Mala05TF           ACAGGCCCTTGTTCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
Mala allele2       ACAGGCCCTTGTTCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
Pah06TR            ACAGGCCCTTGTCCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
Pah19TR            ACAGGCCCTTGTTCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
PDH07TF            ACAGGCCCTTGTCCTCATGTCAATGCACAAAGGATGCACCTCAACACACA
                 151
MA4_64C22          CCAAACTCCAGTTGACTCATCTATACTTGGCCTAAATTGGACGGACTTGG
C410TF             CCAAACTCCAGTTGACTCATCTATACTTGGCCTAAATTGGACGGACTTGG
Mala05TF           CCAAACTCCAGTTGACTCATCTATACTTGGCCTAAATTGGACGGACTTGG
Mala allele2       CCAAACTCCAGTTGACTCATCTATACTTGGCCTAAATTGGACGGACTTGG
Pah06TR            CCAAACTCCAGTTGACTCAGCTATACTTGGCCTAAATTGGACAGACTTGG
Pah19TR            CCAAACTCCAGTTGACTCATCTATACTTGGCCTAAATTGGACGGACTTGG
PDH07TF            CCAAACTCCAGTTGACTCAGCTATACTTGGCCTAAATTGGACAGACTTGG
                 200
MA4_64C22          TAGGACTTGACCTAATTTGGTCAAGCTGGGACAAATTGACCAATTCCAAC
C410TF             TAGGACTTGACCTAATTTGGTCAAGCTGGGACAAATTGACCAATTCCAAC
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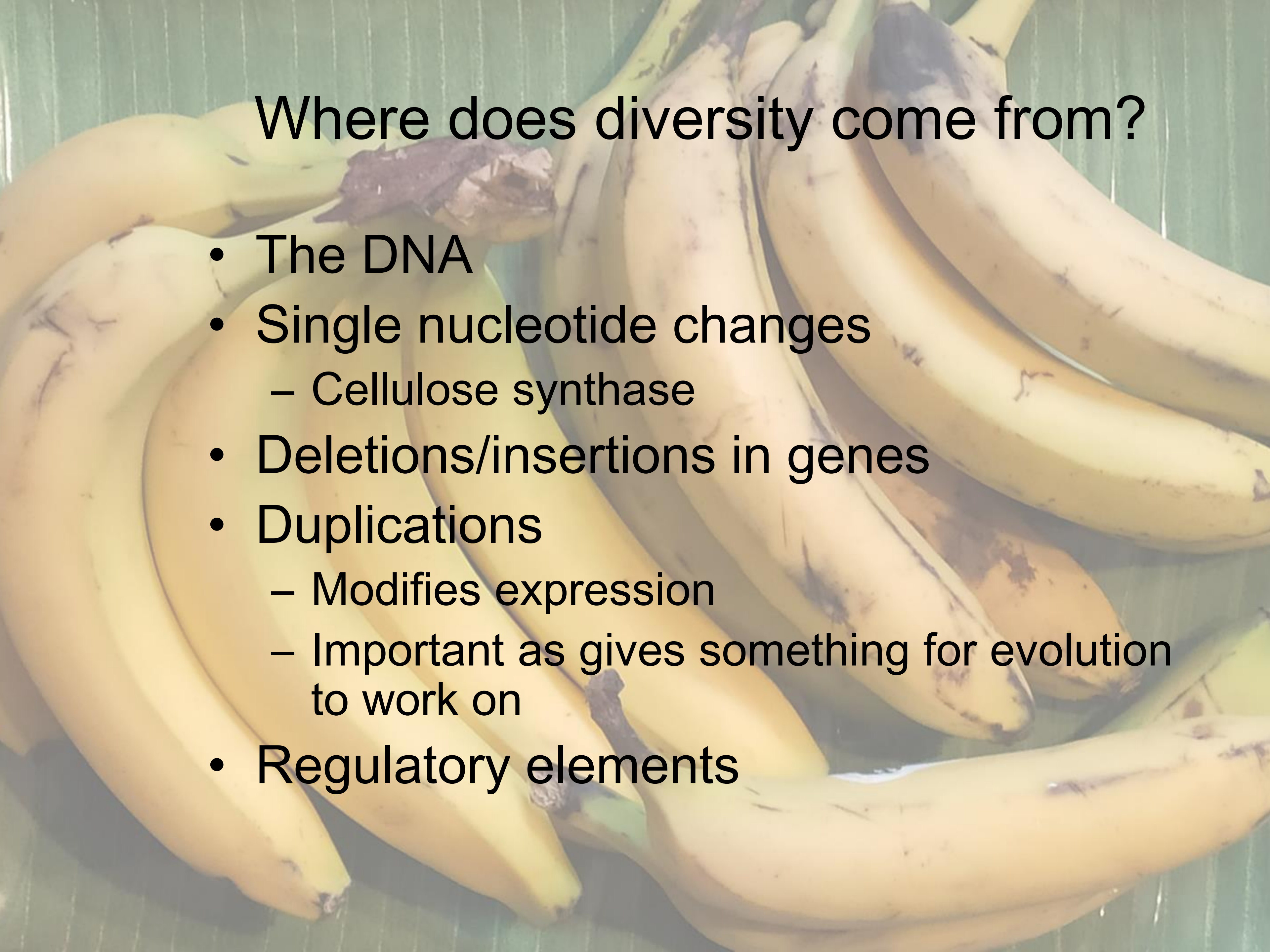

Where does diversity come from?

- The DNA
- Single nucleotide changes
  - Cellulose synthase
- Deletions/insertions in genes
- Duplications
  - Modifies expression
  - Important as gives something for evolution to work on
- Regulatory elements


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EV
LUT
ON

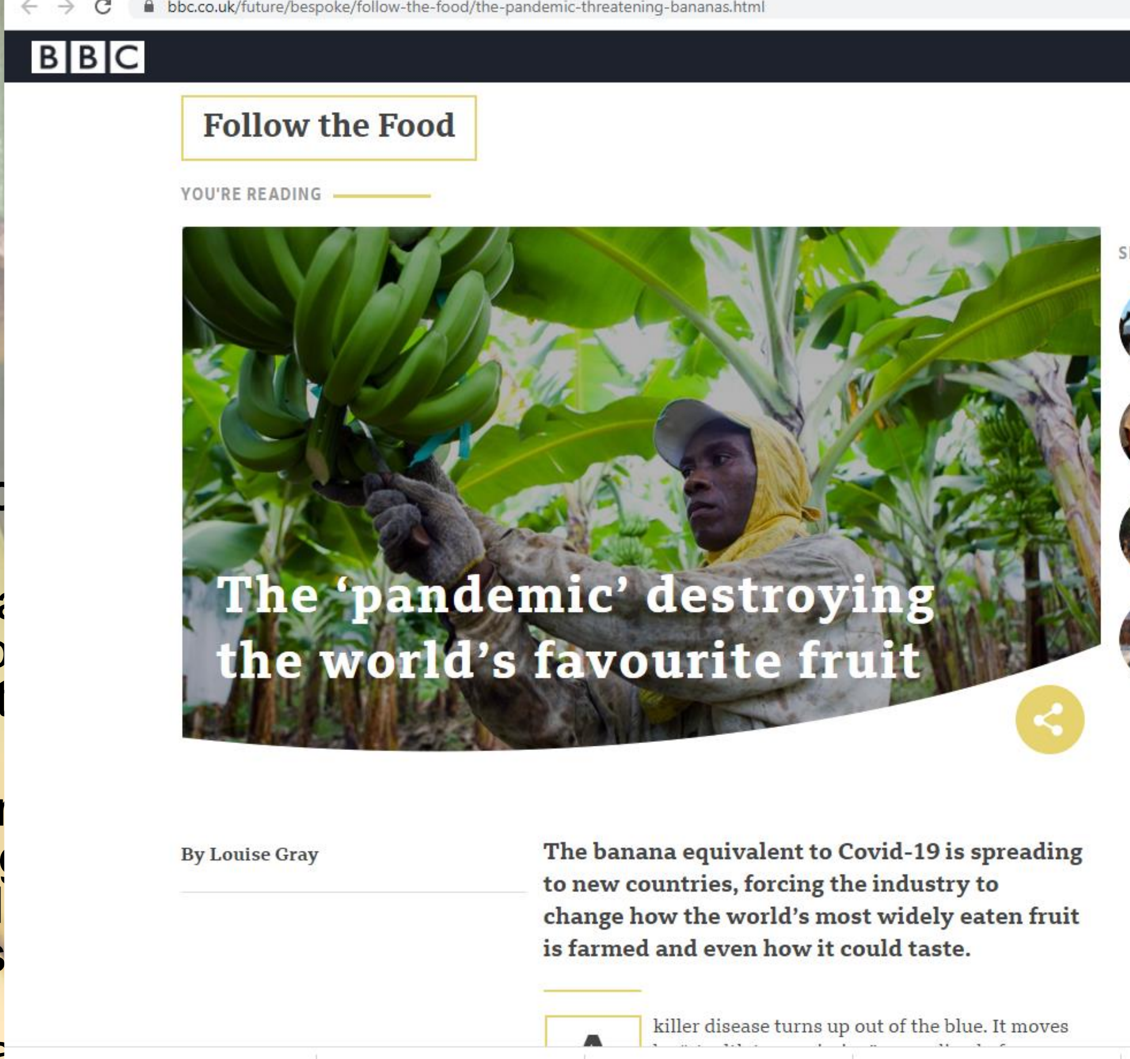
Variety Cavendish

- 15% of banana production worldwide
- The vast majority of export banana to temperate countries
- Controllable ripening but very sensitive to conditions
- First collected in China in 1826 (Telfair), Sold to Duke of Devonshire, Chatsworth
- Distributed worldwide from 1836
- Became dominant variety in 1960s, replacing Gros Michel
- Has various variants: Williams, Dwarf C, Giant C, Grand Naine, Robusta, Poyo …

- Gros Michel in Fusarium (Panama disease) trial in Malaysia

Daily Telegraph

- No 1 banana could face extincti
  Roger Highfield, Science Editor
- The most popular type of banan
  from disease. In the 1950s, Brito
  Gros Michel but it was wiped out
- Now the Cavendish could follow
  to which it was supposed to be i
  plants. So far, the new, more ag
  disease - TR4 - has not reached
  Latin America or Africa but it is s
  Cavendish plantations in Asia - I
  provinces of China and Malaysia.
- In the humid conditions of traditional banana plantations in Central America, the black Sigatoka fungus which attacks leaves, also thrives and the plants must be protected by weekly sprays of fungicides. Although the Cavendish could disappear, experts are confident that a bunch of alternative bananas could fill the void. The caveat is that the taste and texture will be changed forever and there is likely to be a rise in price.



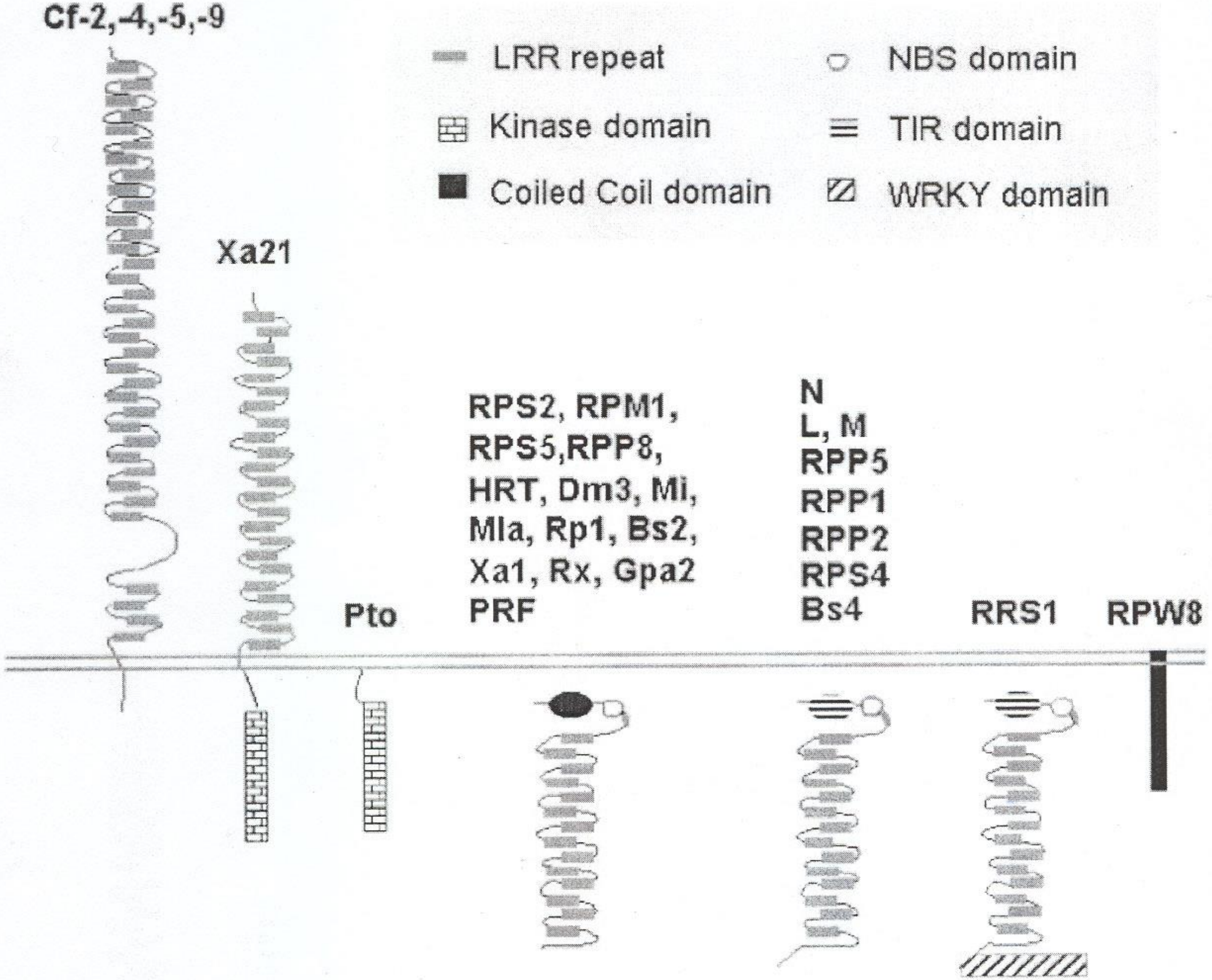
The 'pandemic' destroying the world's favourite fruit

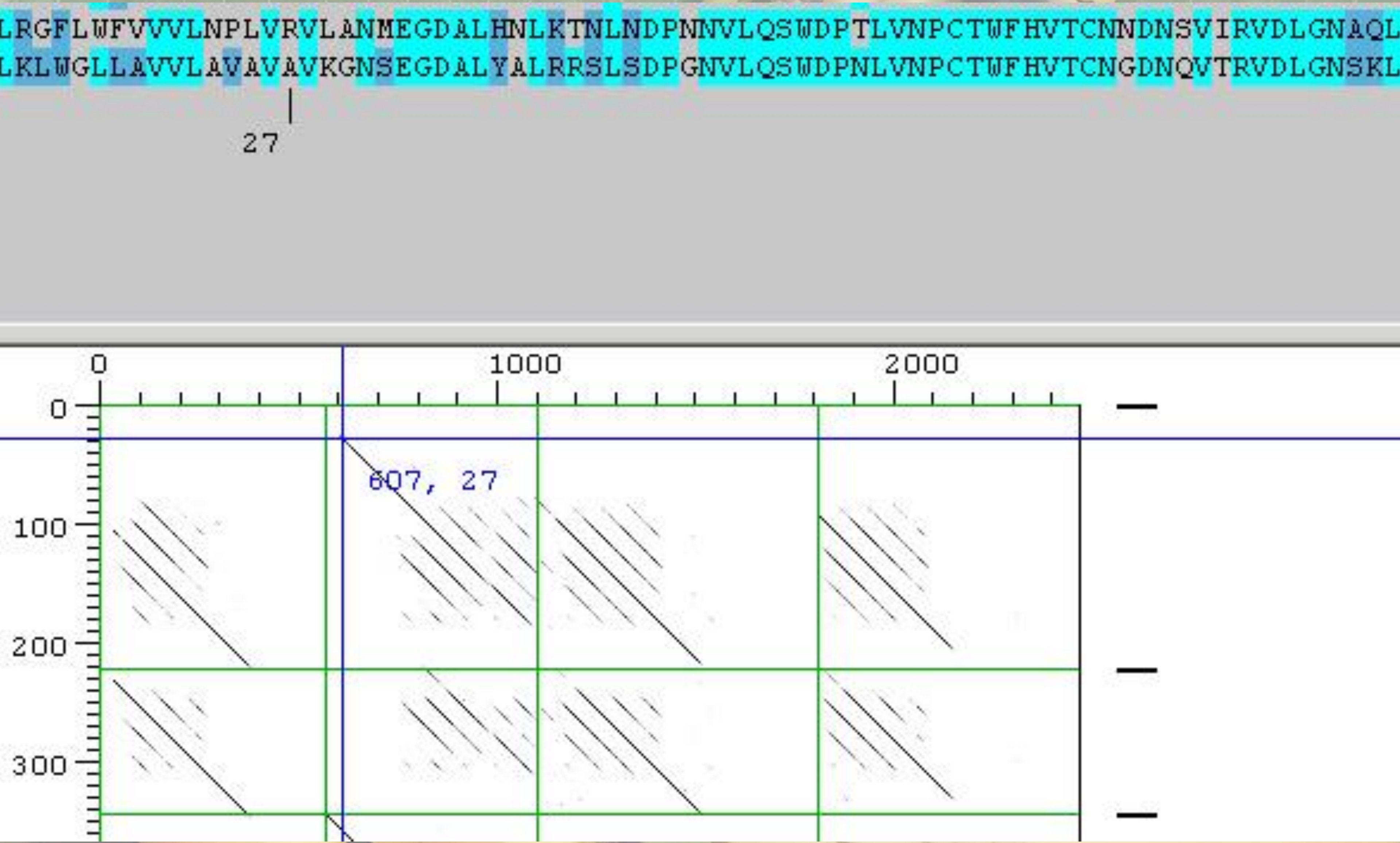
By Louise Gray

The banana equivalent to Covid-19 is spreading to new countries, forcing the industry to change how the world's most widely eaten fruit is farmed and even how it could taste.

A killer disease turns up out of the blue. It moves

RECOGNITION AND RESPONSE IN THE
PLANT IMMUNE SYSTEM
Zachary et al.; Annu. Rev. Genet. 2003. 37:579–609





