

# Genome Organization and Diversity of Major Satellite DNAs in Banana (*Musa spp.*)

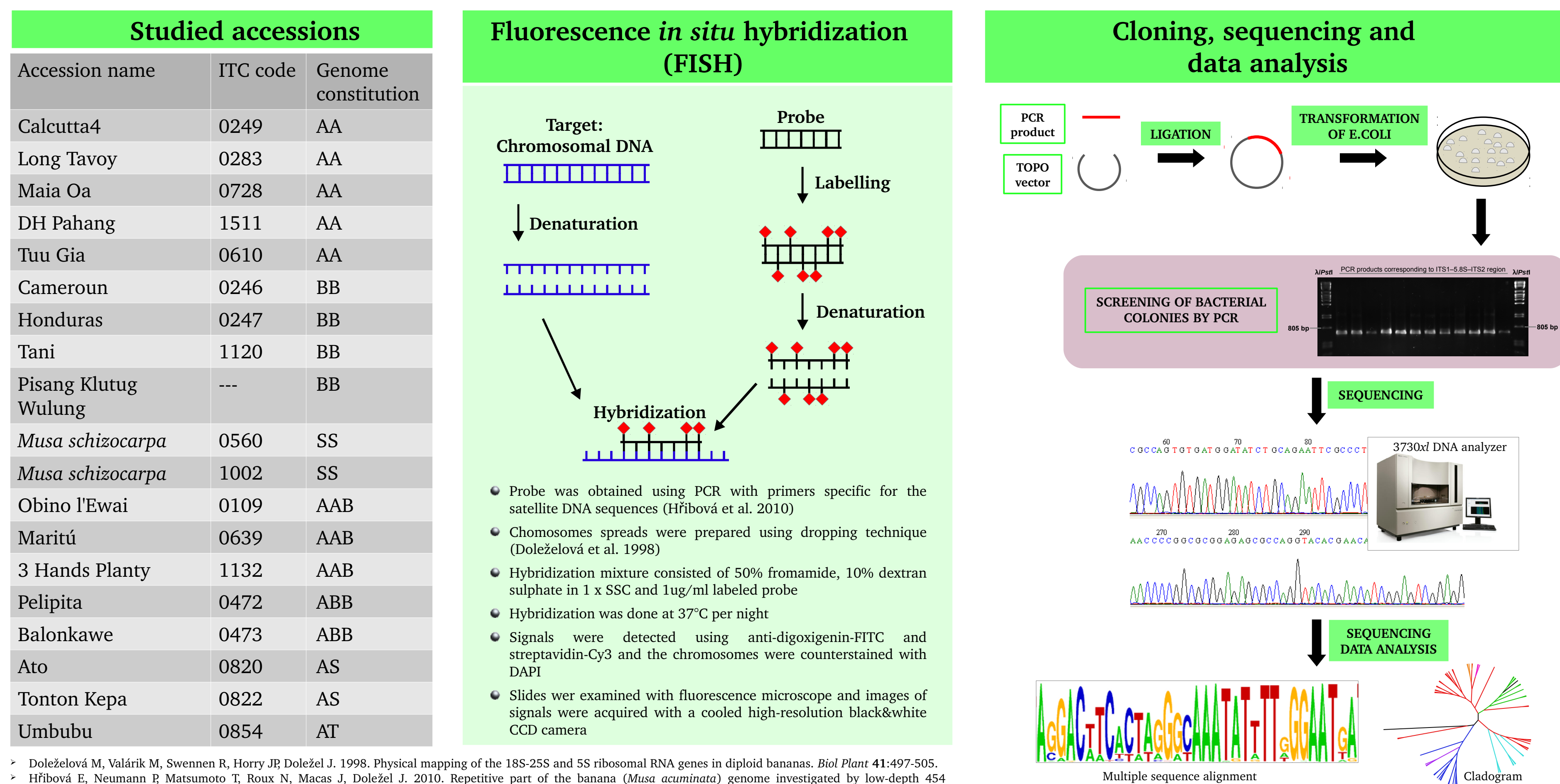
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## Introduction