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LKLWGLLAVVLAVAVAVKGNSEGDALYALRRSLSDPGNVLQSWDPNLVNPCTWFHVTCNGDNQVTRVDLGNSKL
```
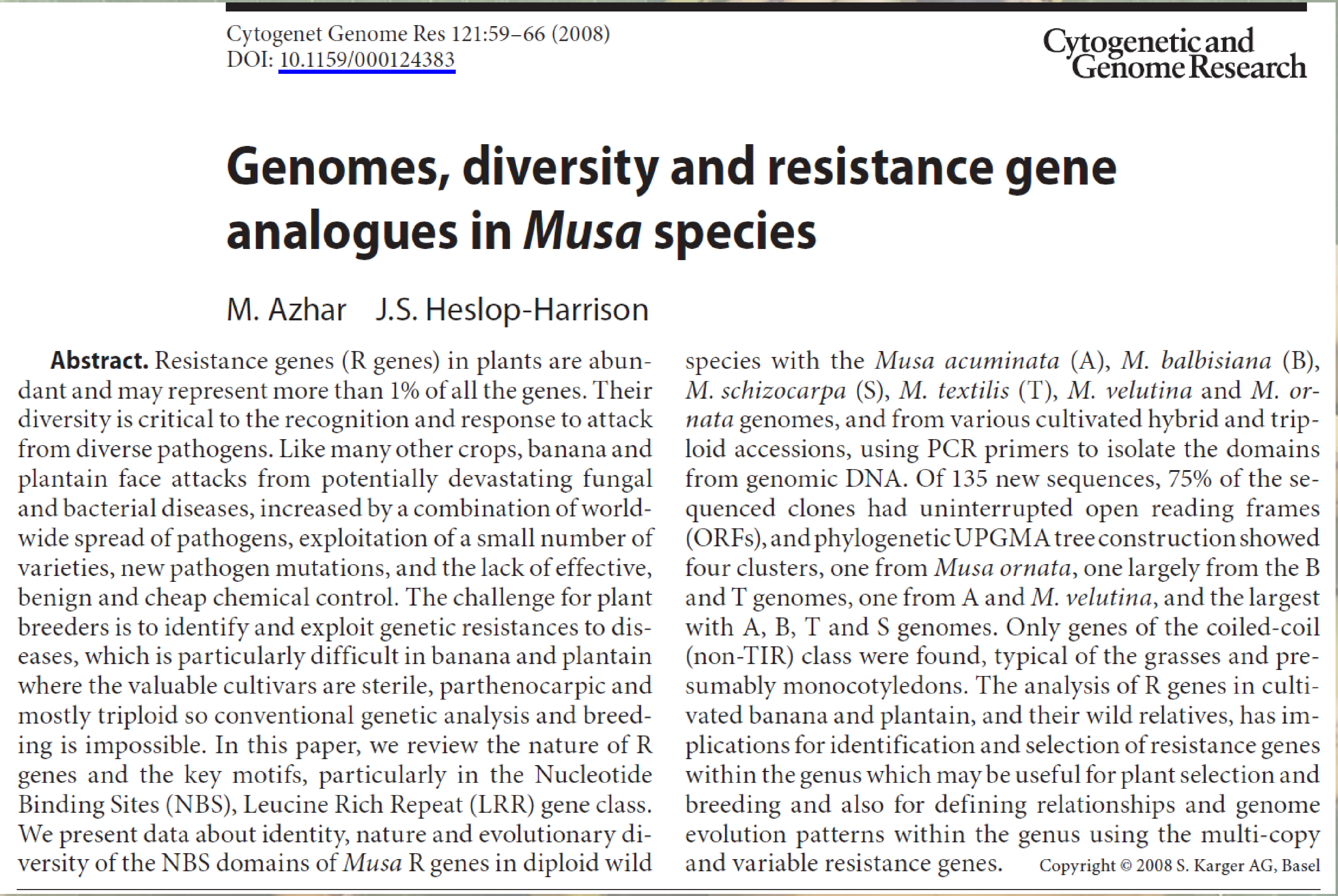

- LRRs in Musa compared to reference Rice



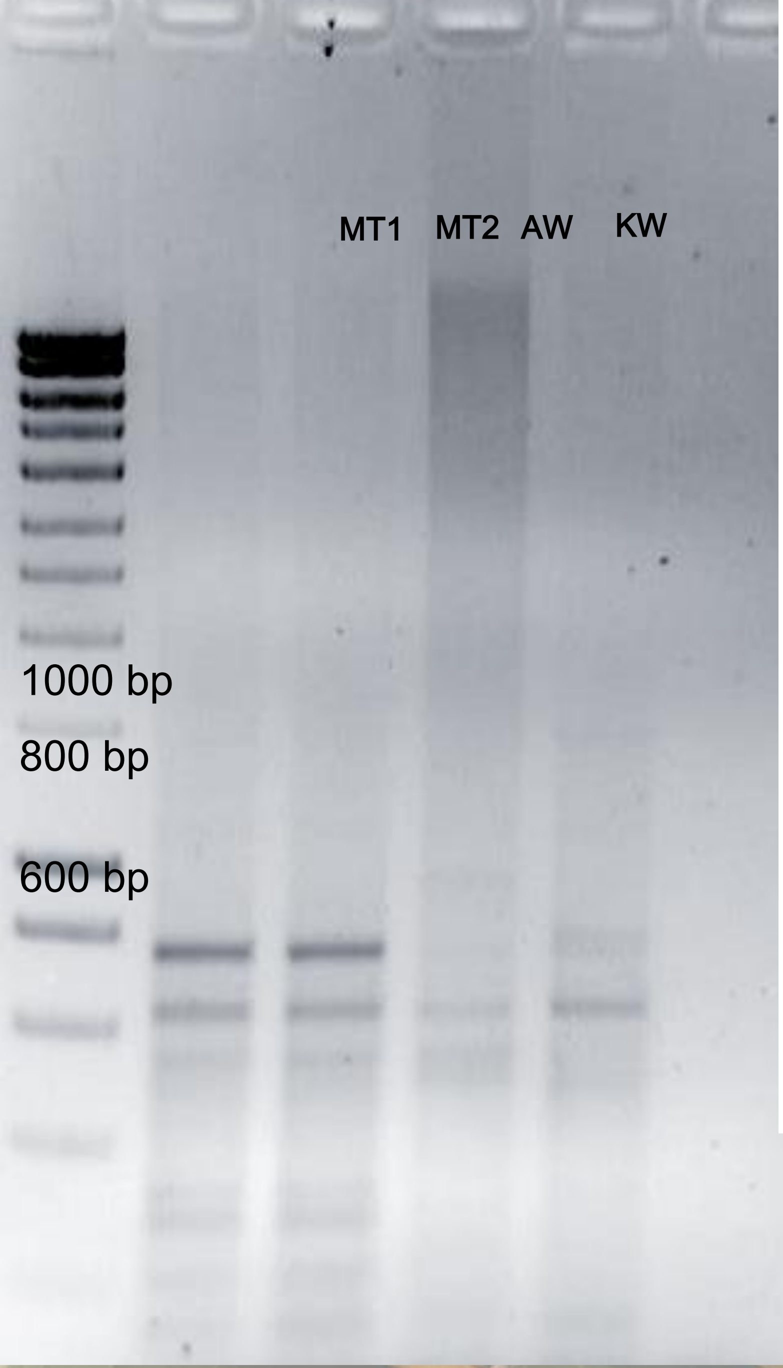
Cytogenet Genome Res 121:59–66 (2008)
DOI: 10.1159/000124383

Cytogenetic and Genome Research

Genomes, diversity and resistance gene analogues in *Musa* species

M. Azhar J.S. Heslop-Harrison

Abstract. Resistance genes (R genes) in plants are abundant and may represent more than 1% of all the genes. Their diversity is critical to the recognition and response to attack from diverse pathogens. Like many other crops, banana and plantain face attacks from potentially devastating fungal and bacterial diseases, increased by a combination of worldwide spread of pathogens, exploitation of a small number of varieties, new pathogen mutations, and the lack of effective, benign and cheap chemical control. The challenge for plant breeders is to identify and exploit genetic resistances to diseases, which is particularly difficult in banana and plantain where the valuable cultivars are sterile, parthenocarpic and mostly triploid so conventional genetic analysis and breeding is impossible. In this paper, we review the nature of R genes and the key motifs, particularly in the Nucleotide Binding Sites (NBS), Leucine Rich Repeat (LRR) gene class. We present data about identity, nature and evolutionary diversity of the NBS domains of *Musa* R genes in diploid wild species with the *Musa acuminata* (A), *M. balbisiana* (B), *M. schizocarpa* (S), *M. textilis* (T), *M. velutina* and *M. ornata* genomes, and from various cultivated hybrid and triploid accessions, using PCR primers to isolate the domains from genomic DNA. Of 135 new sequences, 75% of the sequenced clones had uninterrupted open reading frames (ORFs), and phylogenetic UPGMA tree construction showed four clusters, one from *Musa ornata*, one largely from the B and T genomes, one from A and *M. velutina*, and the largest with A, B, T and S genomes. Only genes of the coiled-coil (non-TIR) class were found, typical of the grasses and presumably monocotyledons. The analysis of R genes in cultivated banana and plantain, and their wild relatives, has implications for identification and selection of resistance genes within the genus which may be useful for plant selection and breeding and also for defining relationships and genome evolution patterns within the genus using the multi-copy and variable resistance genes.



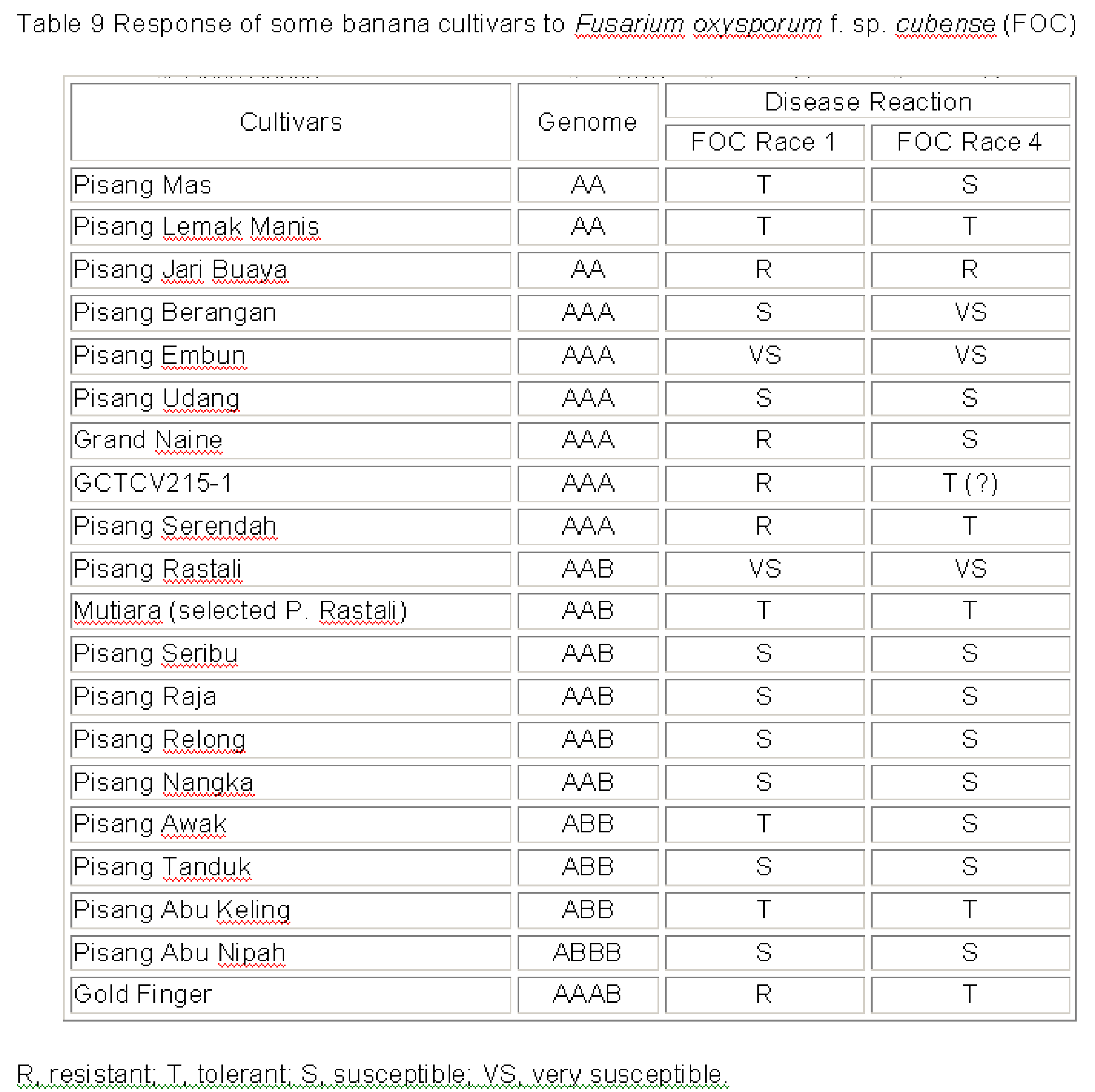


Table 9 Response of some banana cultivars to *Fusarium oxysporum* f. sp. *cubense* (FOC)

Cultivars	Genome	Disease Reaction	
		FOC Race 1	FOC Race 4
Pisang Mas	AA	T	S
Pisang Lemak Manis	AA	T	T
Pisang Jari Buaya	AA	R	R
Pisang Berangan	AAA	S	VS
Pisang Embun	AAA	VS	VS
Pisang Udang	AAA	S	S
Grand Naine	AAA	R	S
GCTCV215-1	AAA	R	T (?)
Pisang Serendah	AAA	R	T
Pisang Rastali	AAB	VS	VS
Mutiara (selected P. Rastali)	AAB	T	T
Pisang Seribu	AAB	S	S
Pisang Raja	AAB	S	S
Pisang Relong	AAB	S	S
Pisang Nangka	AAB	S	S
Pisang Awak	ABB	T	S
Pisang Tanduk	ABB	S	S
Pisang Abu Keling	ABB	T	T
Pisang Abu Nipah	ABBB	S	S
Gold Finger	AAAB	R	T

R, resistant; T, tolerant; S, susceptible; VS, very susceptible.

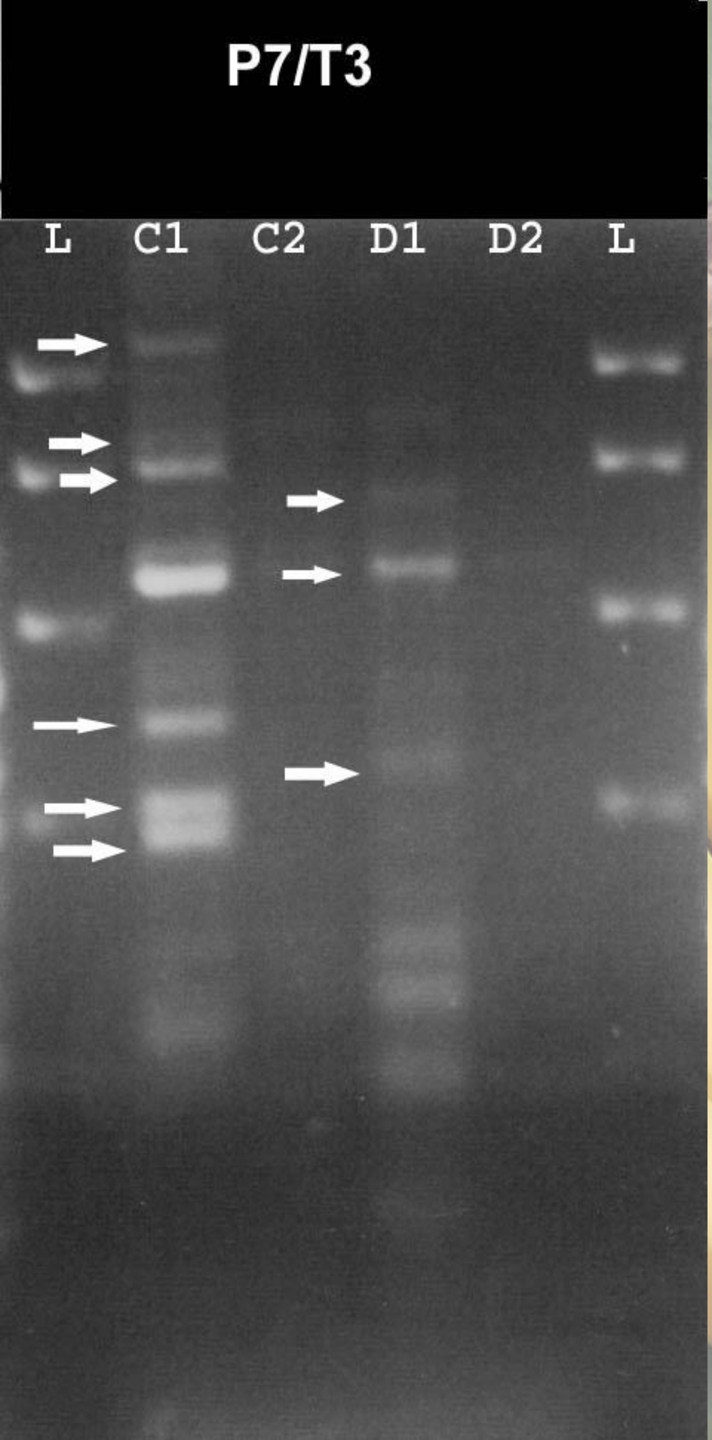
Primers : MLRR1-F and MLRR2-R

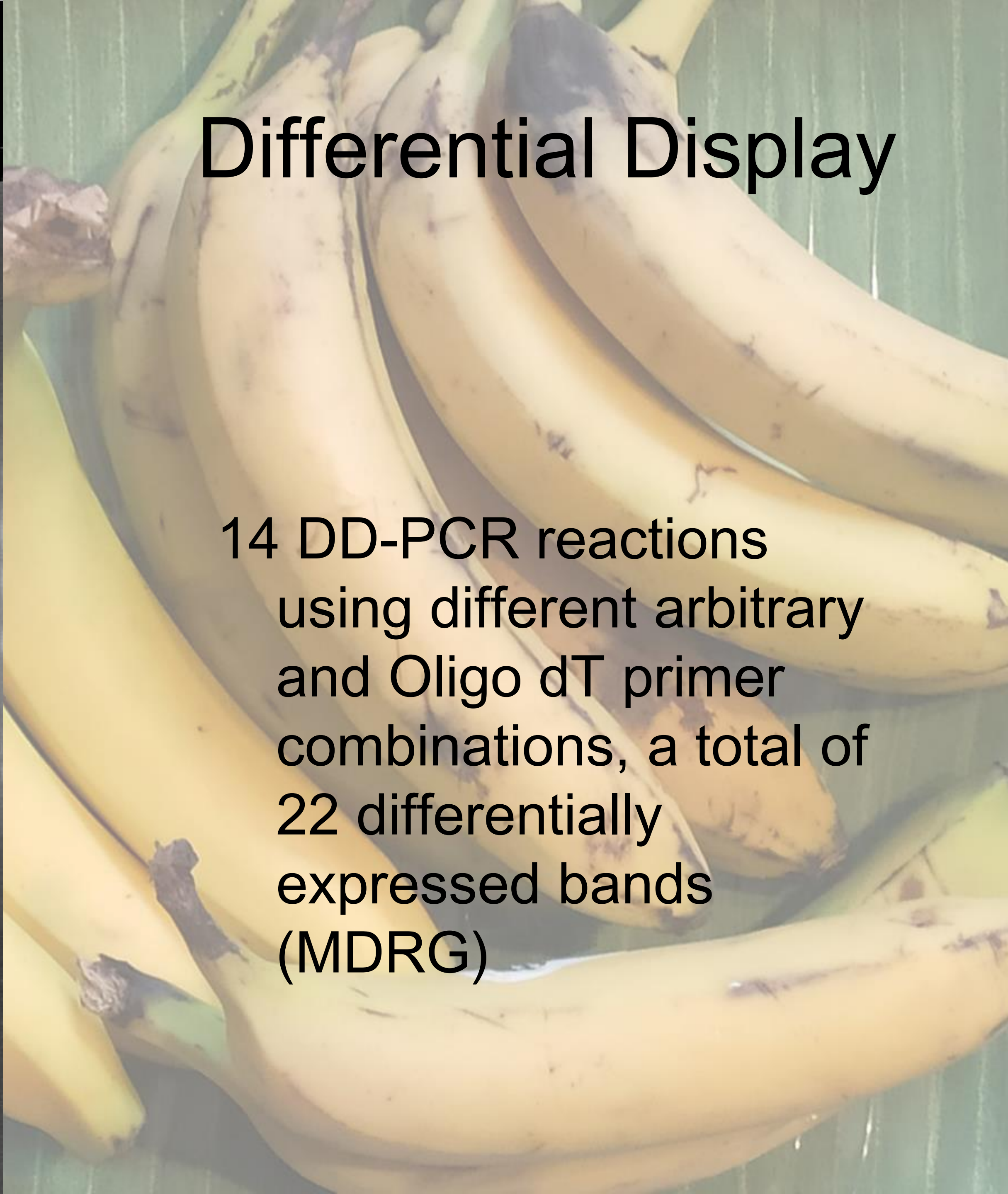
MT1 and MT2 – Mutiara tolerance to FOC
AW - Pisang Awak
KW – Klutuk Wulung

Drought Responsive Genes

- Differential display of genes being expressed from droughted and watered *Musa* lines

Drought Responsive Genes

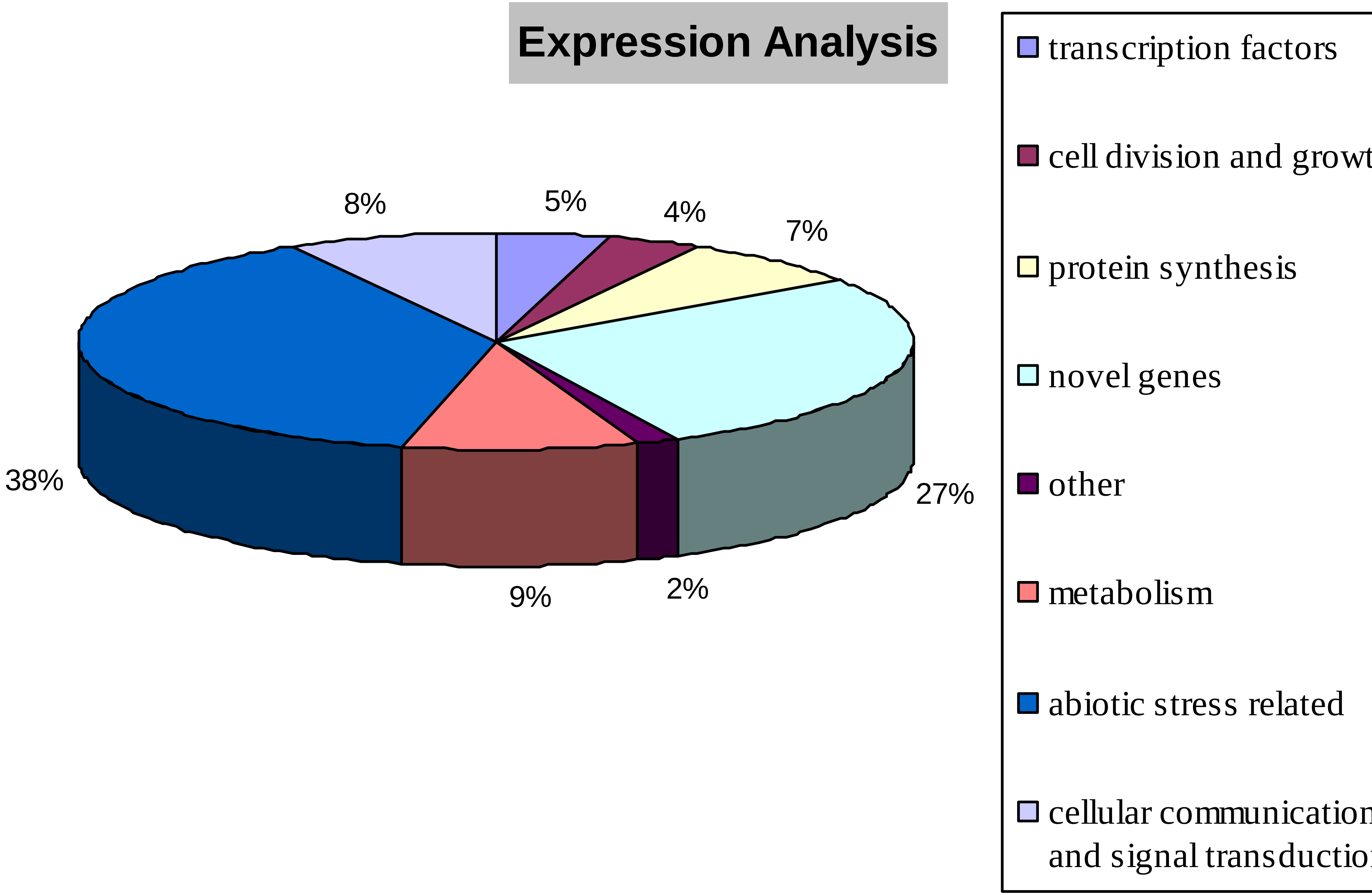




Differential Display

14 DD-PCR reactions using different arbitrary and Oligo dT primer combinations, a total of 22 differentially expressed bands (MDRG)

Expression Analysis



Preliminary data; Dhairyasheel Desai, HH *et al*.

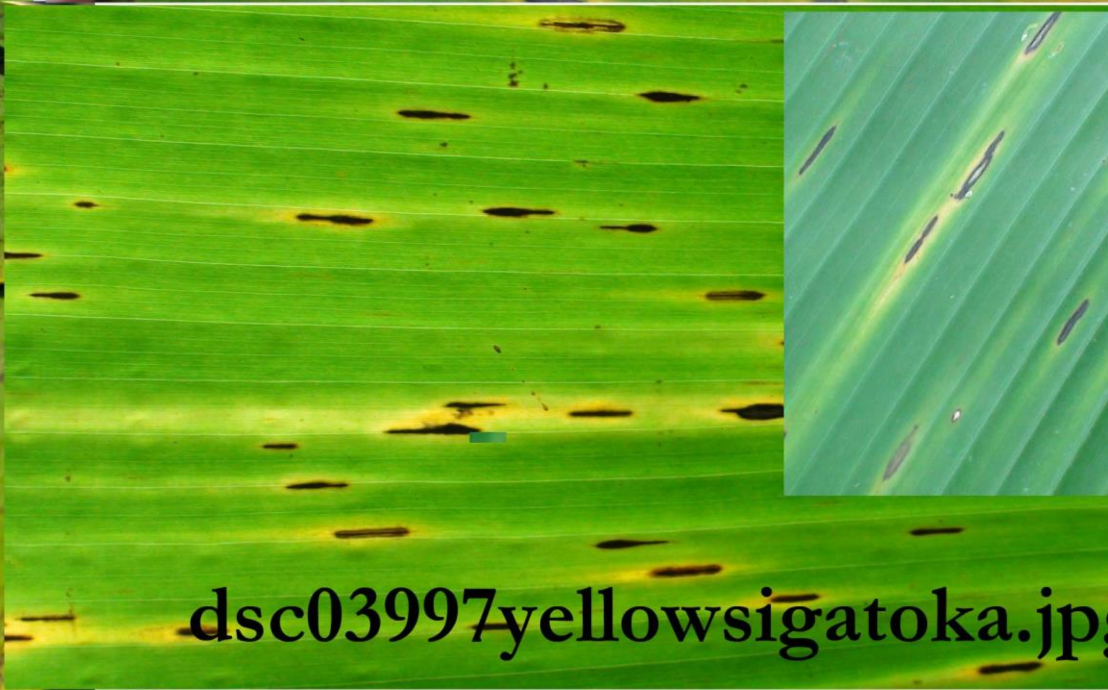



GROS MICHEL


dsc06955lateseriousbsvsymptoms.psd

dsc04004fusarium_banana_leaf.jpg

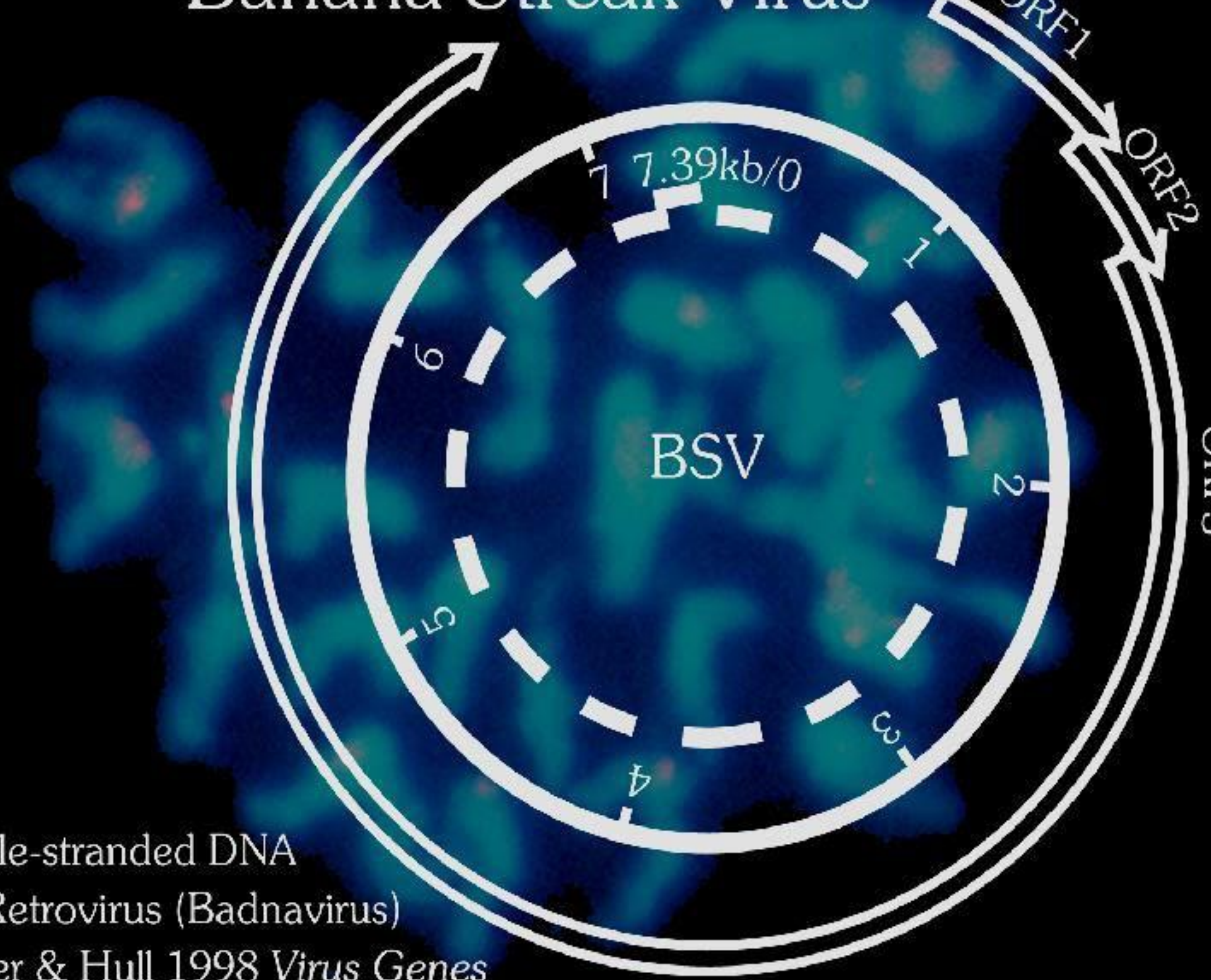
h4812freckle_disease_phyllosticta_guignardia
sae_on_pisangawak.jpg



dsc03997yellowsigatoka.jp

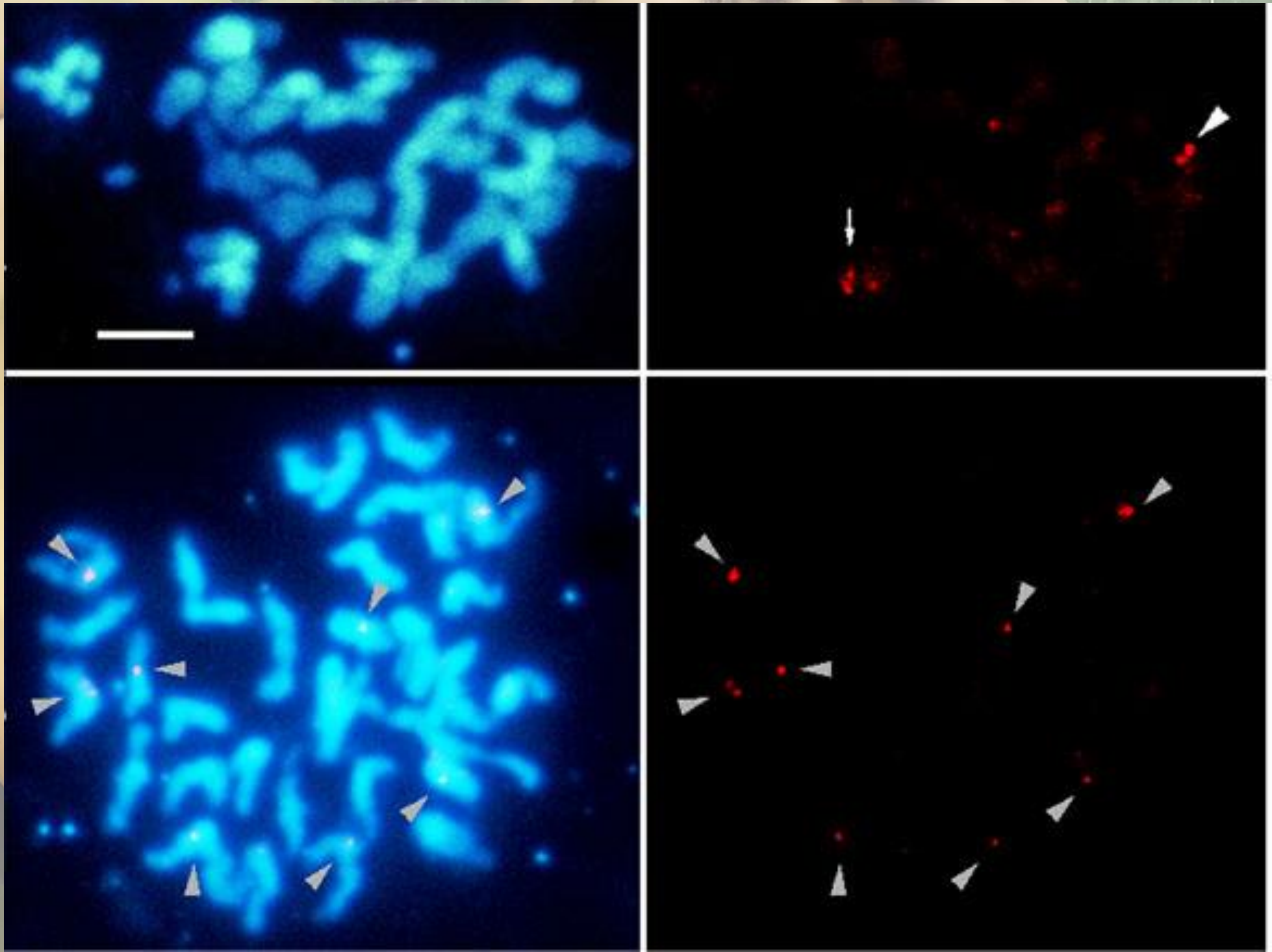
BSV Banana Streak Virus

Banana Streak Virus

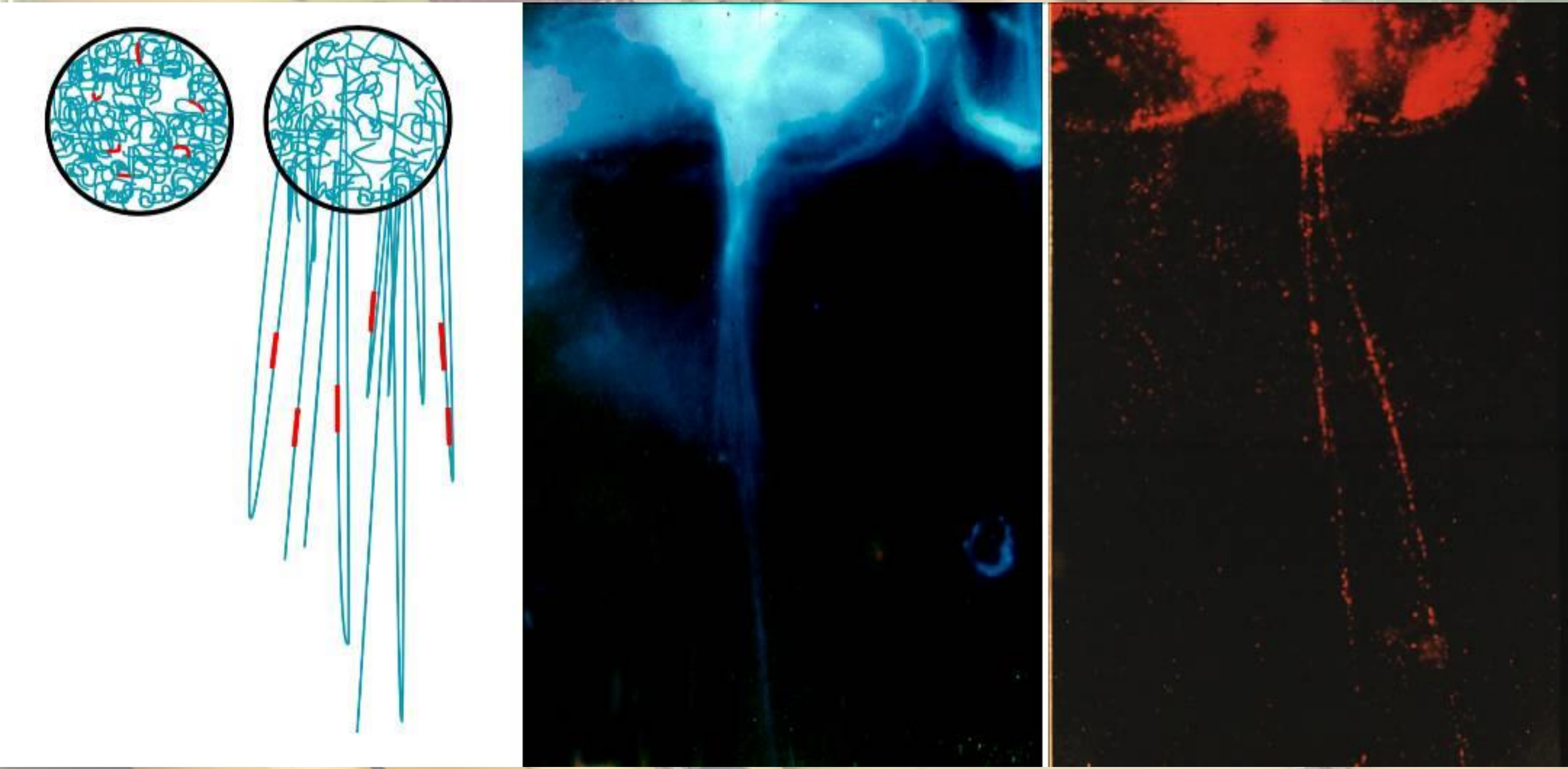


Double-stranded DNA
ParaRetrovirus (Badnavirus)
Harper & Hull 1998 *Virus Genes*

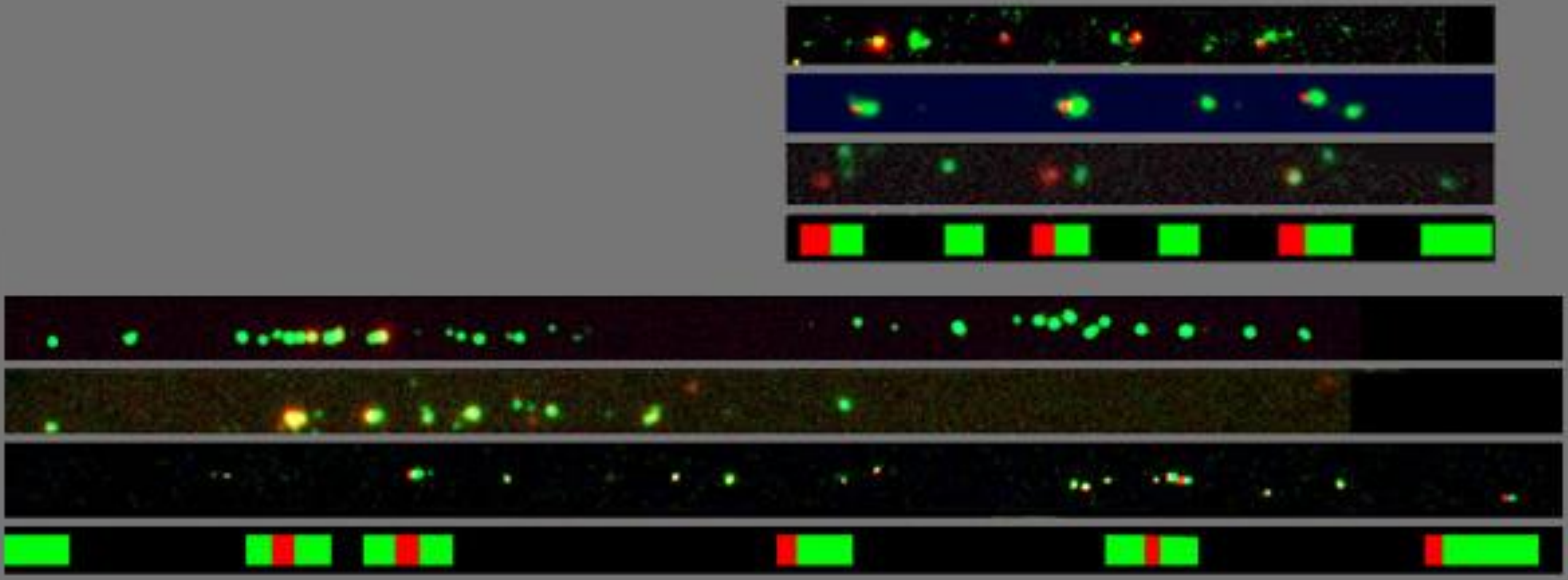
ar Copies of Banana Streak Virus in Banana



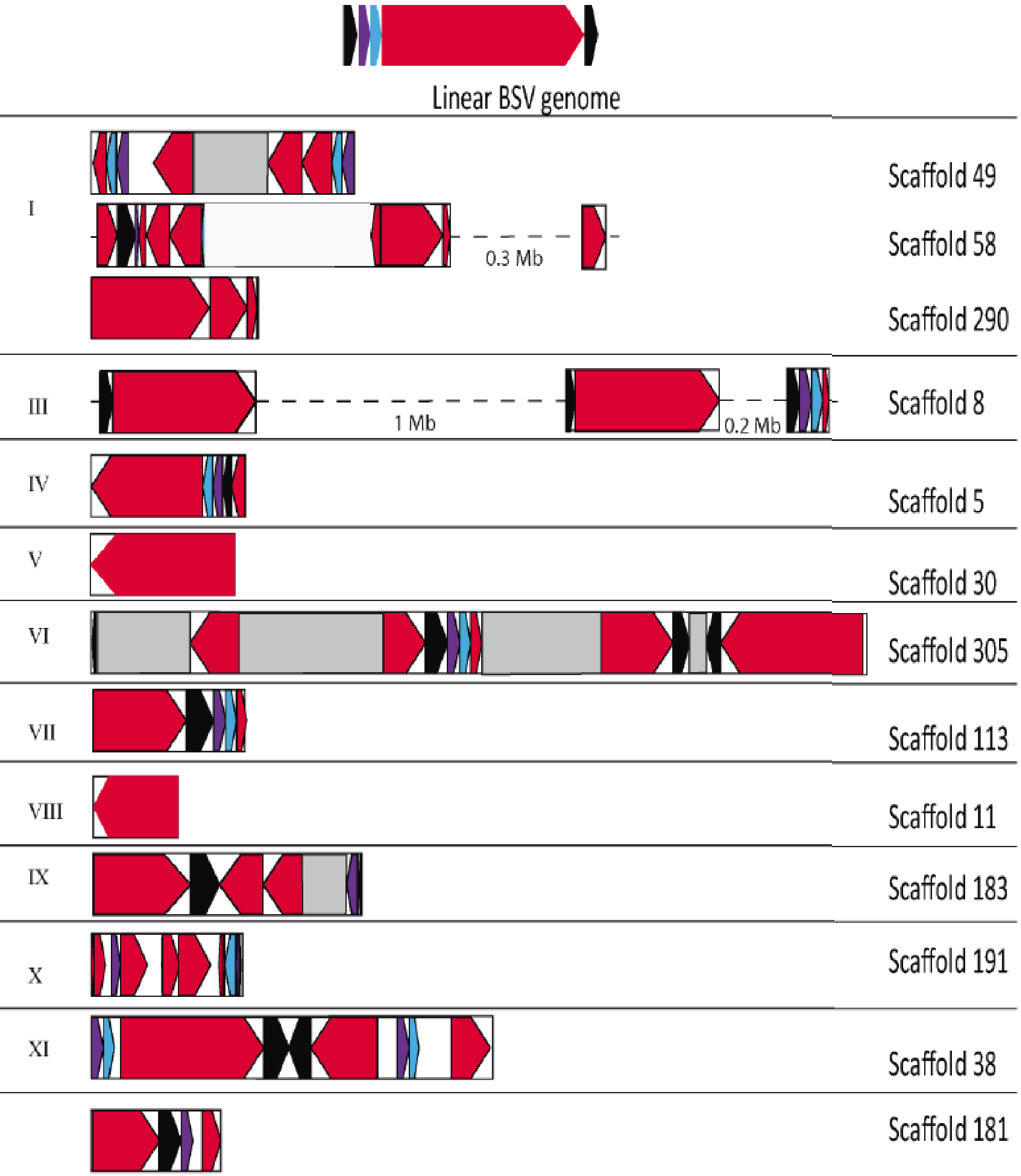
DNA Fibre Hybridization



Nuclear Copies of BSV in Banana



Harper, HH et al., Virology 1999 …



D'Hont, PHH*et al. Nature* 2012 doi:10.1038/nature11241

How to control disease in banana?

Biosecurity

1800 771 163
BANANA FRECKLE HOTLINE
HOTLINE IS OPEN 7 DAYS A WEEK

During the period of the banana freckle response no banana plant material may be moved within, or out of Control and Restricted Areas.

Do not move home grown bananas including fruit

Font Size: S M

How to detect Banana Freckle

The most characteristic symptom of banana freckle is a sandpaper feel to the infected leaves and fruit when rubbed between your fingers. This is caused by the fungal spore structures sticking through the upper leaf surface of the leaf tissue or fruit peel.

DOWNLOAD INFORMATION

Please check your banana plants for banana freckle and if you suspect it is present call the Banana Freckle Hotline on 1800 771 163, 7 days a week

DO NOT ATTEMPT TO DESTROY OR REMOVE THE BANANA PLANTS YOURSELF!

Help make the NT banana freckle free!
Call 1800 771 163 | 7 Days a week


BANANA
GERMPLASM

- Rouging and burning banana plants infected with Banana Bunchy Top Virus


Monceren DS


NSK
NSK

SUMMARY OF THE GLOBAL STRATEGY FOR THE CONSERVATION AND USE OF *MUSA* GENETIC RESOURCES

A consultative document prepared by the Global *Musa* Genetic Resources Network (MusaNet)

October 2016

MusaNet Bioversity International CGIAR

Special appreciation is expressed to the following contributors of the Global Strategy,

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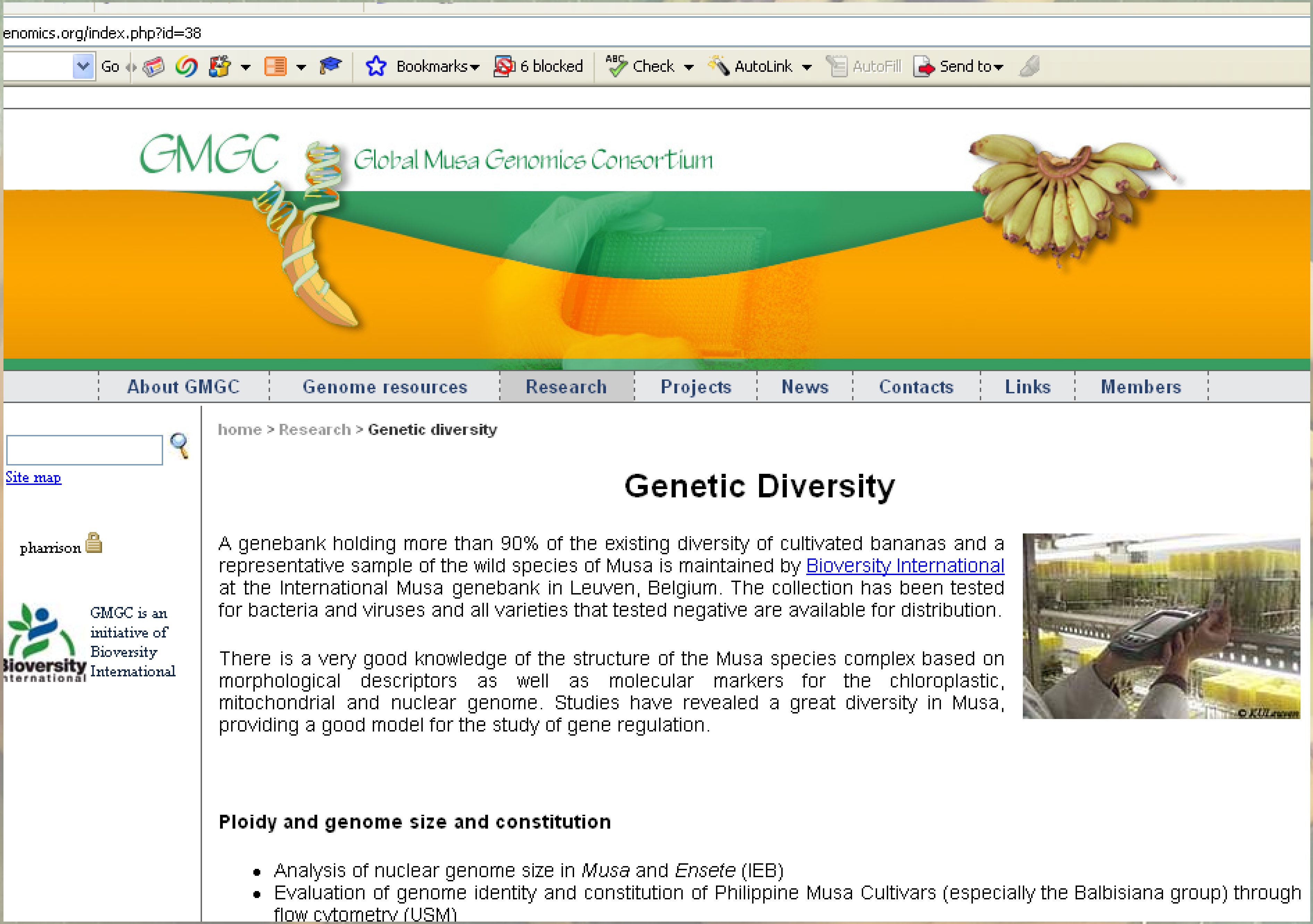
51. Rachel Chase (Bioversity International)


AICRP(TF)
COLLECTION, CONSERVATION AND EVALUATION OF BANANA GERMPLASM
No. OF ACCESSIONS - 256.
No. OF PLANTS/ACCESSION - 5.
SPACING - 2x2.5m.
DATE OF PLANTING - 23.10.2006.



home > Research > Genetic diversity

Genetic Diversity

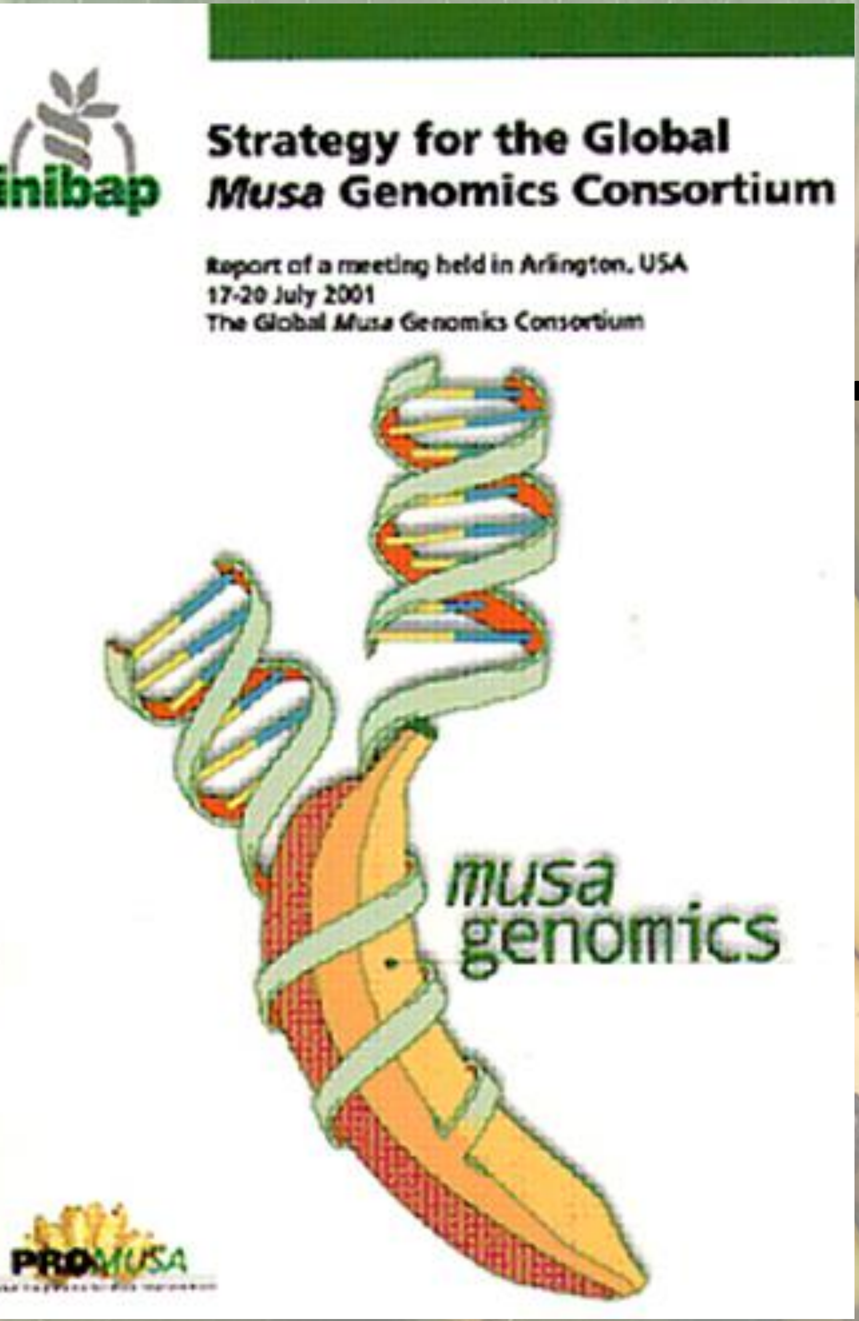
A genebank holding more than 90% of the existing diversity of cultivated bananas and a representative sample of the wild species of Musa is maintained by Bioversity International at the International Musa genebank in Leuven, Belgium. The collection has been tested for bacteria and viruses and all varieties that tested negative are available for distribution.

There is a very good knowledge of the structure of the Musa species complex based on morphological descriptors as well as molecular markers for the chloroplastic, mitochondrial and nuclear genome. Studies have revealed a great diversity in Musa, providing a good model for the study of gene regulation.

Ploidy and genome size and constitution

- Analysis of nuclear genome size in *Musa* and *Ensete* (IEB)
- Evaluation of genome identity and constitution of Philippine Musa Cultivars (especially the Balbisiana group) through flow cytometry (USM)

The Global Musa Genomics Consortium



inibap

Strategy for the Global *Musa* Genomics Consortium

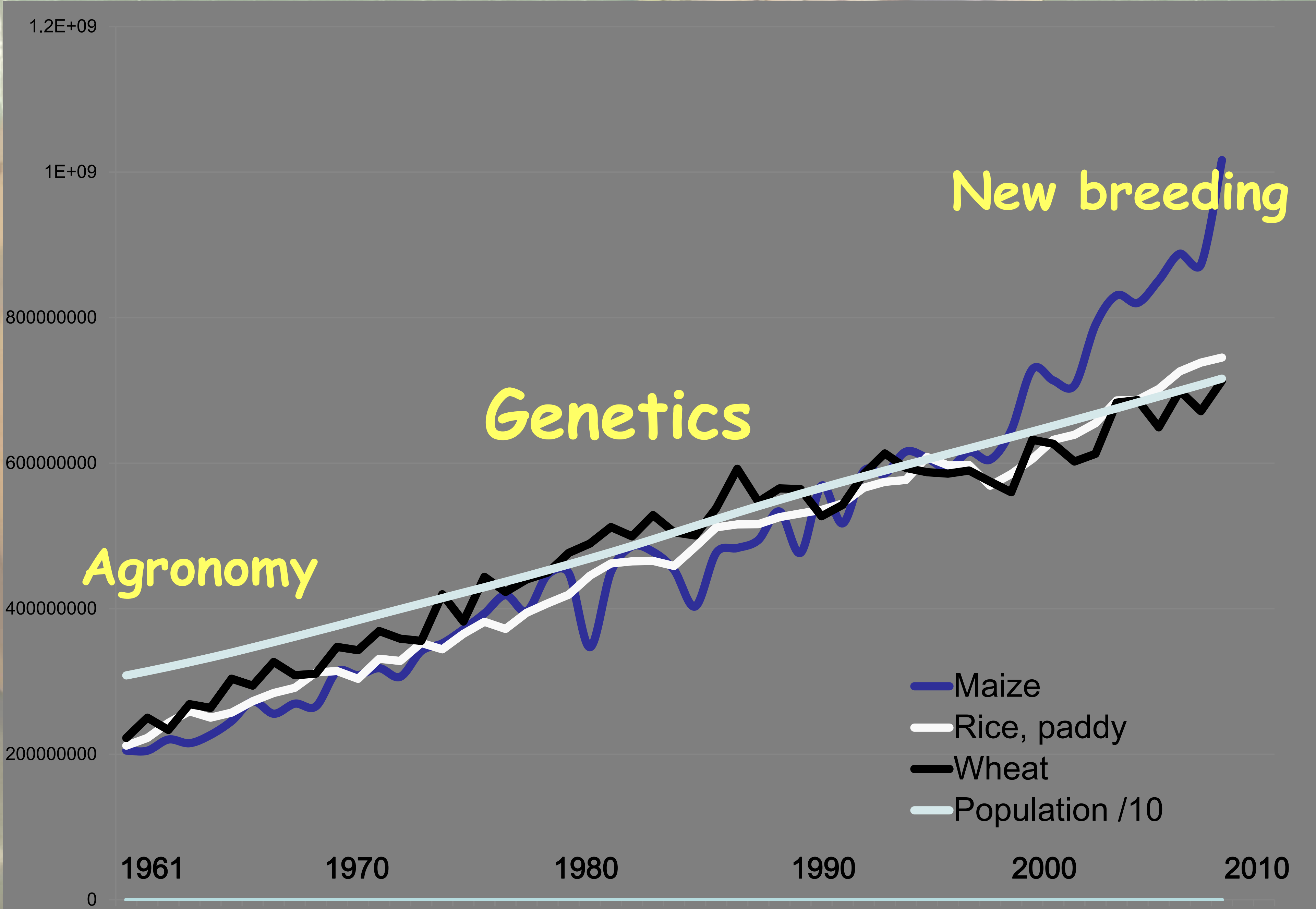
Report of a meeting held in Arlington, USA
17-20 July 2001
The Global *Musa* Genomics Consortium

- To assure the sustainability of banana as a staple food crop by developing an integrated genetic and genomic understanding, allowing targeted breeding, transformation and more efficient use of Musa biodiversity

Plant breeding

- Keeping up with changes
- Biotic stress
  - New disease races are continuously appearing and spreading
  - Fungi, viruses, bacteria
  - Insects, nematodes, weeds …
- Abiotic stresses
  - Drought/flooding/salt, cold …
- Sustainability - inputs
- Socio-economic changes
  - More people to feed on less land
  - Urbanization of population

52 years of plant breeding progress

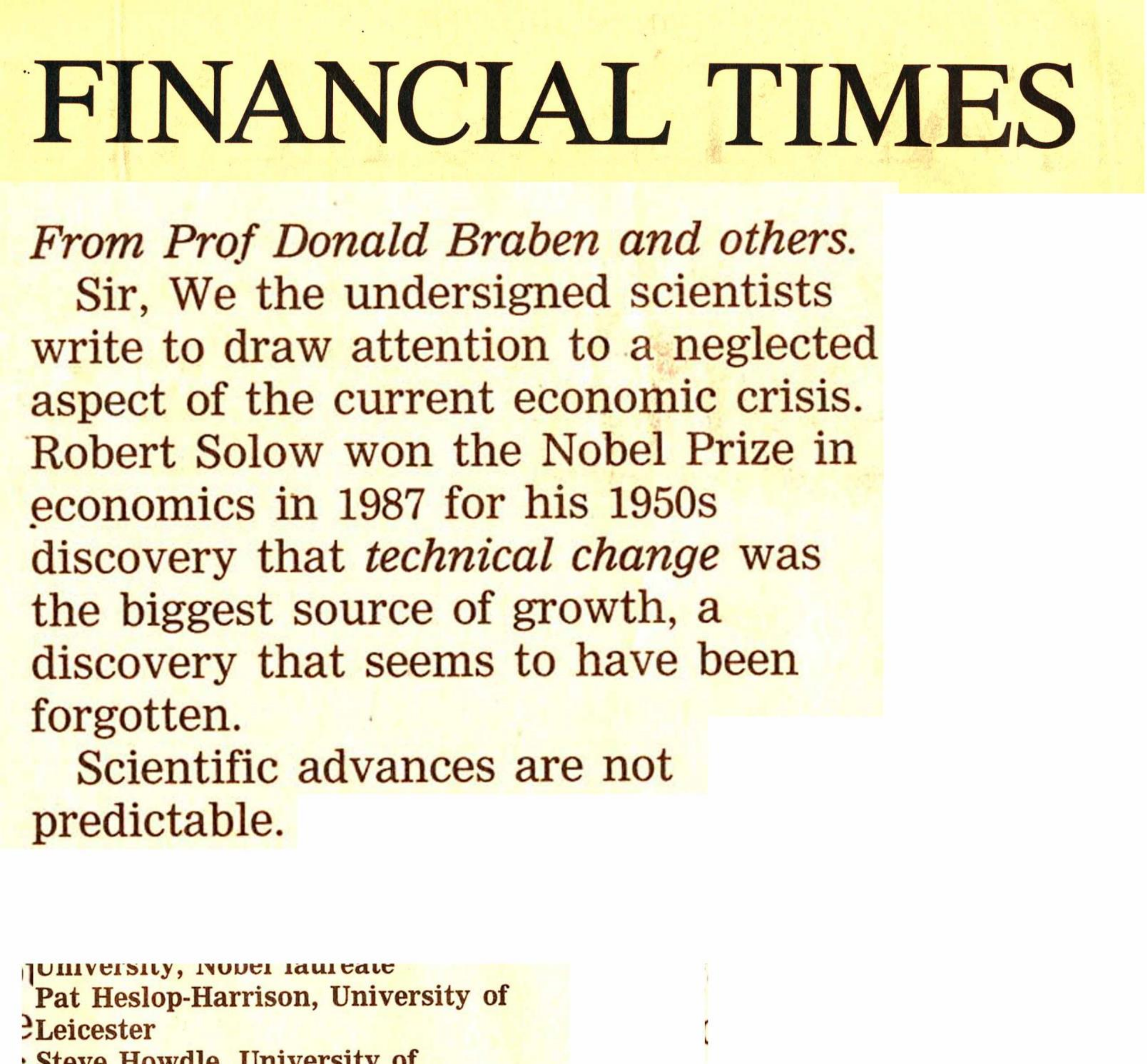


Super-domestication:
The future of banana crops

- The genepool has the diversity there which can meet these challenges

- Breeders need to get better and faster

- Banana has extra challenges
  - Staple food
  - Major income source in many communities
  - Sterile plant
  - Export has transport/ripening requirements



FINANCIAL TIMES

From Prof Donald Braben and others.

Sir, We the undersigned scientists write to draw attention to a neglected aspect of the current economic crisis. Robert Solow won the Nobel Prize in economics in 1987 for his 1950s discovery that *technical change* was the biggest source of growth, a discovery that seems to have been forgotten.

Scientific advances are not predictable.

University, Nobel laureate
Pat Heslop-Harrison, University of Leicester
Steve Howdle, University of

Super-domestication:
Challenges for the future of banana

- Biotic stresses
- Abiotic stresses
- Sustainability
- Production and climate
- Socioeconomic factors

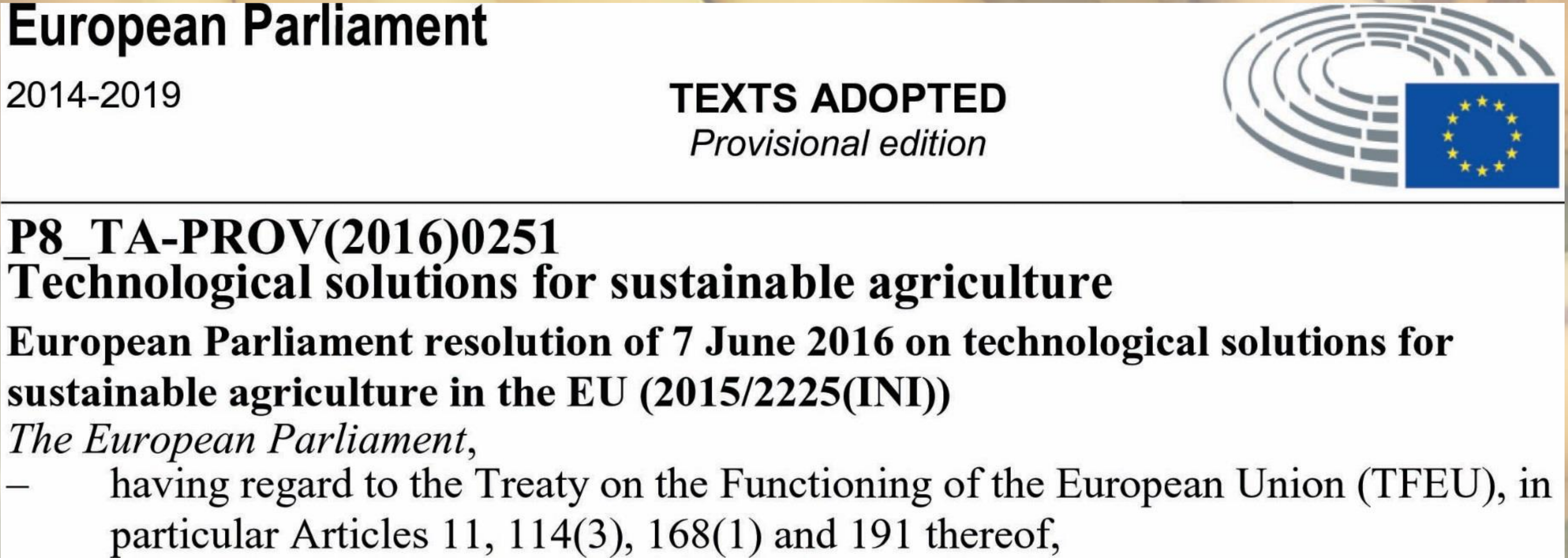
- … all mean current cultivars may not meet future needs
- … but there are solutions


1 NO POVERTY
2 ZERO HUNGER
3 GOOD HEALTH AND WELL-BEING
4 QUALITY EDUCATION
5 GENDER EQUALITY
6 CLEAN WATER AND SANITATION
7 AFFORDABLE AND CLEAN ENERGY
8 DECENT WORK AND ECONOMIC GROWTH
9 INDUSTRY, INNOVATION AND INFRASTRUCTURE
10 REDUCED INEQUALITIES
11 SUSTAINABLE CITIES AND COMMUNITIES
THE GLOBAL GOALS
For Sustainable Development
12 RESPONSIBLE CONSUMPTION AND PRODUCTION
13 CLIMATE ACTION
14 LIFE BELOW WATER
15 LIFE ON LAND
16 PEACE AND JUSTICE STRONG INSTITUTIONS
17 PARTNERSHIPS FOR THE GOALS

European Parliament

REPORT 10 May 2016
on technological solutions for sustainable agriculture in the EU
(2015/2225(INI))
Committee on Agriculture and Rural Development
Rapporteur: Anthea McIntyre

EU Health & Food Commissioner Vytenis Andriukaitis



European Parliament

2014-2019

TEXTS ADOPTED
Provisional edition

P8_TA-PROV(2016)0251
Technological solutions for sustainable agriculture

European Parliament resolution of 7 June 2016 on technological solutions for sustainable agriculture in the EU (2015/2225(INI))

The European Parliament,

– having regard to the Treaty on the Functioning of the European Union (TFEU), in particular Articles 11, 114(3), 168(1) and 191 thereof,

The regulation of genetic technologies

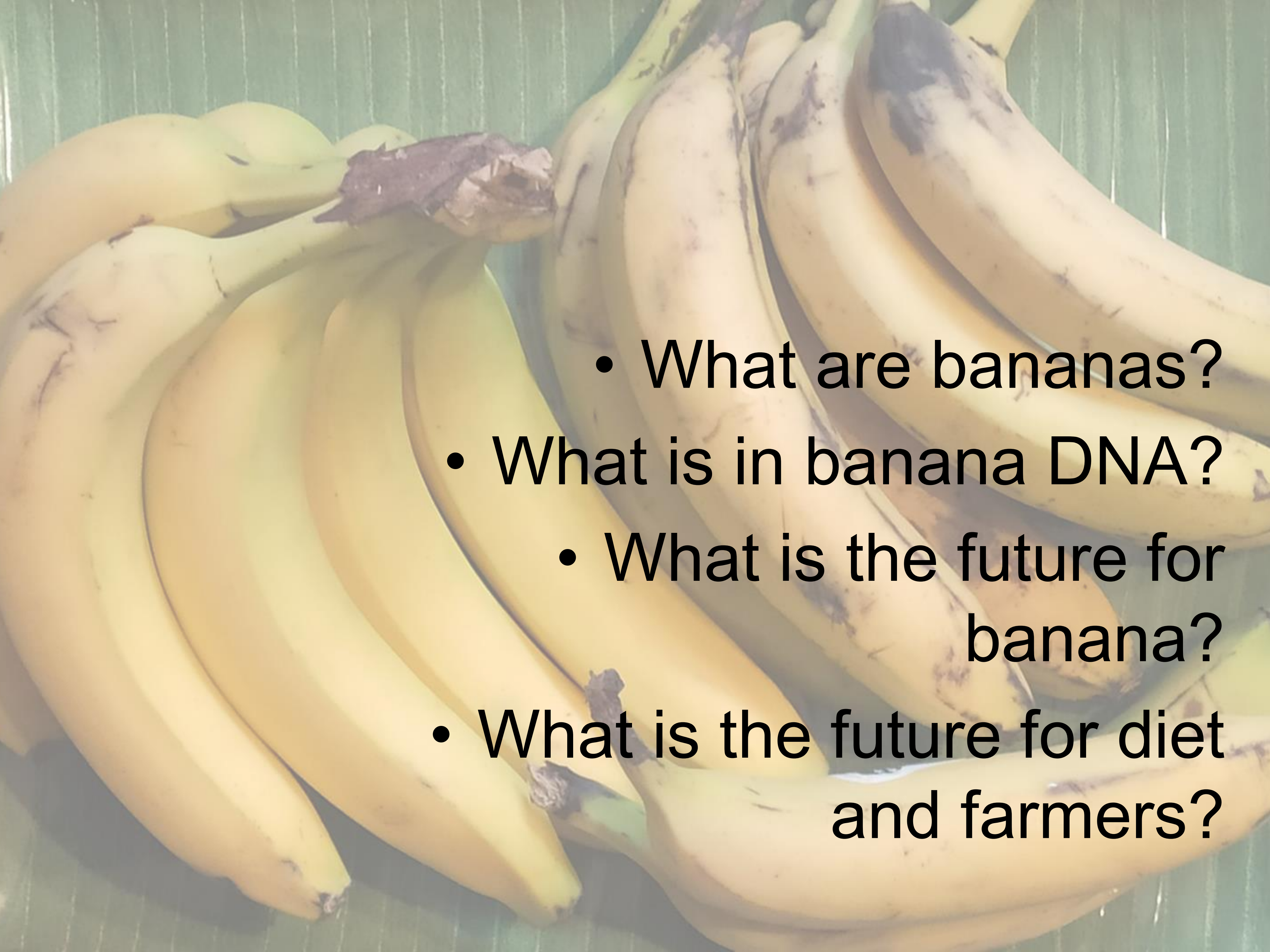
Overview

Closes 17 Mar 2021

This consultation is about the regulation of genetic technologies.
It mainly focuses on the regulation of gene edited (GE) organisms possessing genetic changes which could have been introduced by traditional breeding. This is covered in part 1 of the consultation.

In part 2 of the consultation, we are using this opportunity to engage separately and start gathering views on the wider regulatory framework governing genetically modified organisms (GMOs).

Depending on the results of part 1, Defra may change the legislation to amend the definition of a GMO as it applies in England. Currently GMOs are defined in section 106 of the Environmental Protection Act 1990[1]. This would mean



- What are bananas?
- What is in banana DNA?
- What is the future for banana?
- What is the future for diet and farmers?

Charles Darwin

The final sentences of “The Origin”

> It is interesting to contemplate … many plants of many kinds … from so simple a beginning endless forms most beautiful and most wonderful have been, and are being evolved.

Bananas: past, present and future

Pat Heslop-Harrison

www.molcyt.com

phh@molcyt.com

U3A February 2021

UNIVERSITY OF LEICESTER

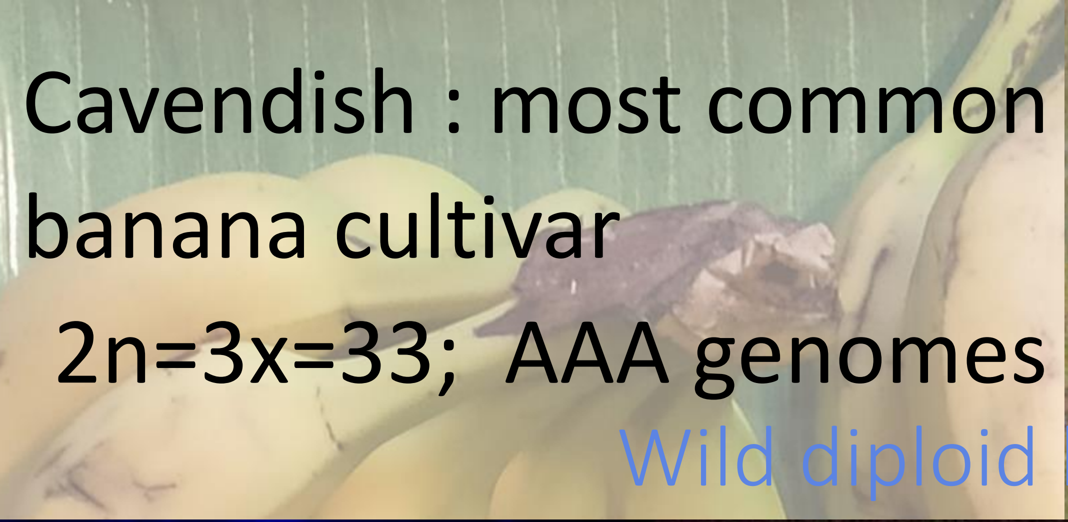
South China Botanical Garden
Chinese Academy of Sciences

The Banana

Pat Heslop-Harrison

www.molcyt.com

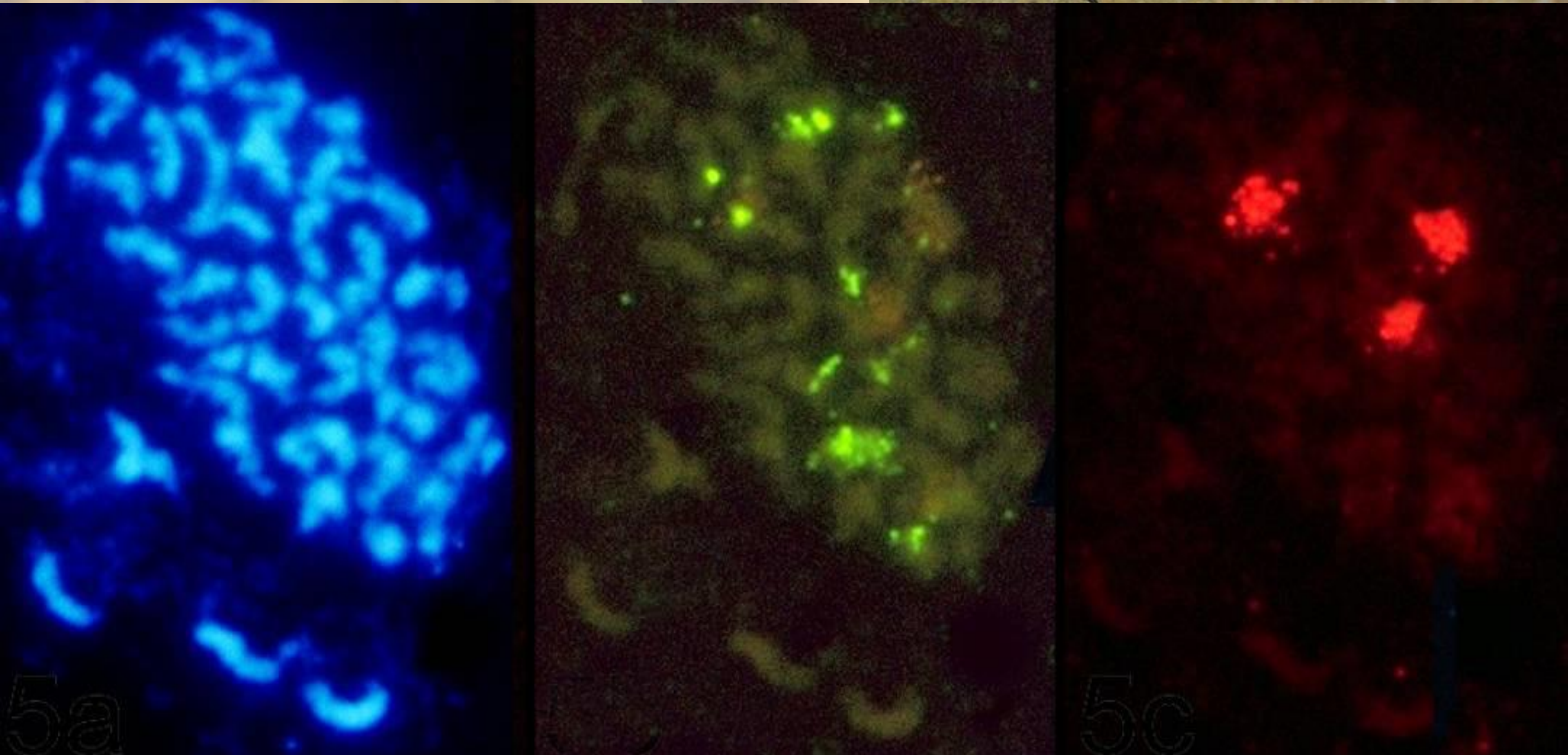
phh4@le.ac.uk



Cavendish : most common banana cultivar

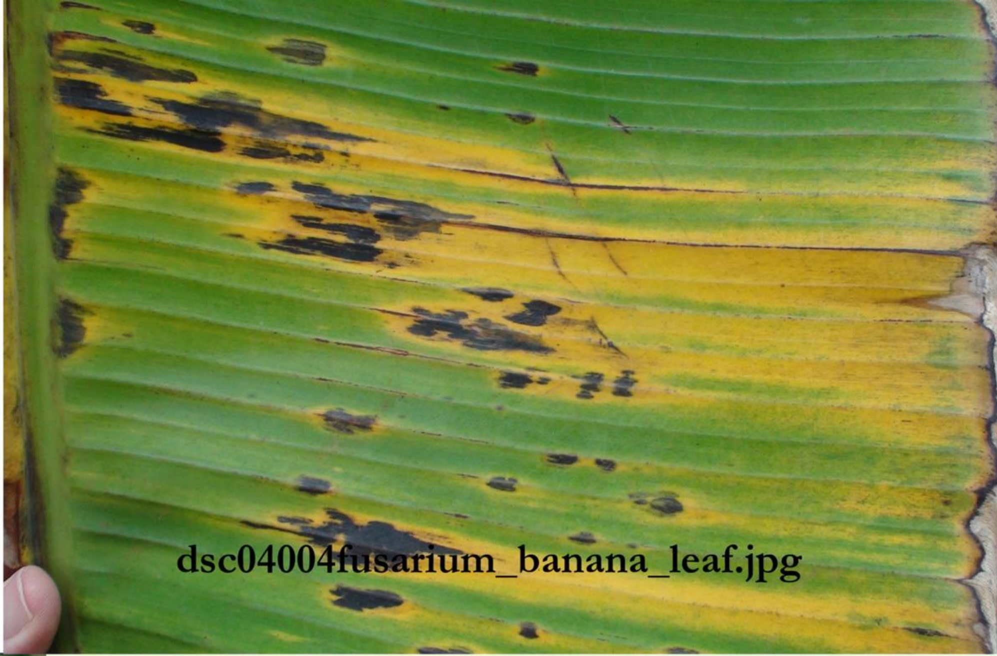
$2n=3x=33$; AAA genomes

Wild diploid banana



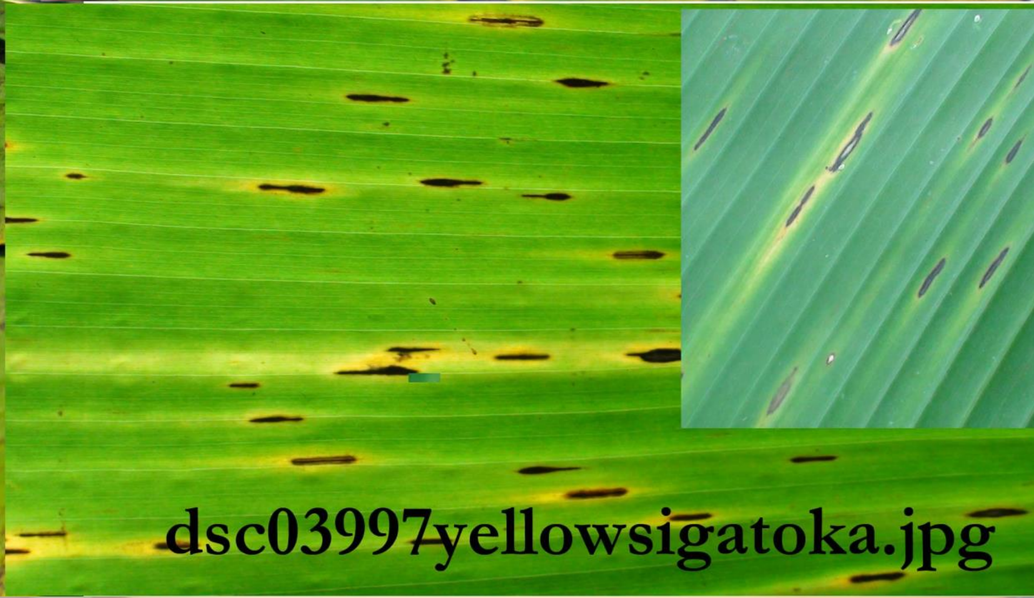
- Aerial spraying to control disease in banana

dsc06955lateseriousbsvsymptoms.psd



dsc04004fusarium_banana_leaf.jpg

_phh4812freckle_disease_phyllosticta_guignardia musae_on_pisangawak.jpg

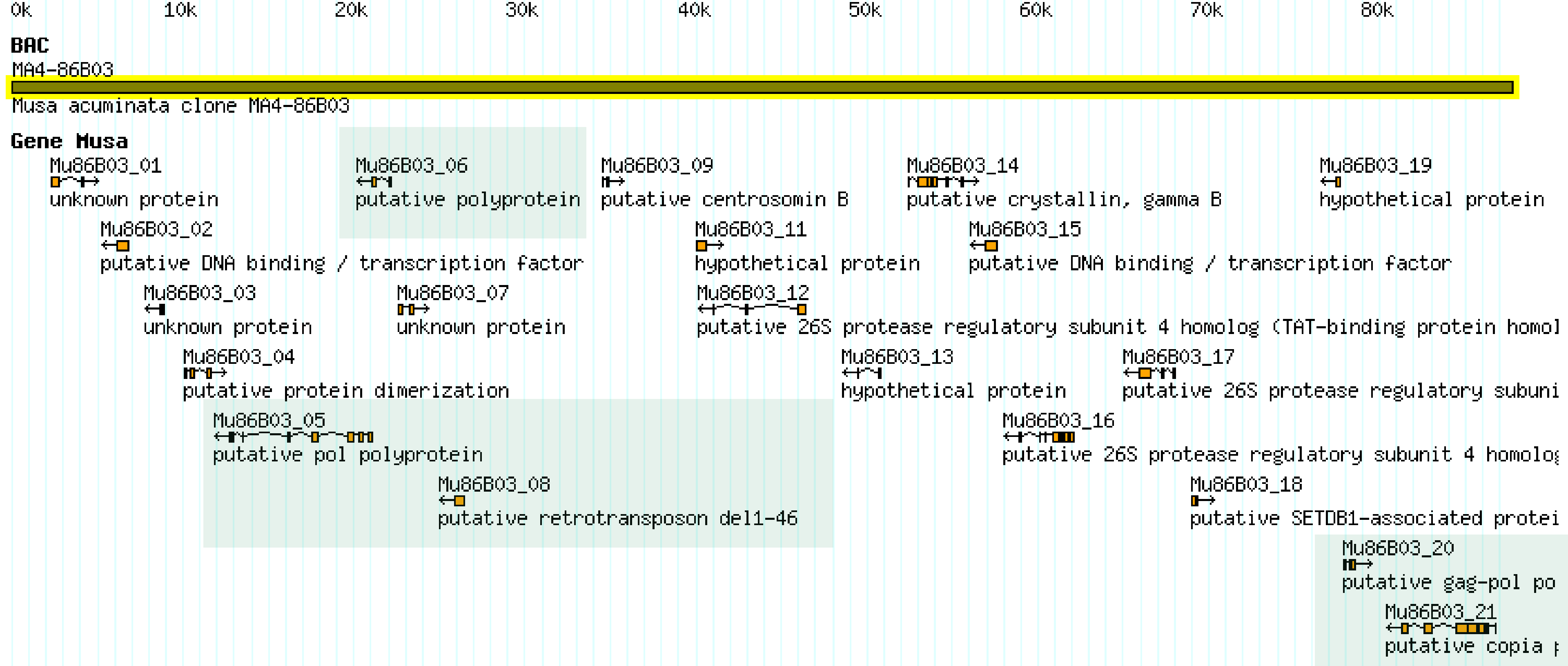


dsc03997yellowsigatoka.jpg

Retroelements

Sequences which amplify through an RNA intermediate

- 50% of all the DNA!



BAC

MA4-86B03

Musa acuminata clone MA4-86B03

Gene Musa

Mu86B03_01
unknown protein

Mu86B03_02
putative DNA binding / transcription factor

Mu86B03_03
unknown protein

Mu86B03_04
putative protein dimerization

Mu86B03_05
putative pol polyprotein

Mu86B03_06
putative polyprotein

Mu86B03_07
unknown protein

Mu86B03_08
putative retrotransposon del1-46

Mu86B03_09
putative centrosomin B

Mu86B03_11
hypothetical protein

Mu86B03_12
putative 26S protease regulatory subunit 4 homolog (TAT-binding protein homol

Mu86B03_13
hypothetical protein

Mu86B03_14
putative crystallin, gamma B

Mu86B03_15
putative DNA binding / transcription factor

Mu86B03_16
putative 26S protease regulatory subunit 4 homolog

Mu86B03_17
putative 26S protease regulatory subuni

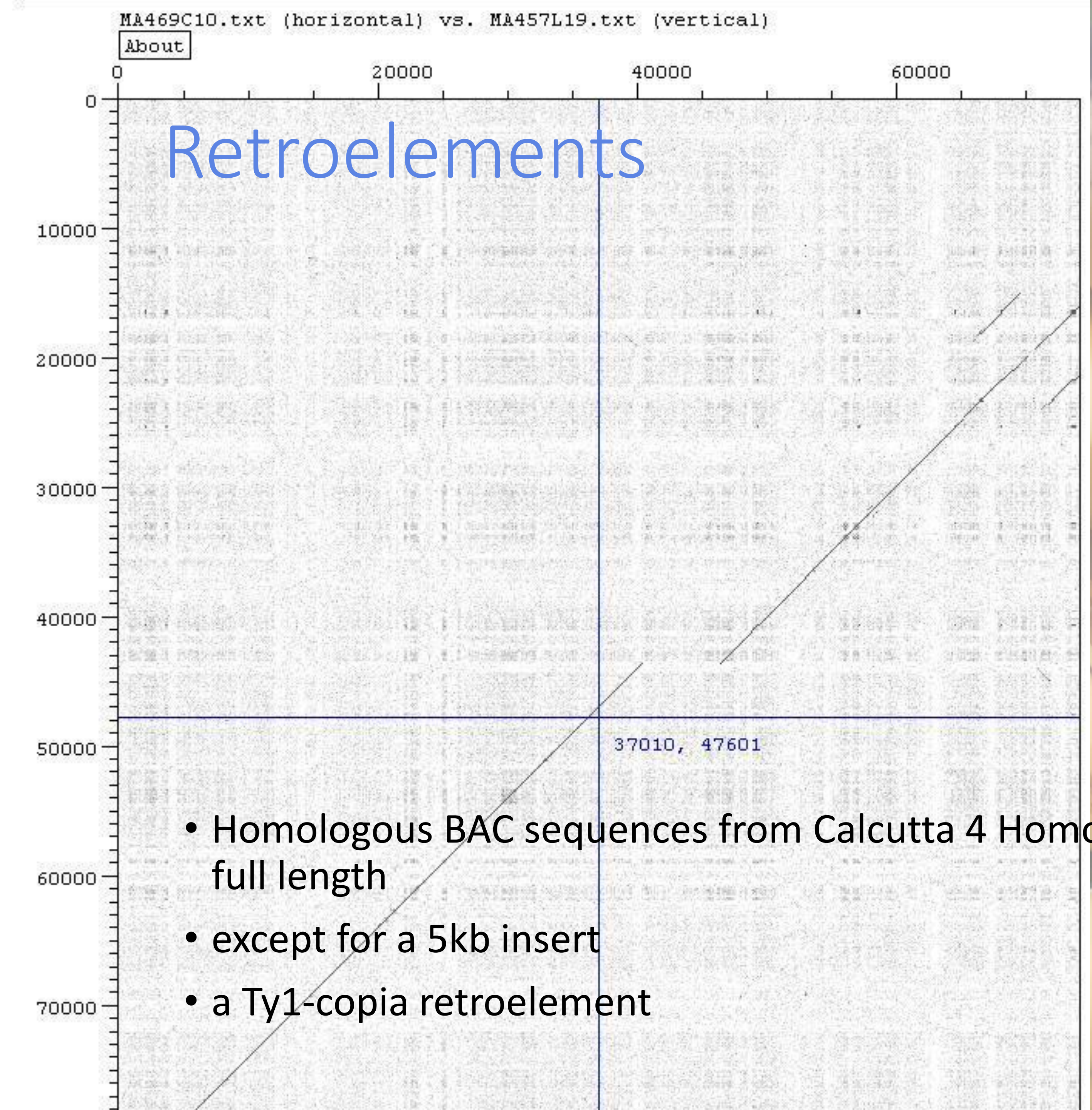
Mu86B03_18
putative SETDB1-associated protei

Mu86B03_19
hypothetical protein

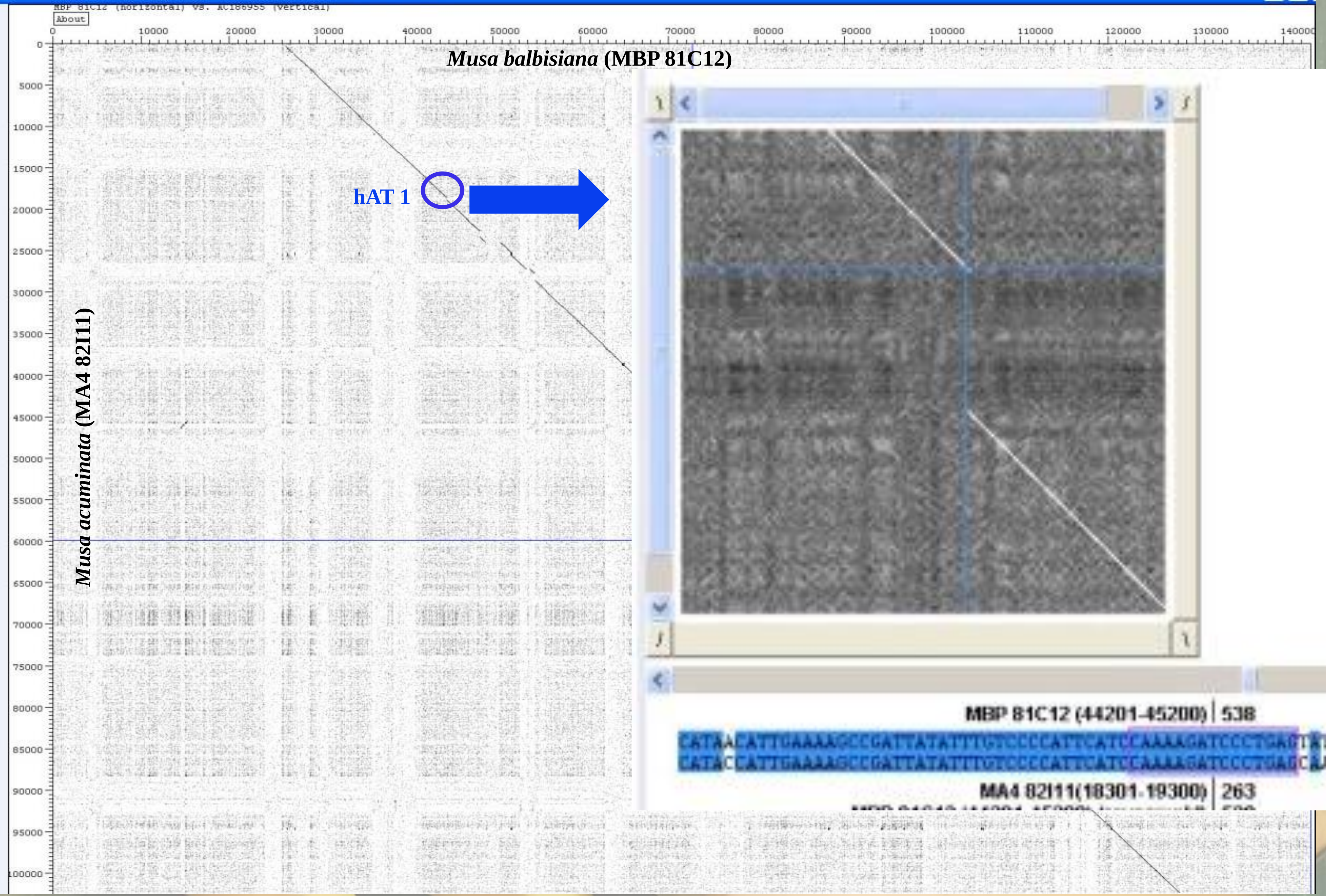
Mu86B03_20
putative gag-pol po

Mu86B03_21
putative copia

Retroelements



- Homologous BAC sequences from Calcutta 4 Homologous over the full length
- except for a 5kb insert
- a Ty1-copia retroelement

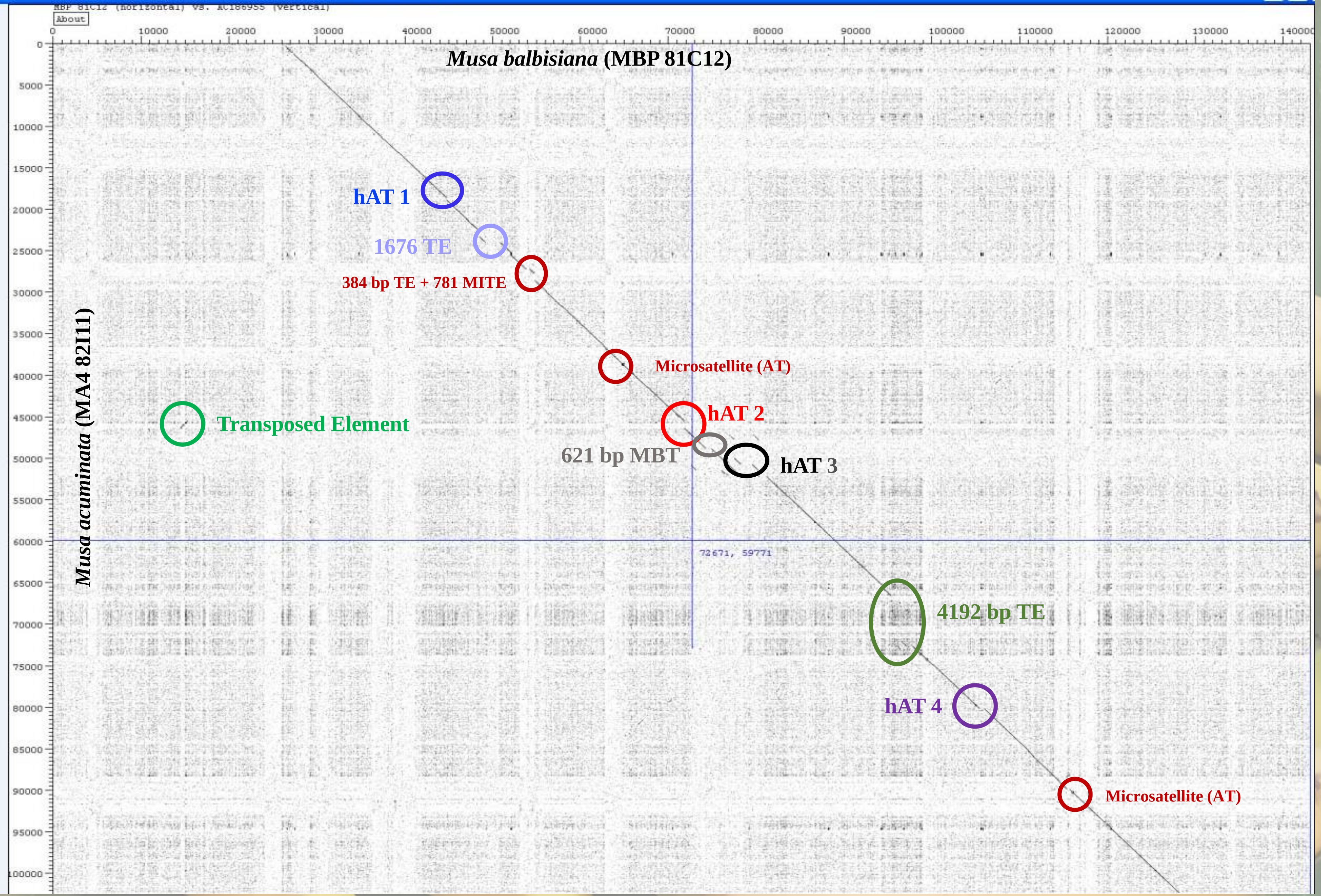


MBP 81C12 (44201-45200) | 538

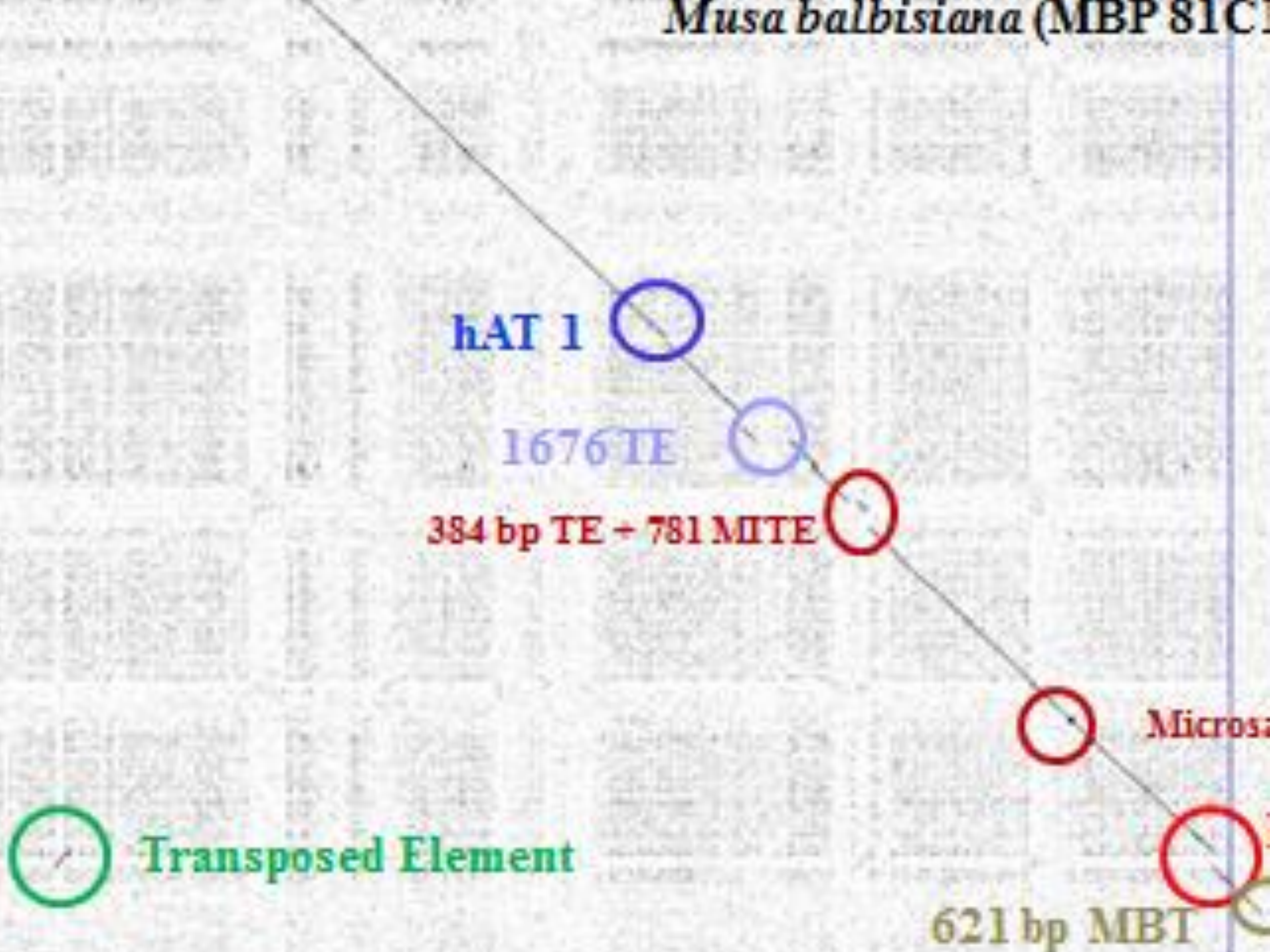
CATAACATTGAAAAGCCGATTATATTTGTCCCCATTCATCCAAAAGATCCCTGAGTA
CATACCATTGAAAAGCCGATTATATTTGTCCCCATTCATCCAAAAGATCCCTGAGCA

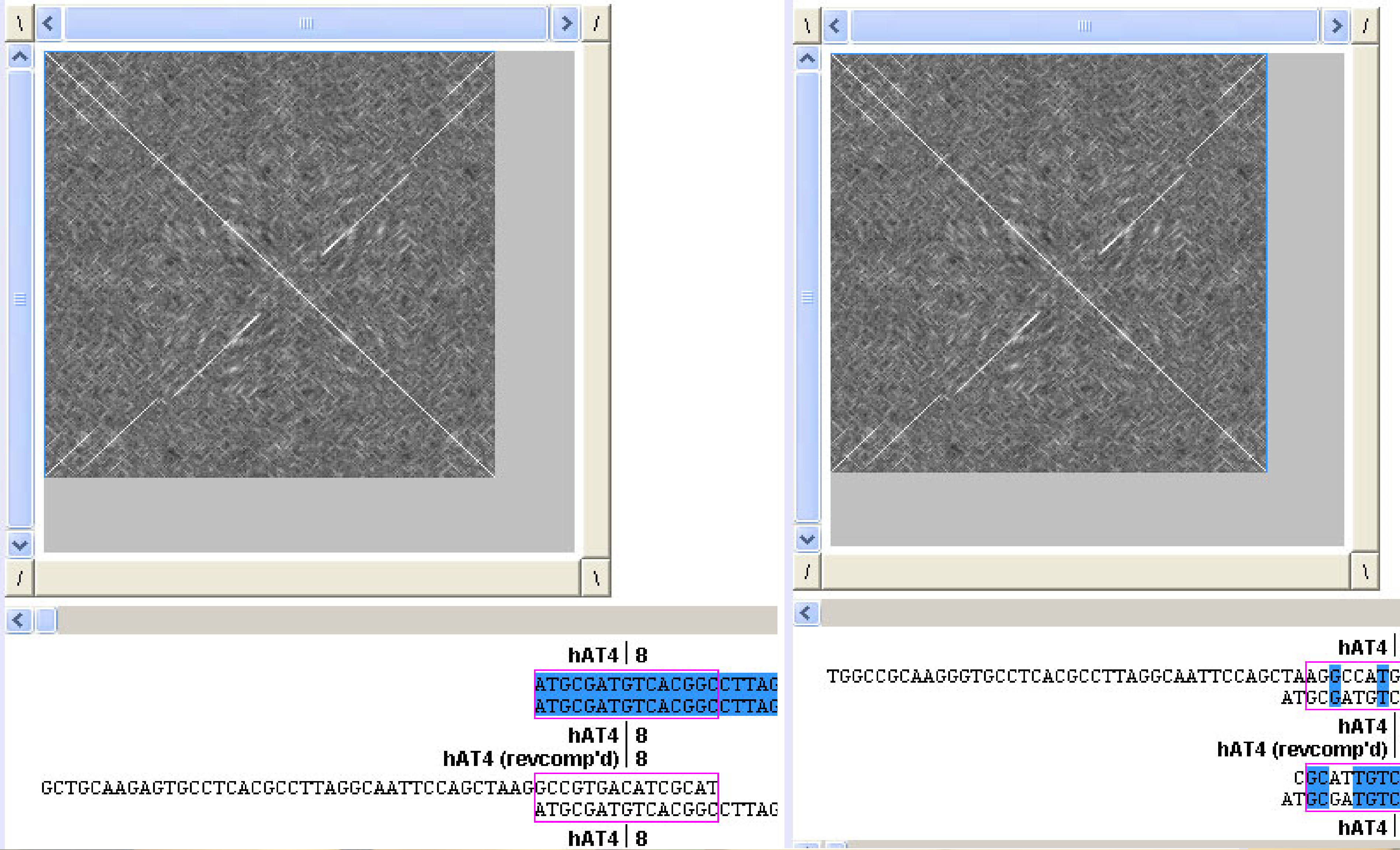
MA4 82I11(18301-19300) | 263

MBP 81C12 (*M. balbisiana*) x MA4 82I11 (*M. acuminata*) BACs.



MBP 81C12 (*M. balbisiana*) x MA4 82I11 (*M. acuminata*) BACs.


Musa balbisiana (MBP 81C
hAT 1
1676 TE
384 bp TE + 781 MITE
Microsa
Transposed Element
621 bp MBT



```
hAT4 | 8
ATGCGATGTCACGGCCTTAG
ATGCGATGTCACGGCCTTAG
hAT4 | 8
hAT4 (revcomp'd) | 8
GCTGCAAGAGTGCCTCACGCCTTAGGCAATTCCAGCTAAGGCCGTGACATCGCAT
                                        ATGCGATGTCACGGCCTTAG
hAT4 | 8
```

```
                                                  hAT4 |
TGGCCGCAAGGGTGCCTCACGCCTTAGGCAATTCCAGCTAAGGCCATG
                                       ATGCGATGTC
                                                  hAT4 |
                                      hAT4 (revcomp'd) |
                                        CGCATTGTC
                                       ATGCGATGTC
                                                  hAT4 |
```

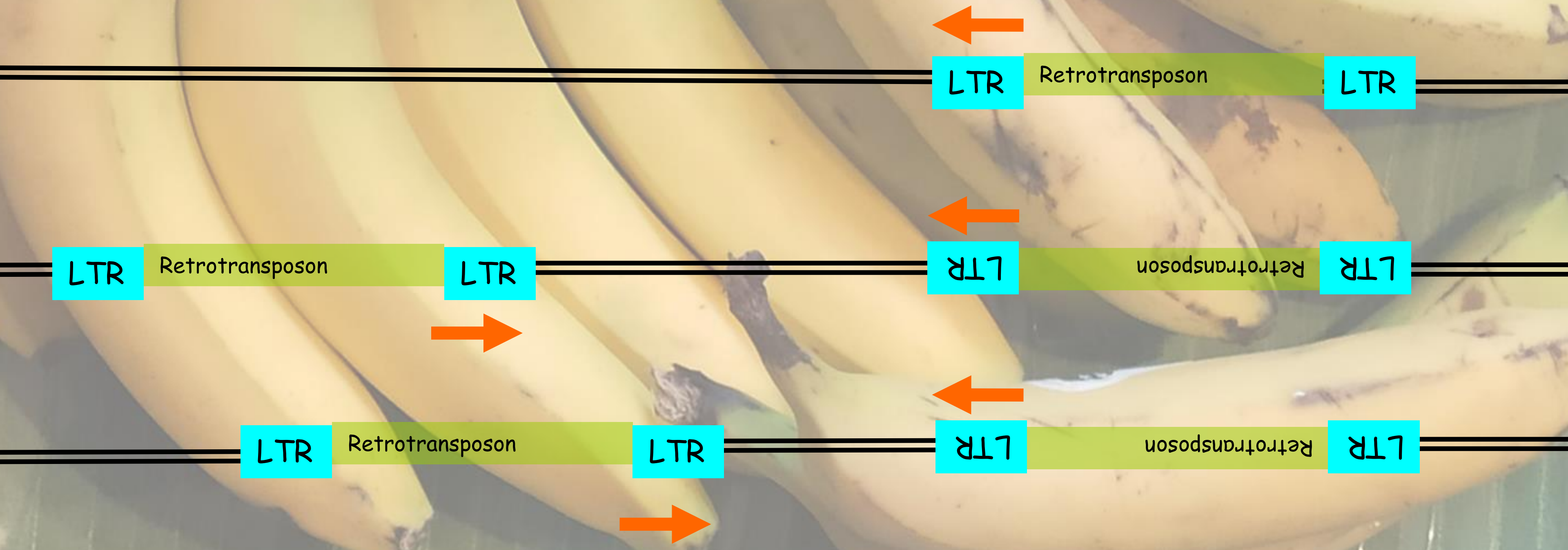
Dot plot showing the complete Inverted repeat.

Retroelement Markers

Insertion

LTR
Retrotransposon
LTR

IRAP - InterRetroelement PCR

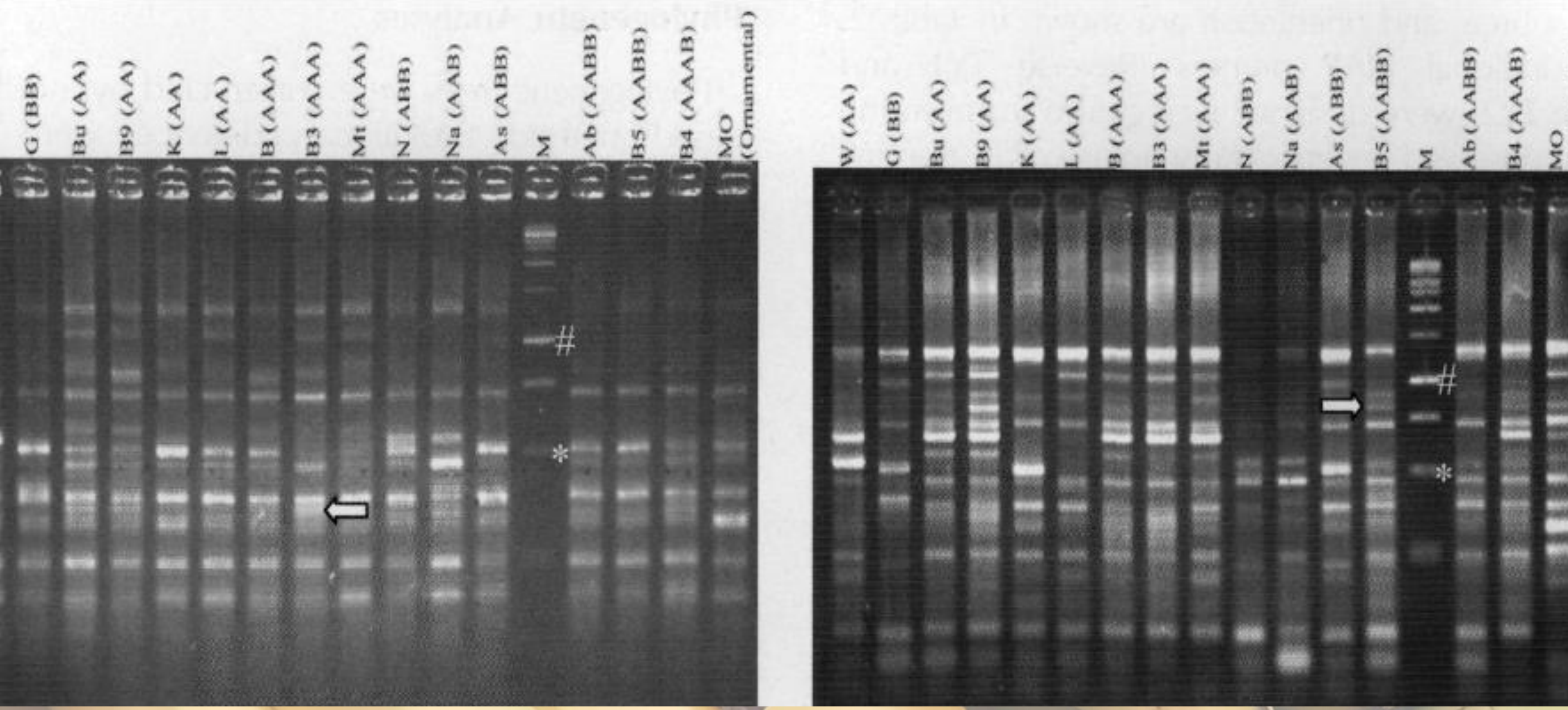


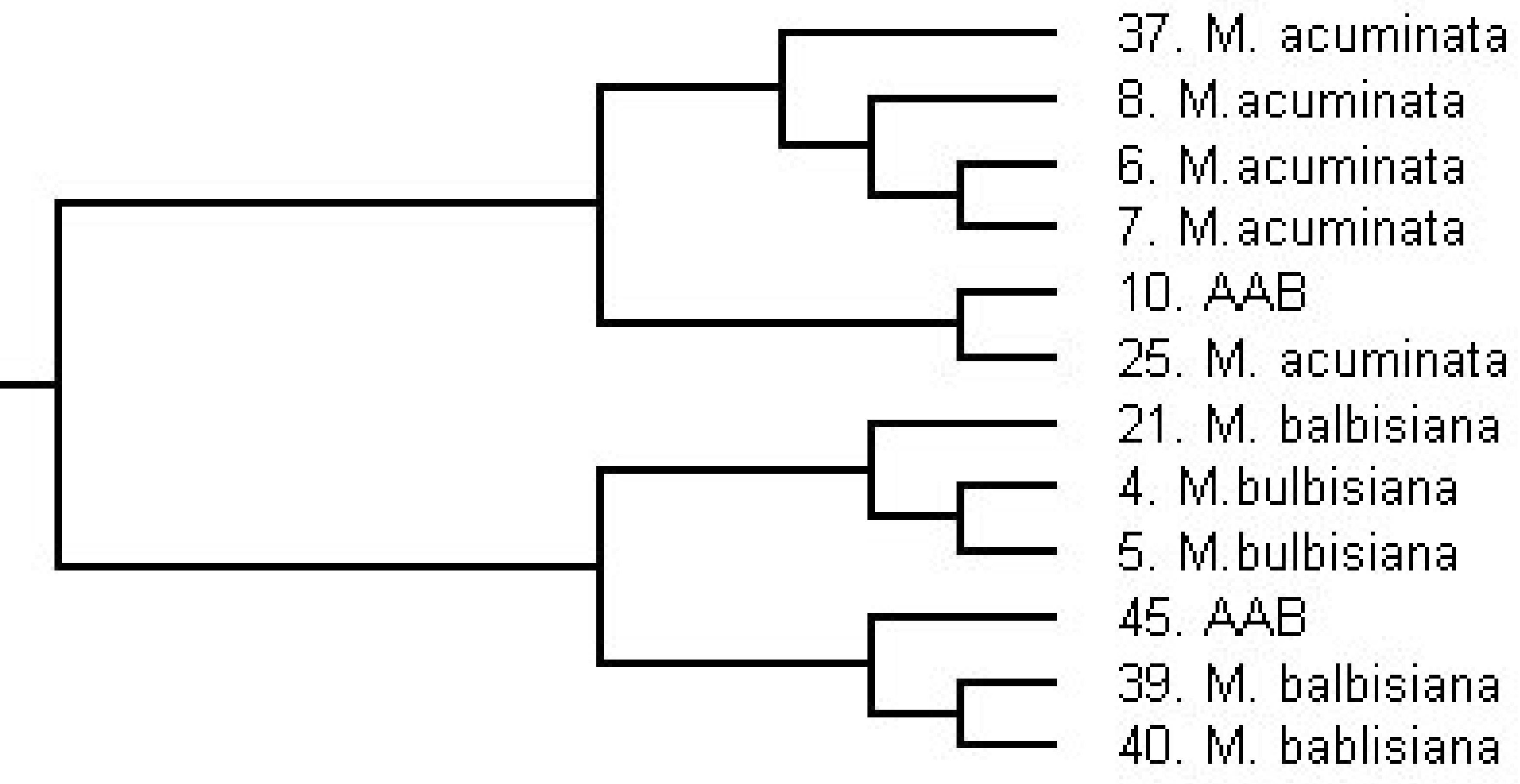
LTR
Retrotransposon
LTR

LTR
Retrotransposon
LTR
LTR
Retrotransposon
LTR

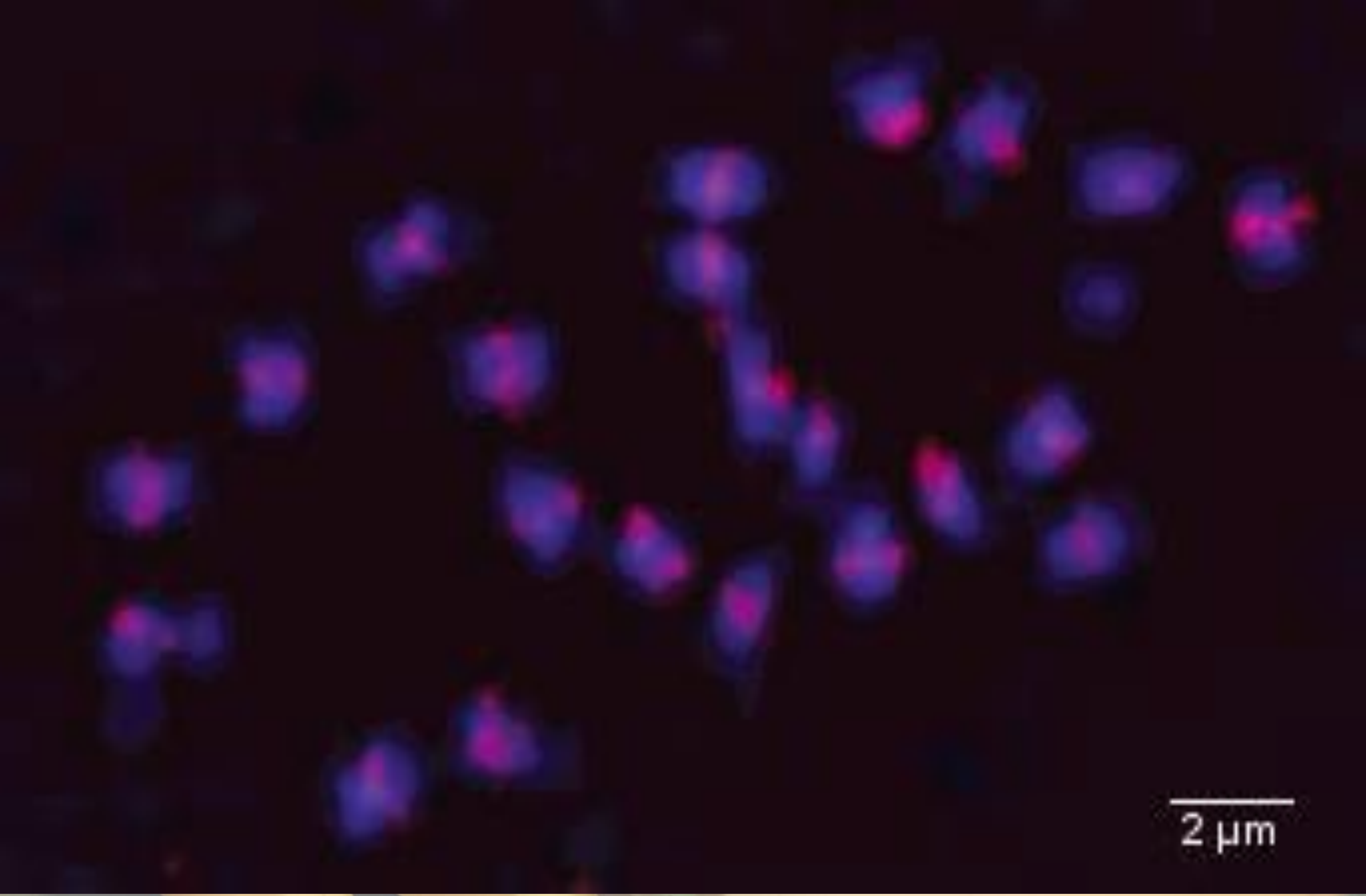
LTR
Retrotransposon
LTR
LTR
Retrotransposon
LTR

"Fingerprint" gels showing diversity in different banana varieties

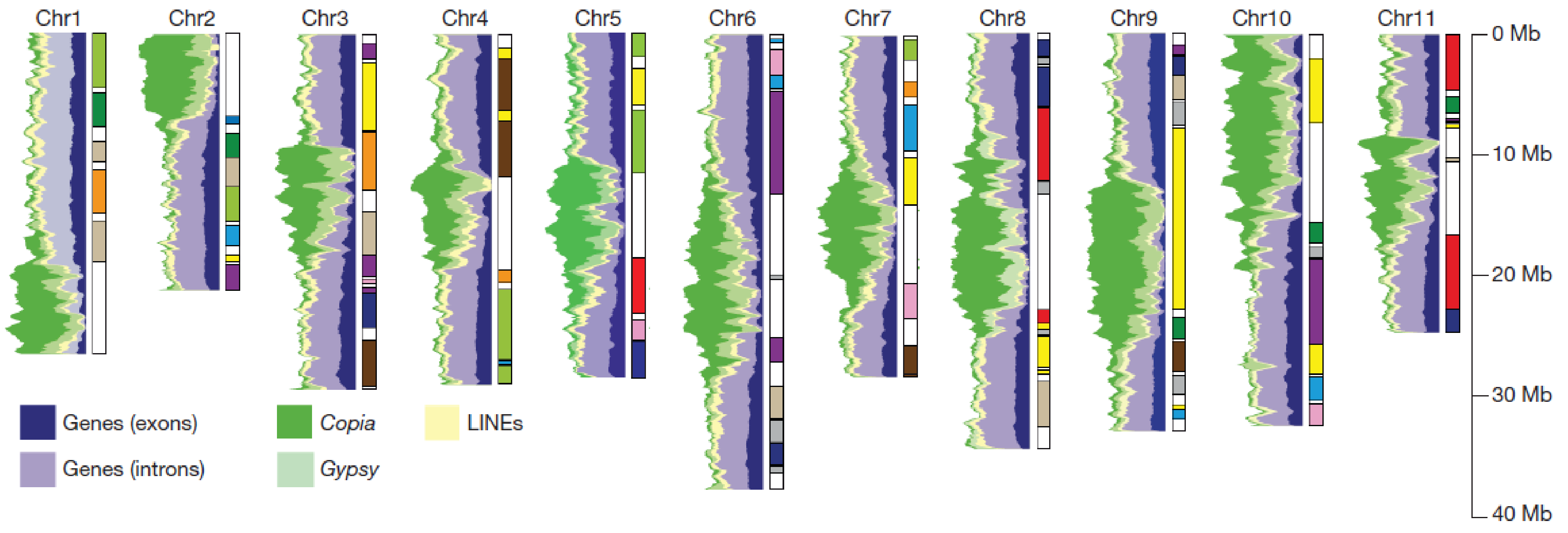


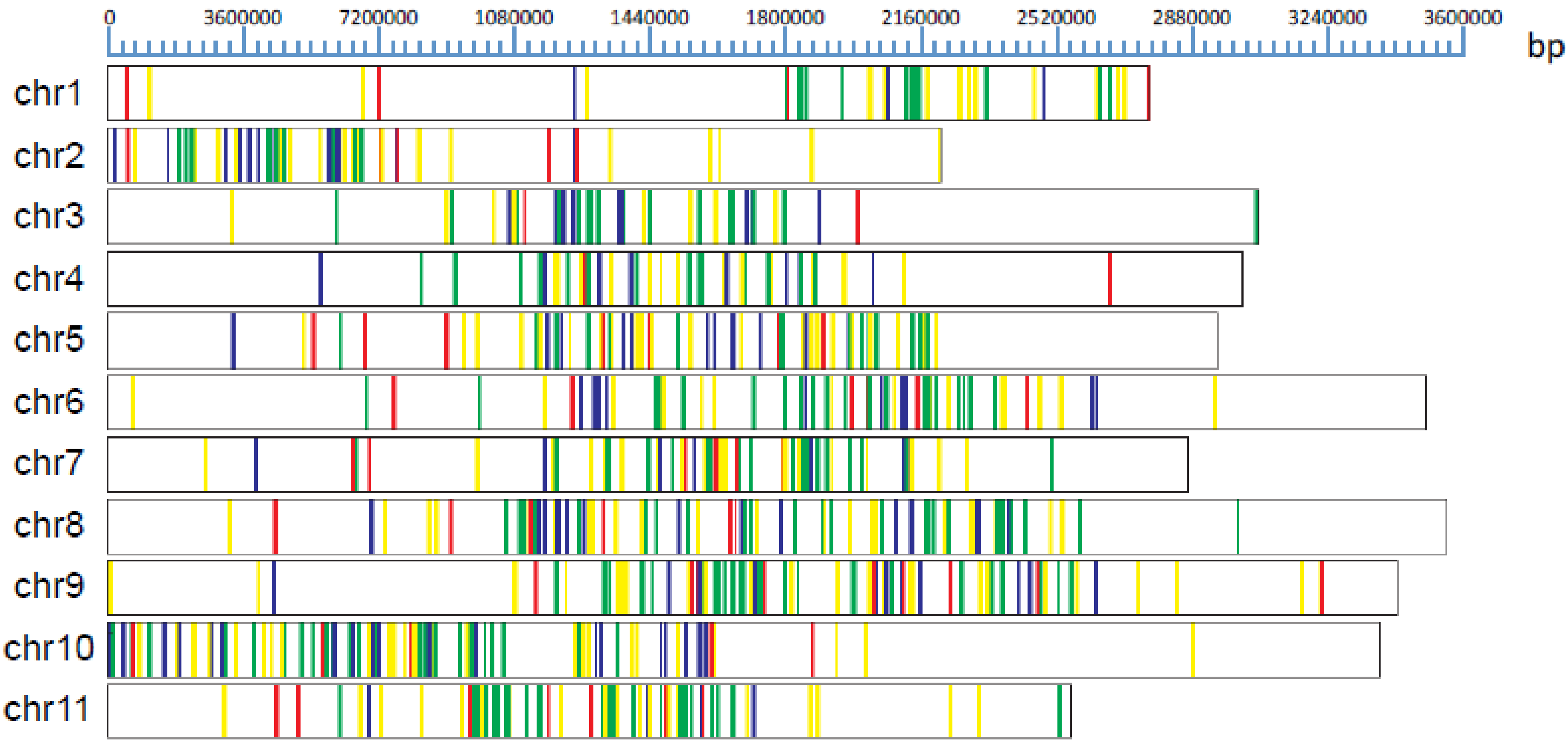


Phylogenetic analysis of *Musa* genomes – separating species. Teo, Schwarzacher et al.



Diploid 2n=2x=22 Musa / banana metaphase probed red with transposable element

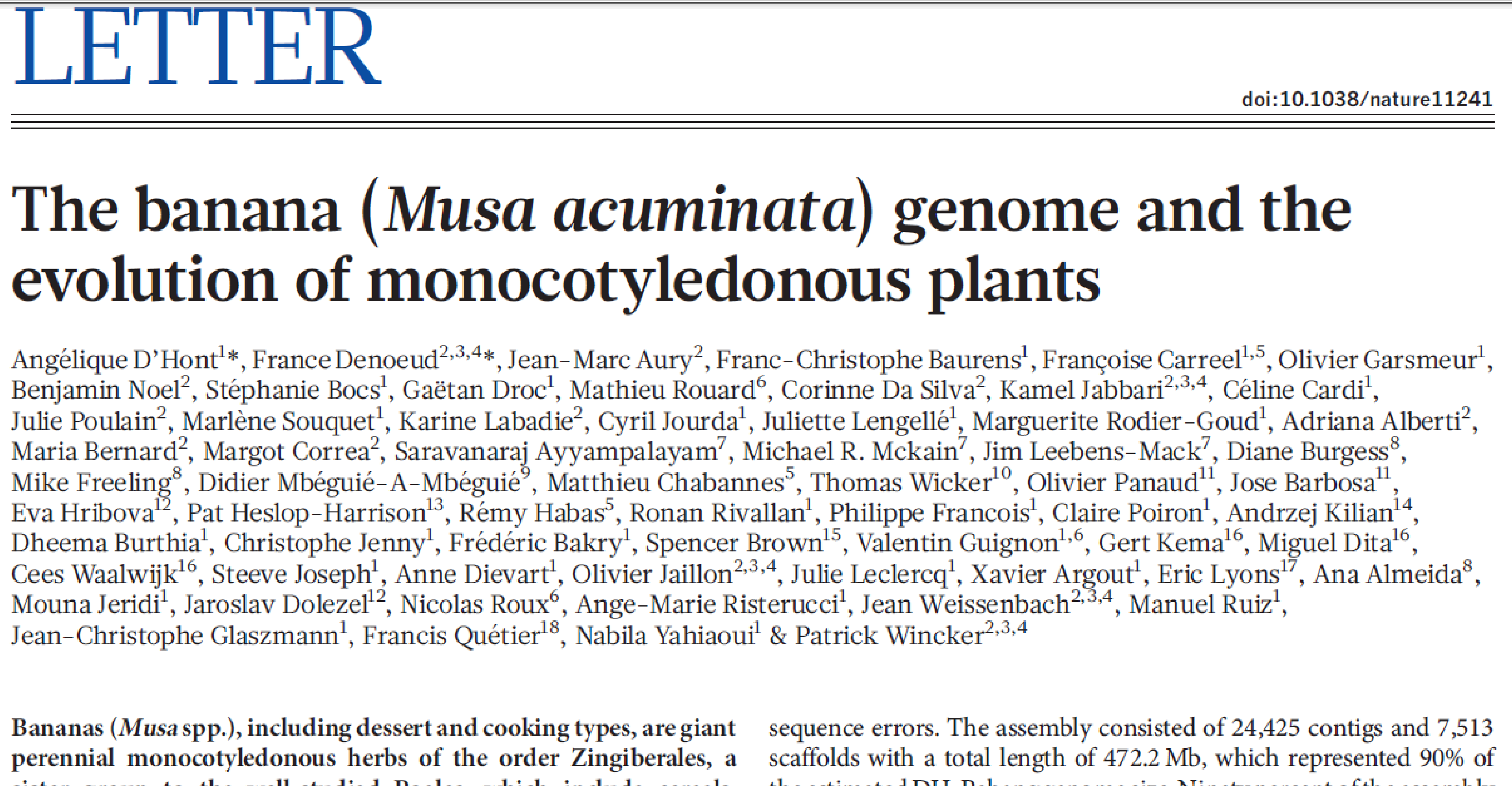

Chr1
Chr2
Chr3
Chr4
Chr5
Chr6
Chr7
Chr8
Chr9
Chr10
Chr11
0 Mb
10 Mb
20 Mb
30 Mb
40 Mb
Genes (exons)
Genes (introns)
Copia
Gypsy
LINEs



Timing of LTR Retrotransposon insertion in Musa
Red 0 to 2 Mya, yellow 2 to 4 Mya, green 4 to 6 Mya and blue older
D'Hont et al. 2012

The Banana Genome

- Seven countries + international organization coordinated by Angelique D’Hont - France (CIRAD, Genoscope)



LETTER

doi:10.1038/nature11241

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

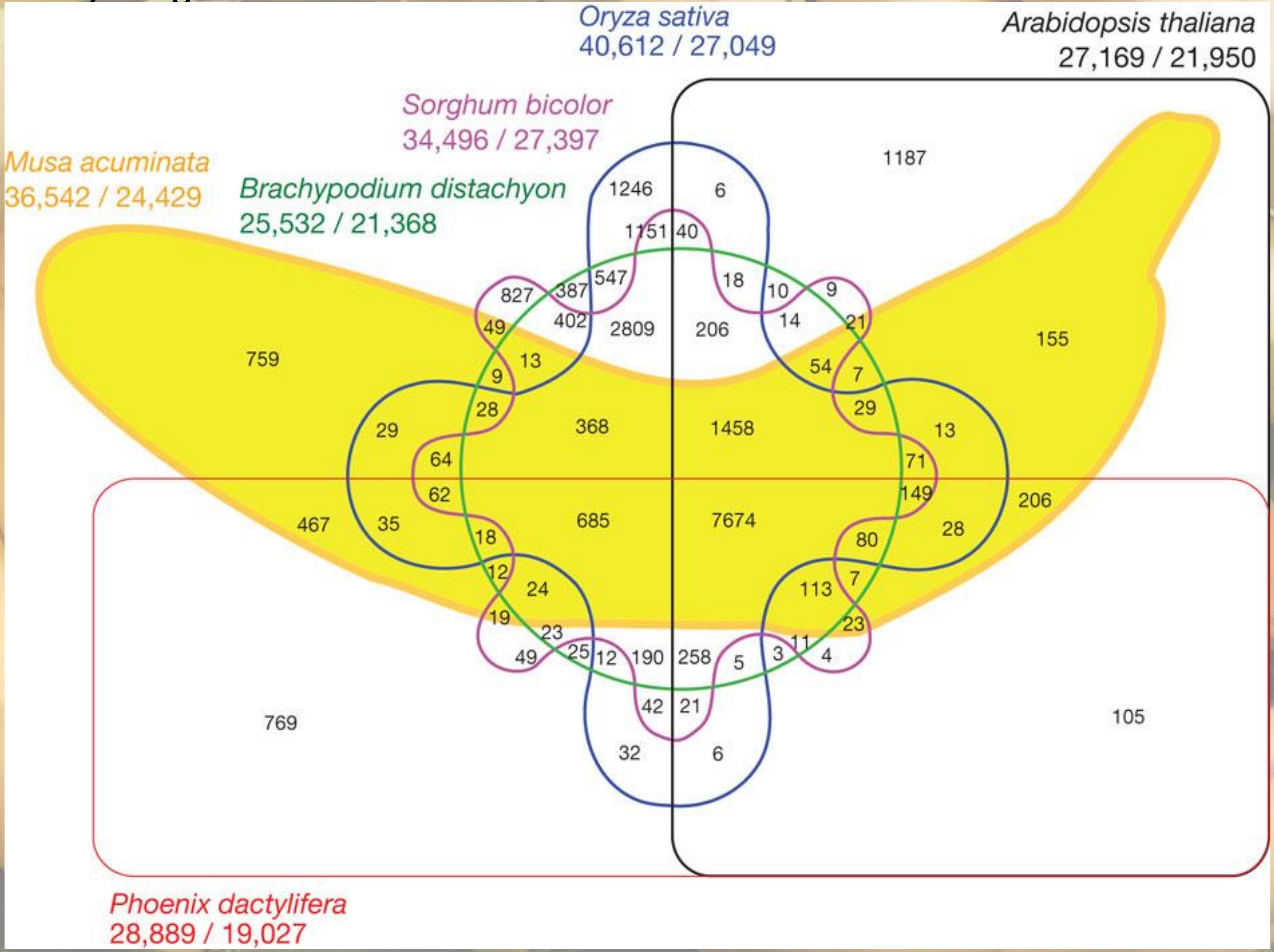
Angélique D’Hont[1]*, France Denoeud[2,3,4]*, Jean-Marc Aury[2], Franc-Christophe Baurens[1], Françoise Carreel[1,5], Olivier Garsmeur[1], Benjamin Noel[2], Stéphanie Bocs[1], Gaëtan Droc[1], Mathieu Rouard[6], Corinne Da Silva[2], Kamel Jabbari[2,3,4], Céline Cardi[1], Julie Poulain[2], Marlène Souquet[1], Karine Labadie[2], Cyril Jourda[1], Juliette Lengellé[1], Marguerite Rodier-Goud[1], Adriana Alberti[2], Maria Bernard[2], Margot Correa[2], Saravanaraj Ayyampalayam[7], Michael R. Mckain[7], Jim Leebens-Mack[7], Diane Burgess[8], Mike Freeling[8], Didier Mbéguié-A-Mbéguié[9], Matthieu Chabannes[5], Thomas Wicker[10], Olivier Panaud[11], Jose Barbosa[11], Eva Hribova[12], Pat Heslop-Harrison[13], Rémy Habas[5], Ronan Rivallan[1], Philippe Francois[1], Claire Poiron[1], Andrzej Kilian[14], Dheema Burthia[1], Christophe Jenny[1], Frédéric Bakry[1], Spencer Brown[15], Valentin Guignon[1,6], Gert Kema[16], Miguel Dita[16], Cees Waalwijk[16], Steeve Joseph[1], Anne Dievart[1], Olivier Jaillon[2,3,4], Julie Leclercq[1], Xavier Argout[1], Eric Lyons[17], Ana Almeida[8], Mouna Jeridi[1], Jaroslav Dolezel[12], Nicolas Roux[6], Ange-Marie Risterucci[1], Jean Weissenbach[2,3,4], Manuel Ruiz[1], Jean-Christophe Glaszmann[1], Francis Quétier[18], Nabila Yahiaoui[1] & Patrick Wincker[2,3,4]

Bananas (*Musa* spp.), including dessert and cooking types, are giant perennial monocotyledonous herbs of the order Zingiberales, a

sequence errors. The assembly consisted of 24,425 contigs and 7,513 scaffolds with a total length of 472.2 Mb, which represented 90% of

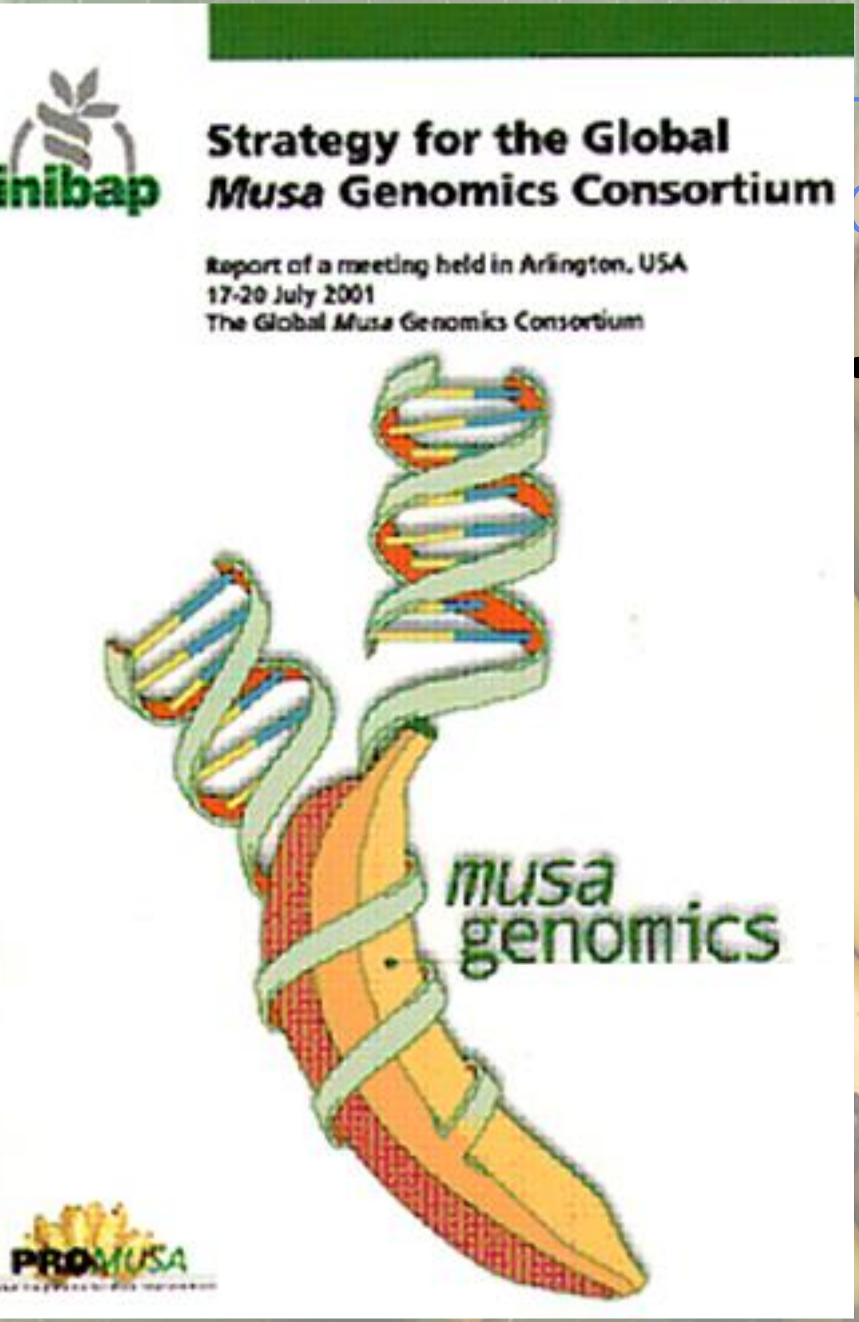
- 523 Mb DH-Pahang genome size (flow cytometry)
- 27.5 million Roche/454 single reads 16 x coverage
- 2.1 million Sanger reads 4 x coverage
- 50.3 x of Illumina data
- 54 BAC sequences (1%)

Six-way Venn diagram showing the distribution of shared gene families (sequence clusters) among *M. acuminata, P. dactylifera, Arabidopsis thaliana, Oryza sativa, Sorghum bicolor and Brachypodium distachyon* genomes.



A D'Hont *et al. Nature* **000**, 1-5 (2012) doi:10.1038/nature11241

The Global Musa Genomics Consortium



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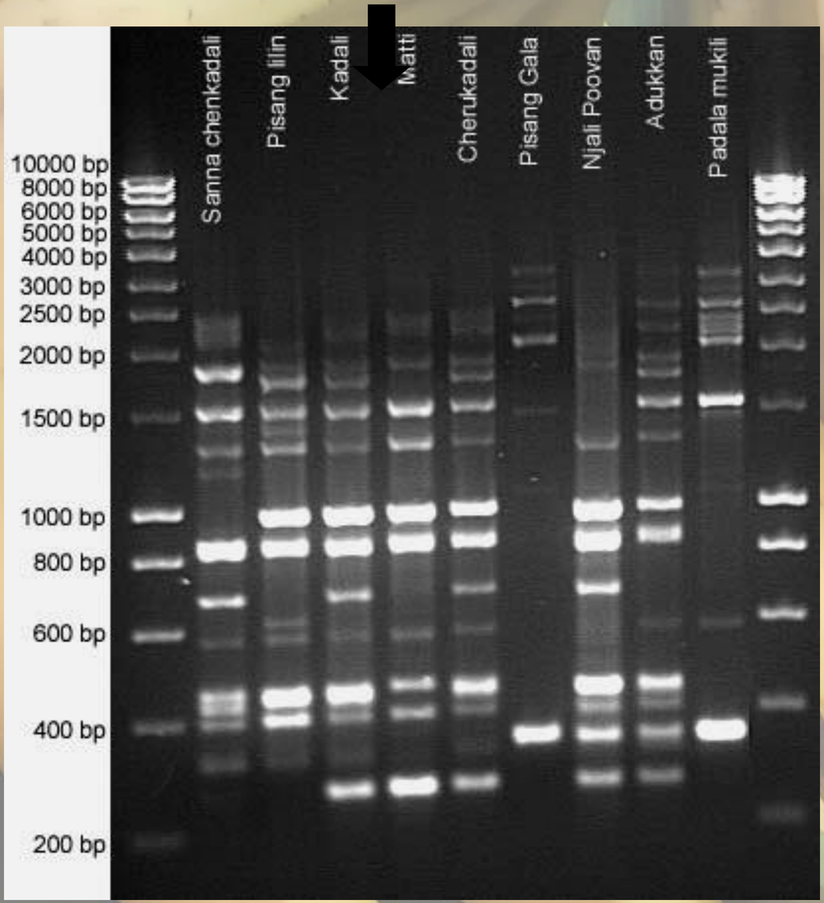
Strategy for the Global *Musa* Genomics Consortium

Report of a meeting held in Arlington, USA
17-20 July 2001
The Global *Musa* Genomics Consortium

musa genomics

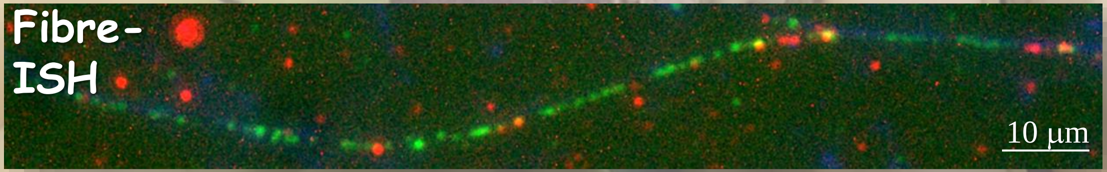
PROMUSA

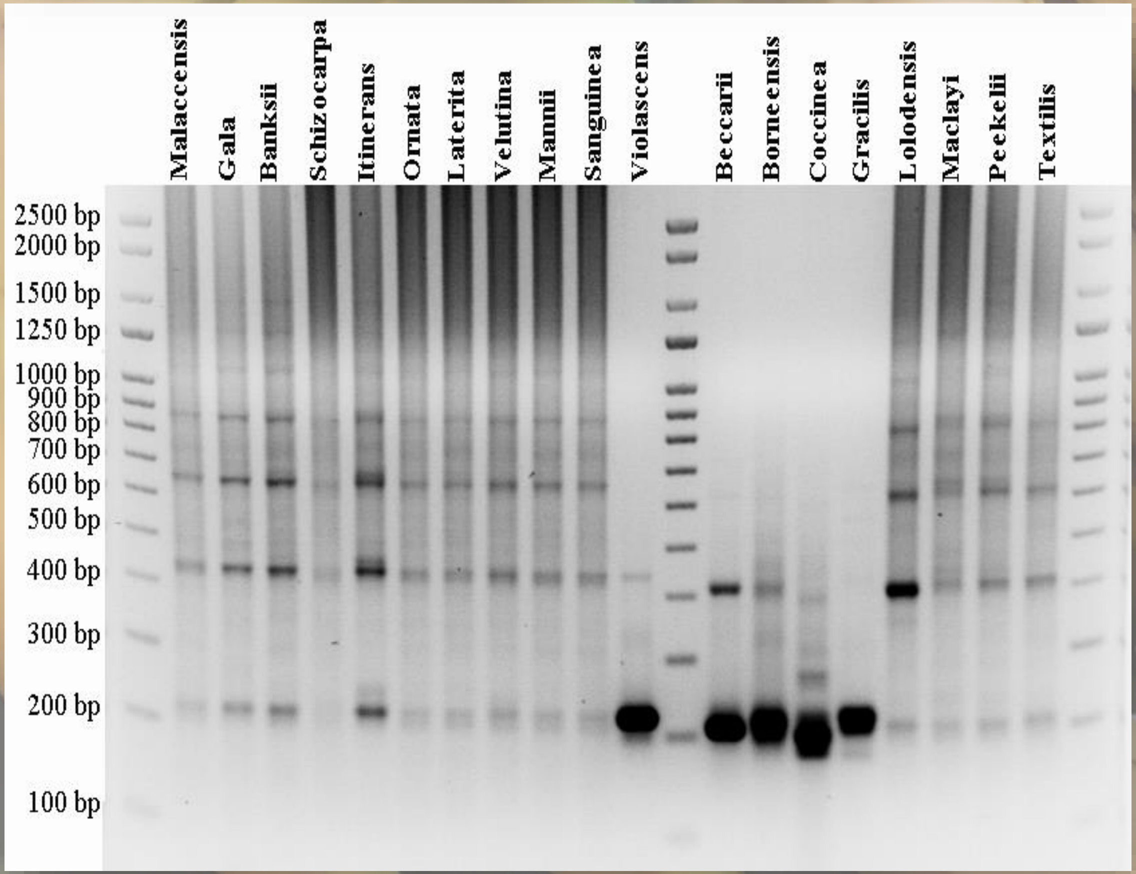
- To assure the sustainability of banana as a staple food crop by developing an integrated genetic and genomic understanding, allowing targeted breeding, transformation and more efficient use of Musa biodiversity



C.H Teo and Schwarzacher

MuTR is organised as tandem repeat

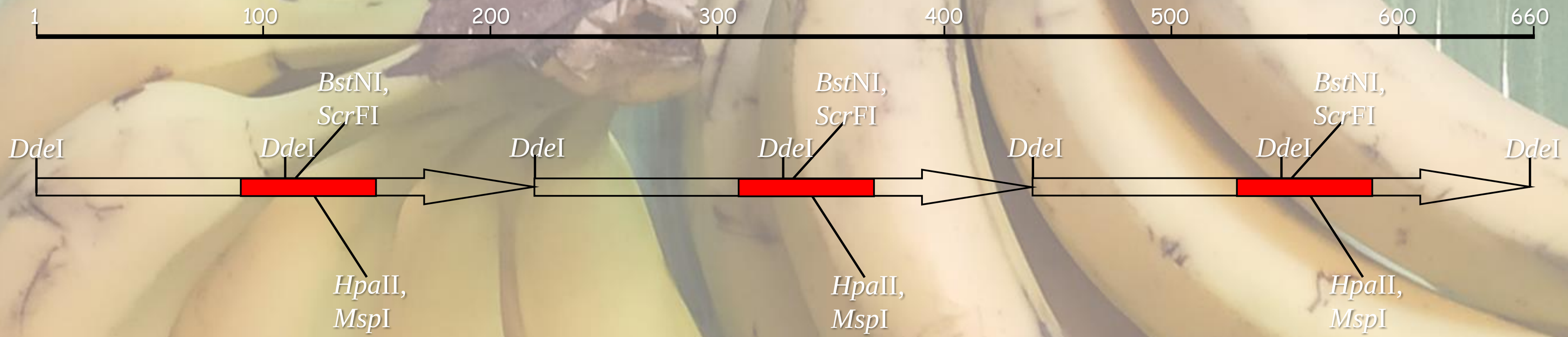




Present in many Musa species as ladder with a 220bp monomer plus degenerations

C.H Teo and Schwarzacher

MuTR is organised as tandem repeat



🟥 63bp box
with ≥ 90% homology to the LTR region of the *Monkey retrotransposon sequence (M. acuminata* 'Grande Naine'; AF143332), a member of genus *Chromovirus* of *Metaviridae* element family

This box is responsible for the PCR amplification

C.H Teo and Schwarzacher

MuTR, 220bp tandem repeats are located at NORs

and some centromeres

Absent or very low copy

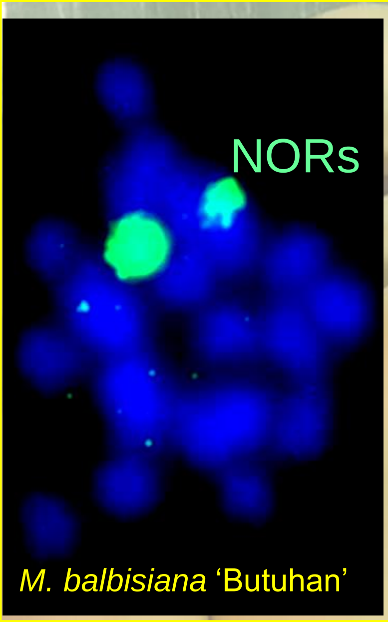
In B, A and O genome

Some amplification

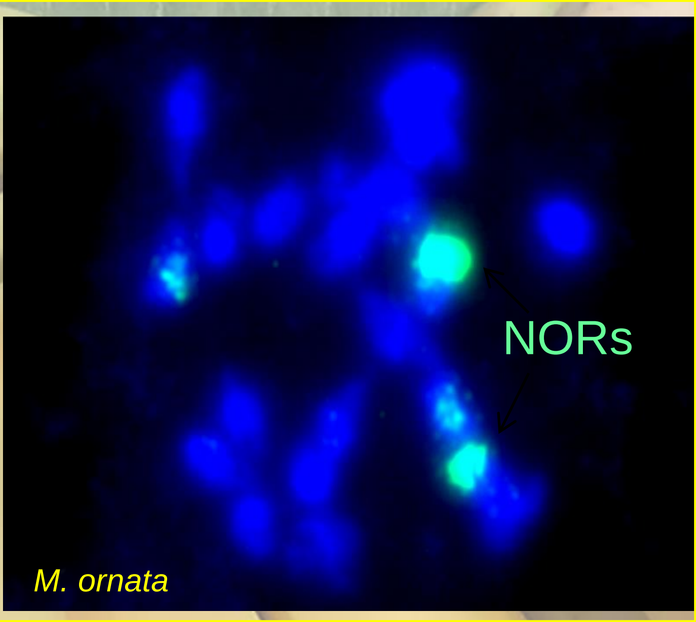
in variant A genomes

Highly amplified

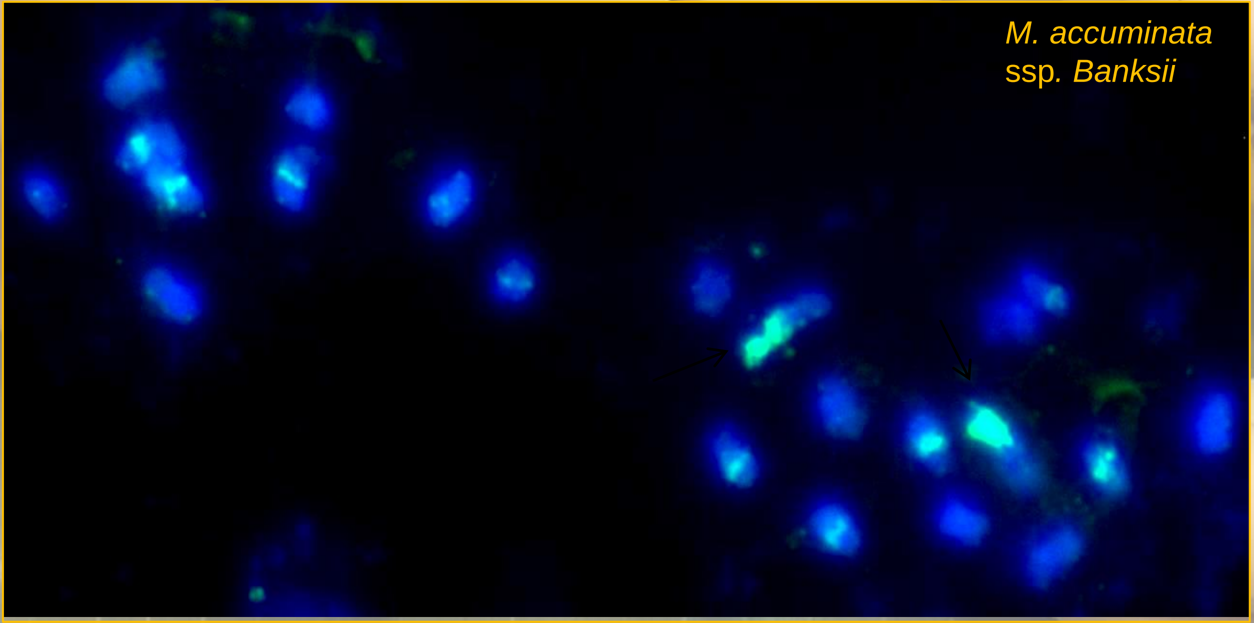
in other Musa genomes



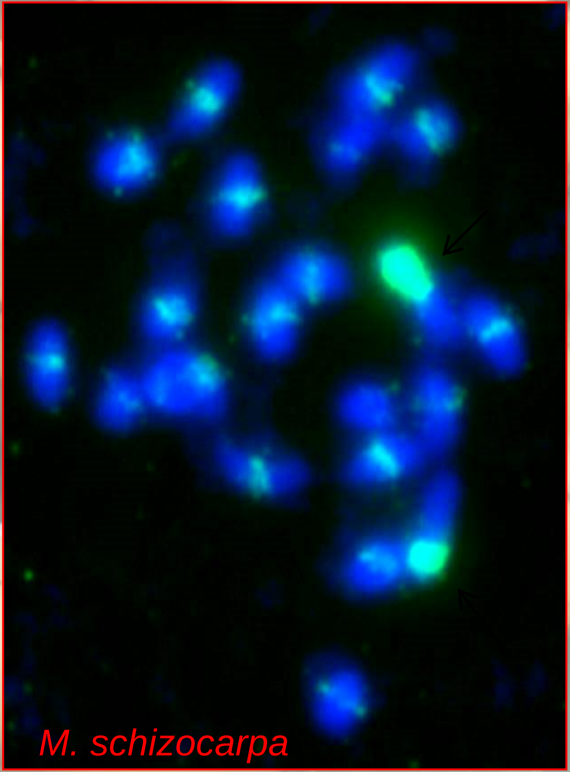
M. balbisiana ‘Butuhan’



M. ornata

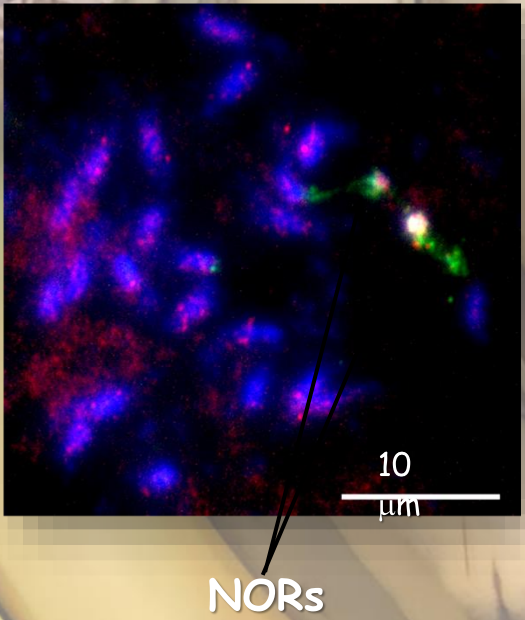


M. accuminata ssp. *Banksii*



M. schizocarpa

MuTRs & *Metaviridae* (Monkey LTRs) found In IGS and ITS of the 45S rRNA



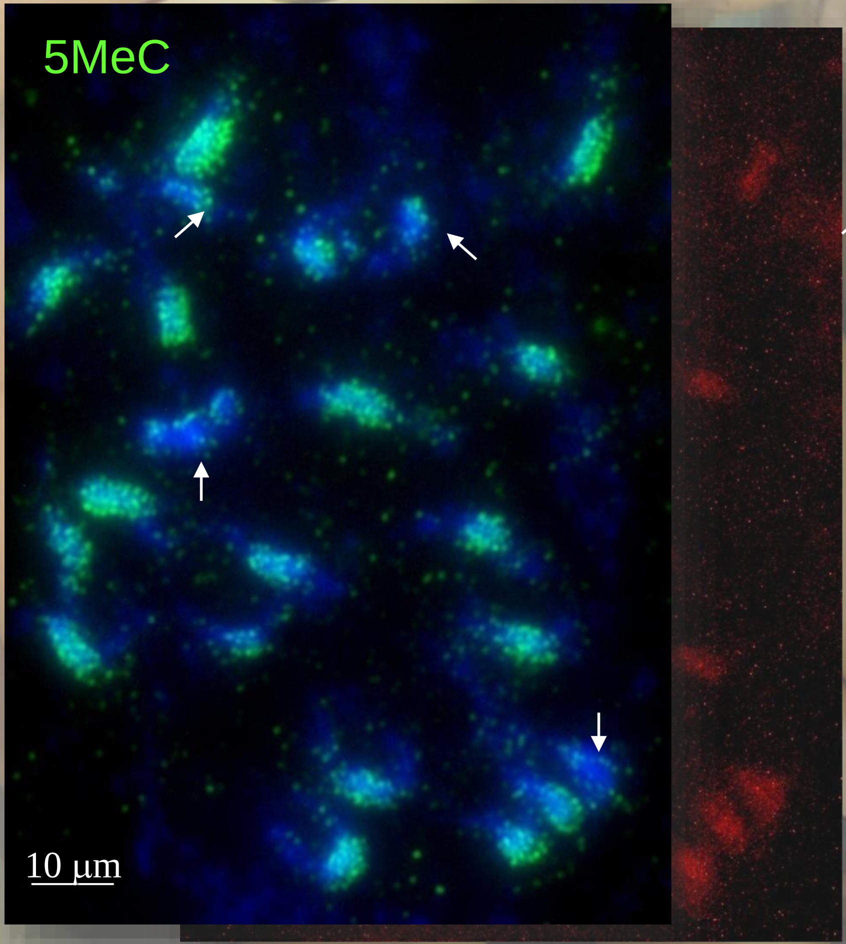
PCR using outward *Metaviridae* LTR & 18S rRNA primers

C.H Teo and Schwarzacher

Functional aspects of the Musa repeats

- DNA methylation
- Expression
- Silencing

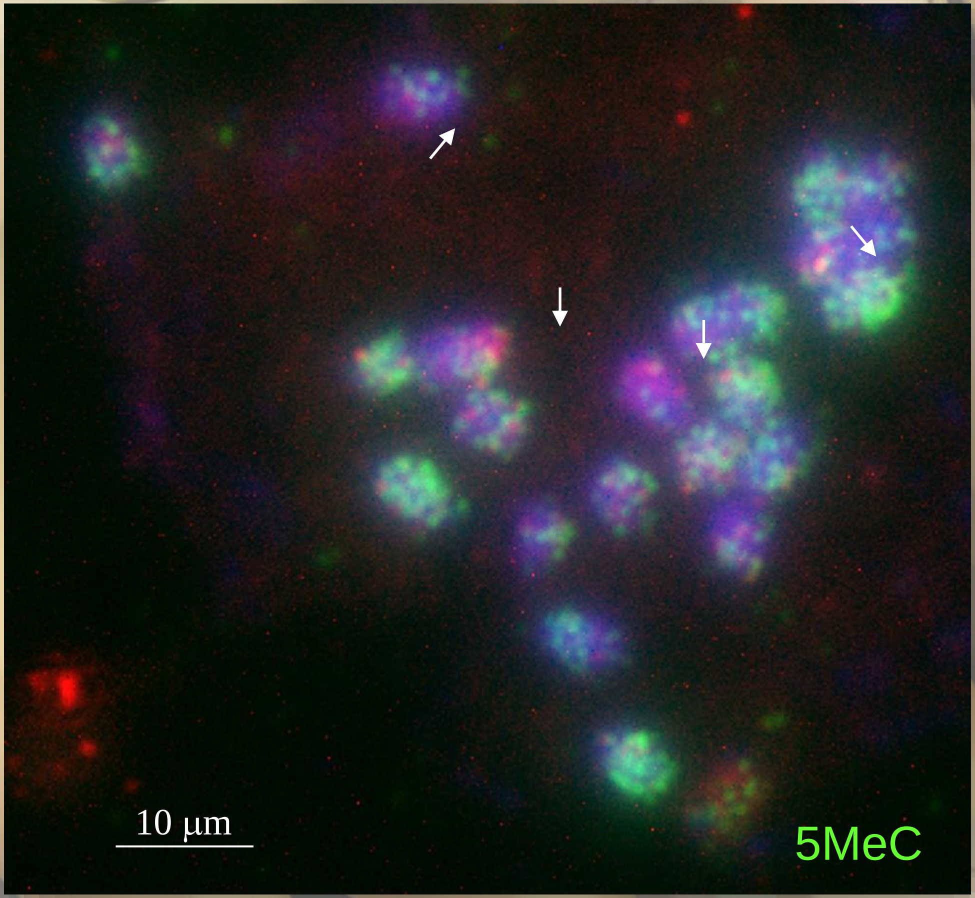
DNA methylation is unevenly distributed on *Musa* chromosomes



***Pseudoviridae* (copia) elements**

in methylated regions, but also in some low methylated regions (arrows)

DNA methylation is unevenly distributed on *Musa* chromosomes

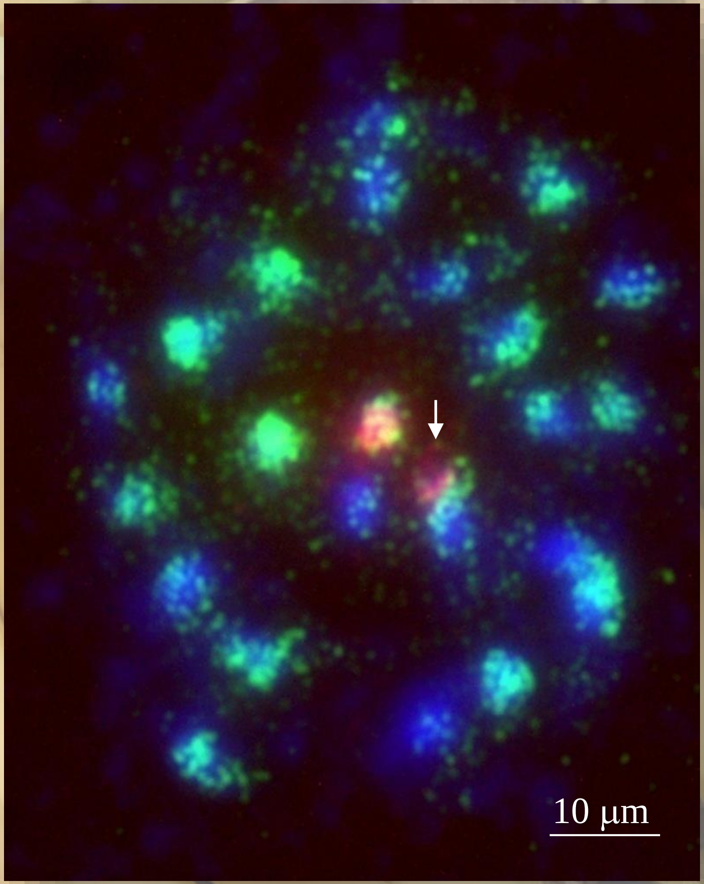


Metaviridae (gypsy) elements

in methylated regions, but also in some low methylated regions (arrows)

C.H Teo and Schwarzacher

DNA methylation is unevenly distributed on *Musa* chromosomes

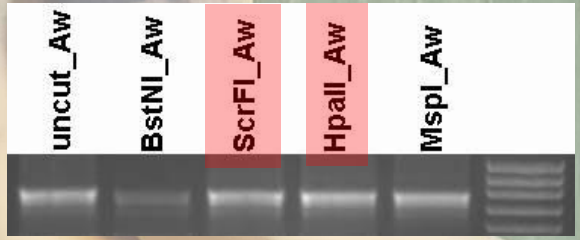


MuTR repeats

are located both at the high and low methylated part of the NOR

C.H Teo and Schwarzacher

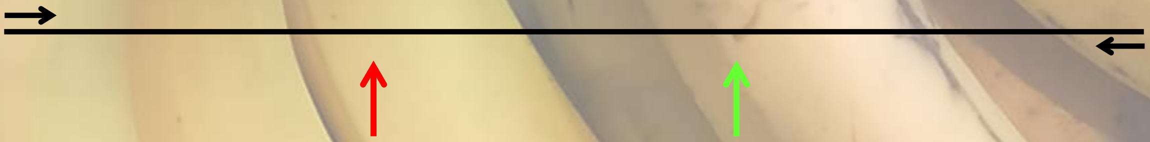
Methylation sensitive PCR analysis



Site present, methylated

No sites

Some sites



CCGG

CCNGG

Methylation sensitive enzyme (*Hpa*II, *BstN*I)
site methylated: amplification as uncut
site not methylated: no amplification

Compare the methylation sensitive enzymes with uncut lane

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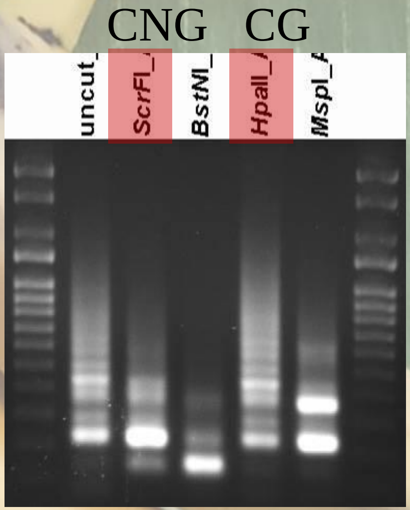
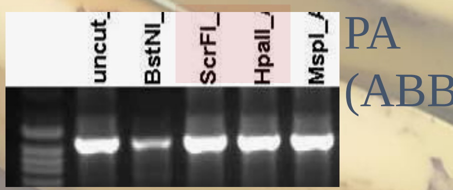
Methylation sensitive PCR



MuTR

Many CG sites: methylated
Many CNG sites: some methylated

Metaviridae (Gypsy)



Reverse transcriptase domain

CG sites are not present
some CNG sites present and methylated

Flanking sequences

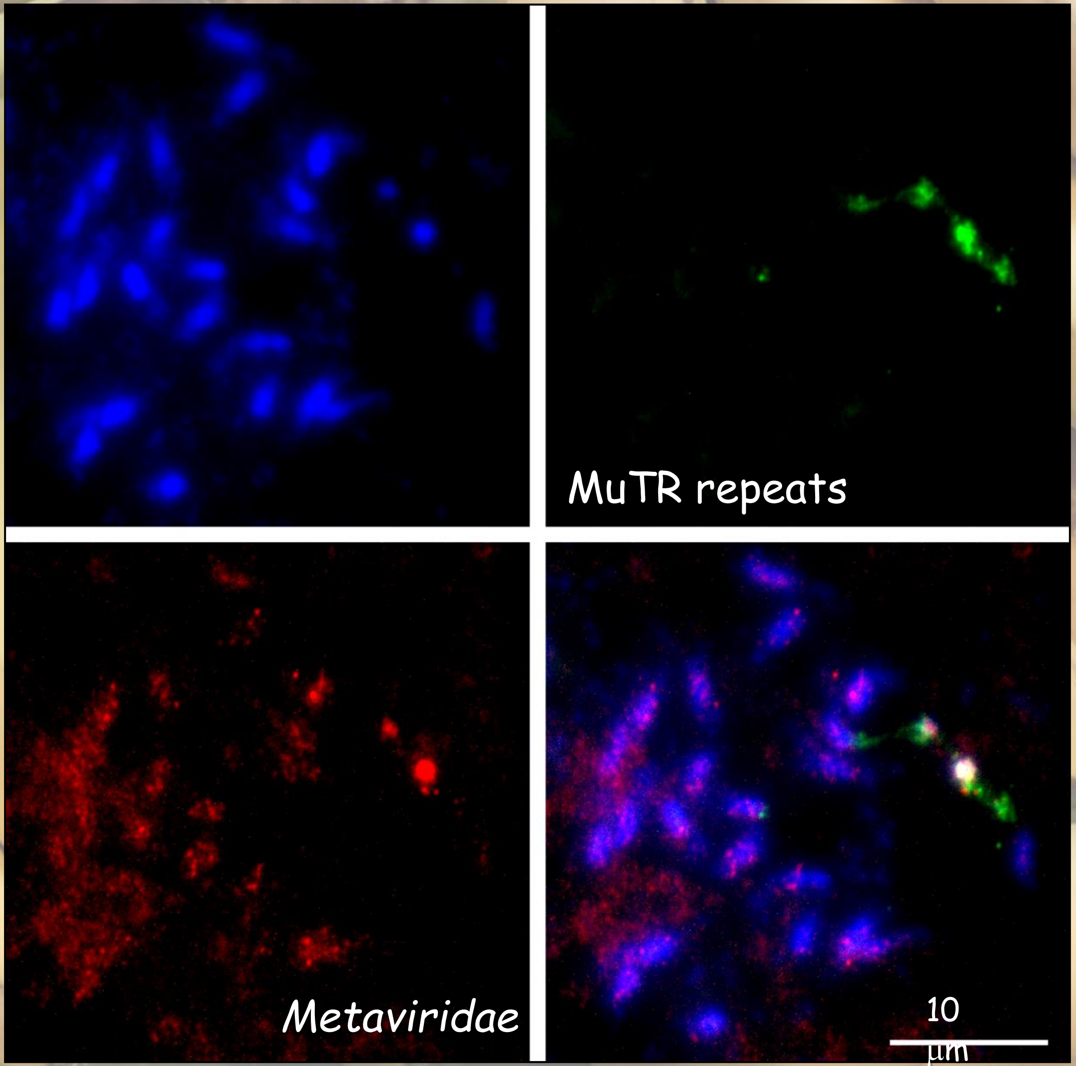
(using outward facing LTR primers)

CG sites are not present
CNG sites present and methylated

Is methylation low because no Cs are available?

C.H Teo and Schwarzacher

MuTRs repeats are visible in the extended part of the 45S rDNA array



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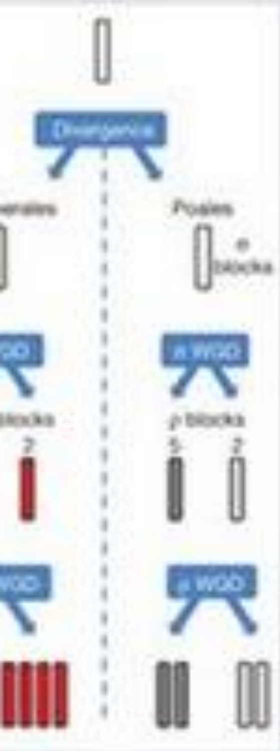
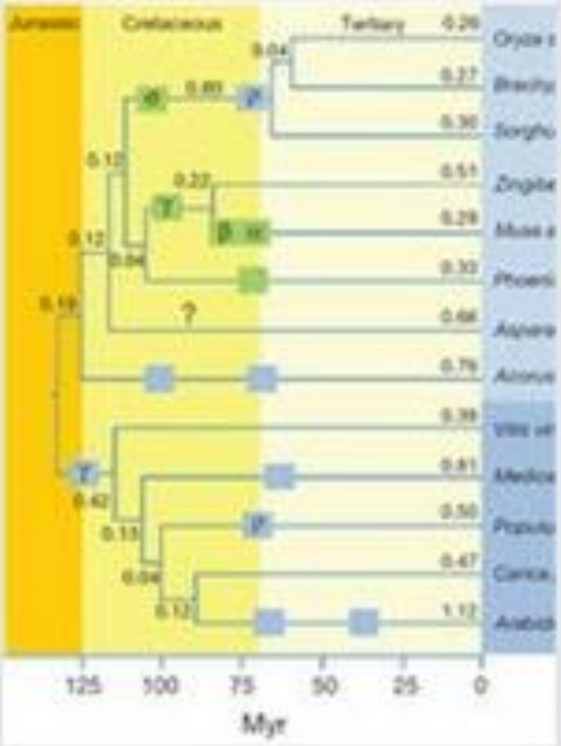
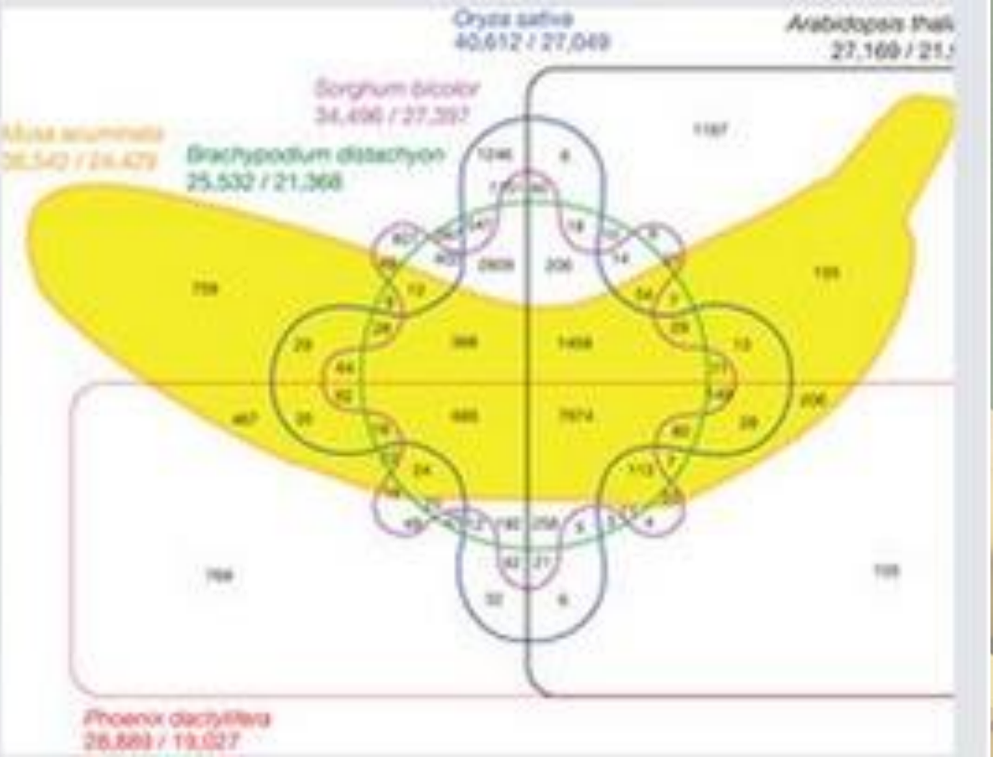

Divergence
Poales
blocks
WGD
α WGD
β blocks
β WGD

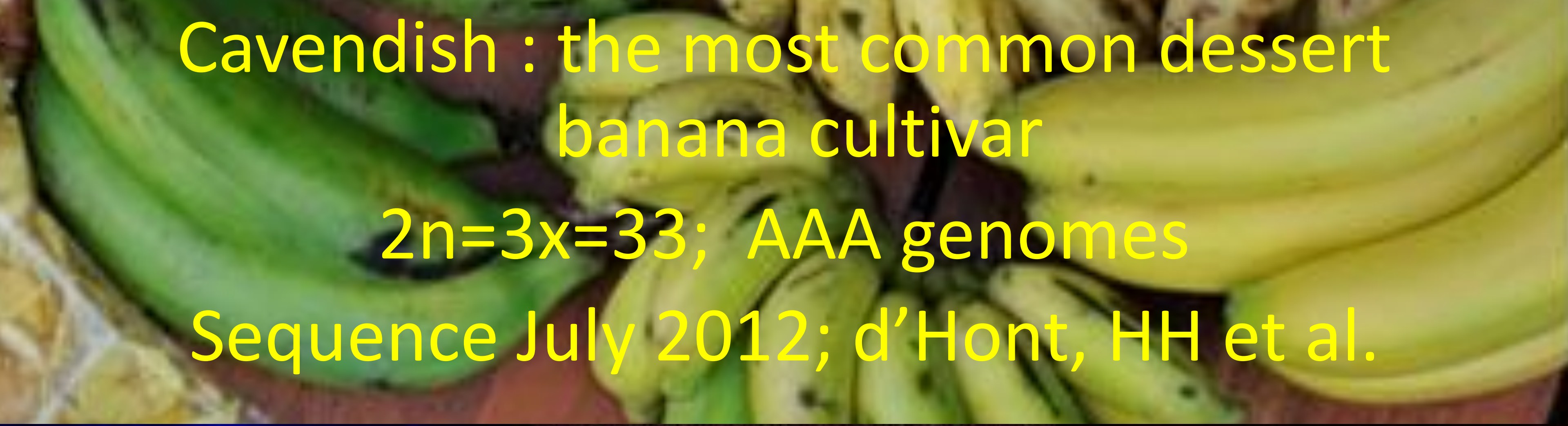

Jurassic
Cretaceous
Tertiary
?
125
100
75
50
25
0
Myr

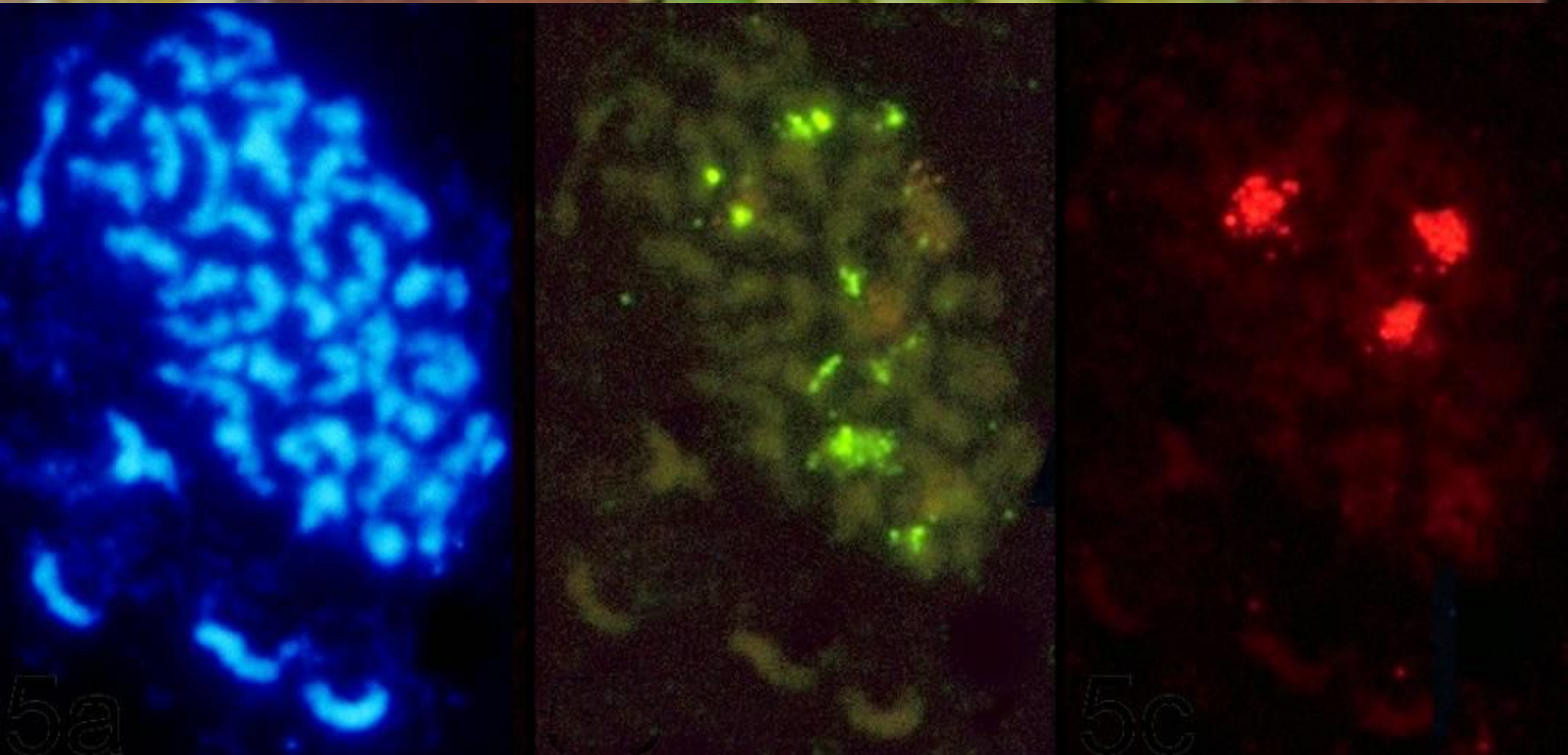

Oryza sativa
40,612 / 27,049
Arabidopsis thali
Sorghum bicolor
Musa acuminata
Brachypodium distachyon
25,532 / 21,368
Phoenix dactylifera
28,889 / 19,027

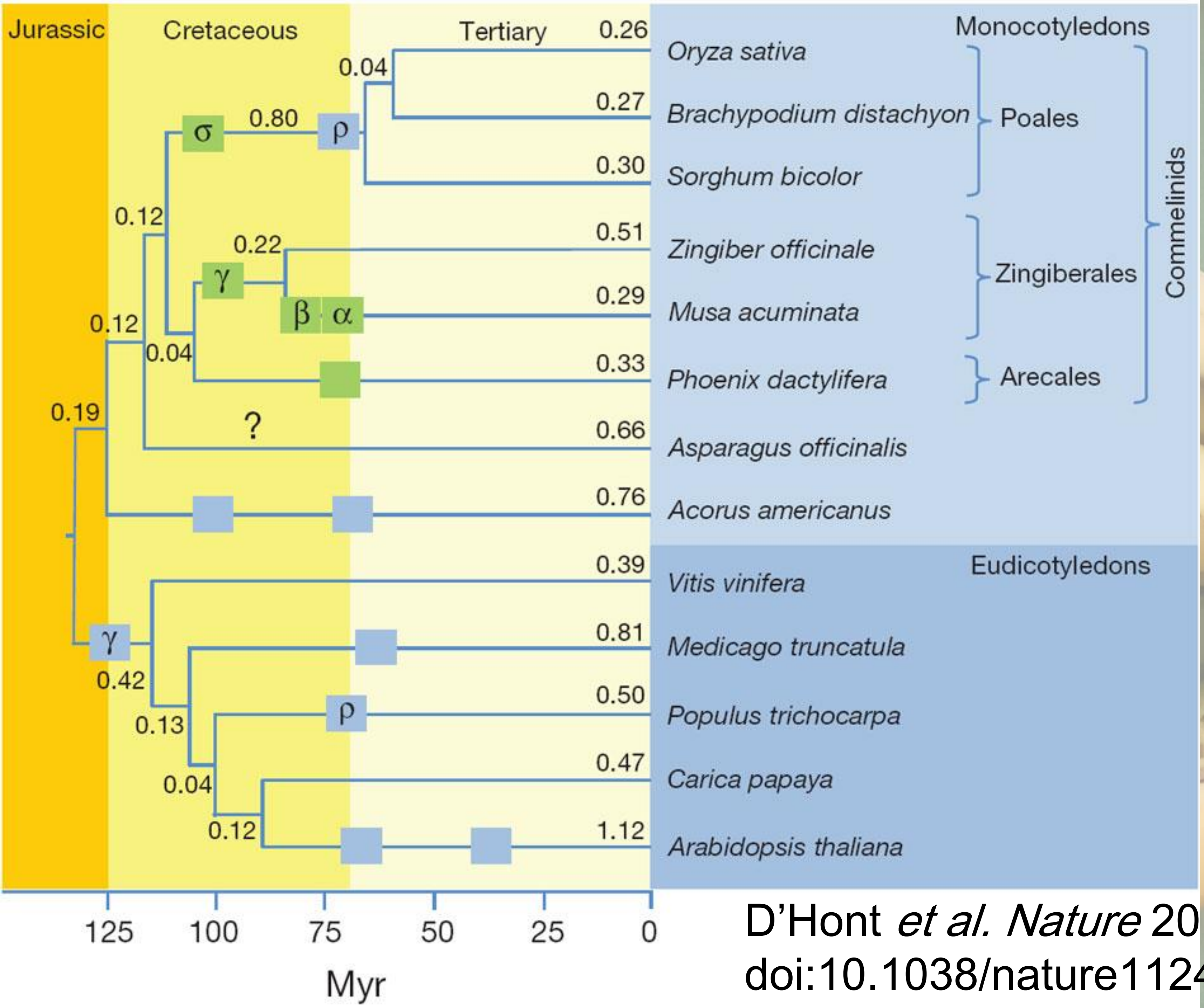
Cavendish : the most common dessert banana cultivar

2n=3x=33; AAA genomes

Sequence July 2012; d'Hont, HH et al.







D'Hont *et al.* *Nature* 2012
doi:10.1038/nature11241

SUMMARY OF THE GLOBAL STRATEGY FOR THE CONSERVATION AND USE OF *MUSA* GENETIC RESOURCES

A consultative document prepared by the Global *Musa* Genetic Resources Network (MusaNet)

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Special appreciation is expressed to the following contributors of the Global Strategy,

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