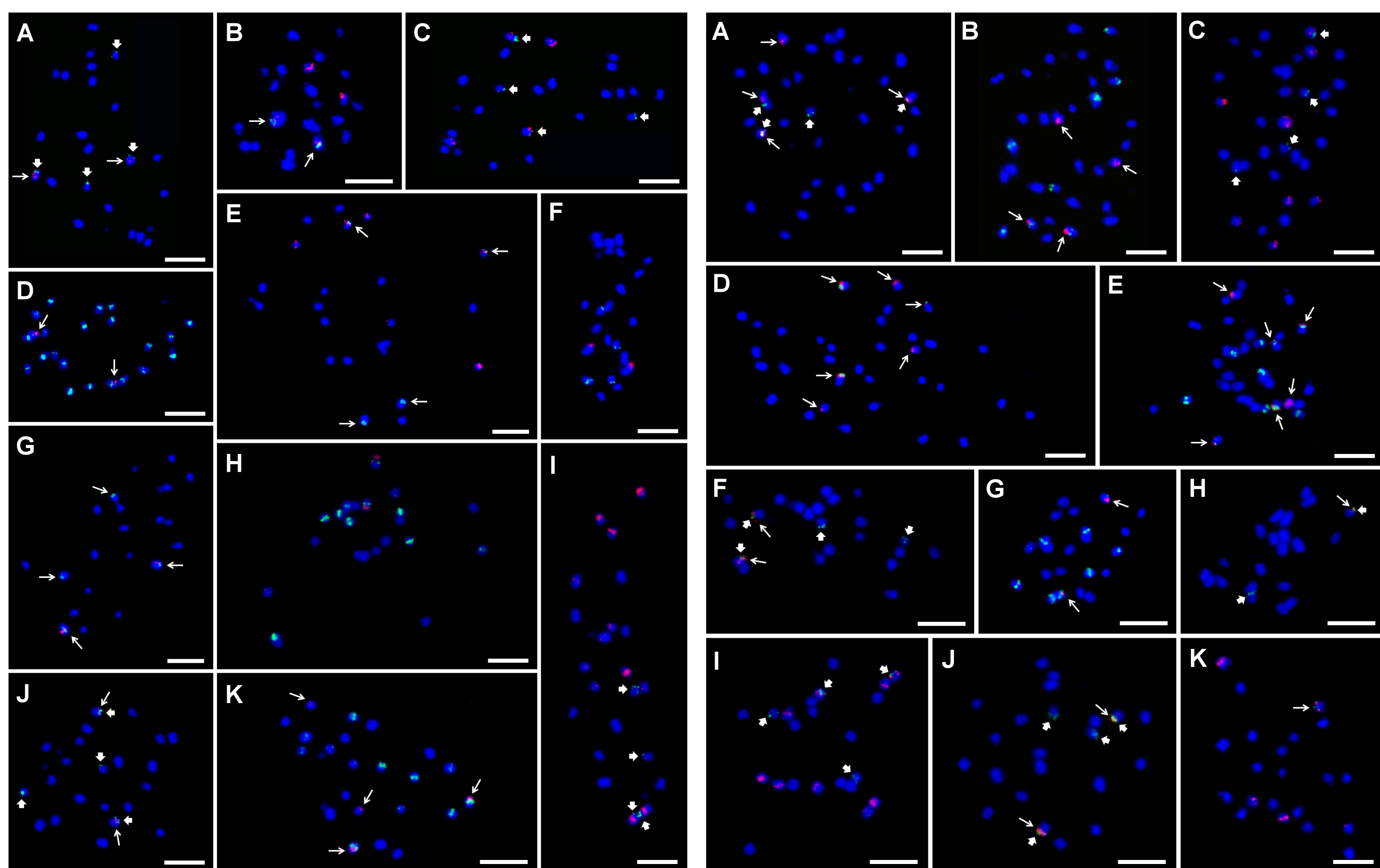
- Bananas are giant perennial tropical plants within genus *Musa*
- Most of cultivated clones originated from natural inter- and intra-individual crosses of two wild diploid species: *M. acuminata* (A genome) and *M. balbisiana* (B genome)
- Previous study showed closely related nature of A and B genomes, including highly similar repetitive DNA fraction
- 454 sequencing of *M. acuminata* 'Calcutta4' enable to identify two different satellites DNA sequences in the nuclear genome
- Satellite DNAs consist of thousands or even millions of tandemly arranged repetitive units in head-to-tail orientations
- Satellite DNAs show specific banding pattern on chromosomes and may be genus- or species-specific

## Materials and Methods



## Results

### Fluorescence in situ hybridization of satellite CL18 and CL33



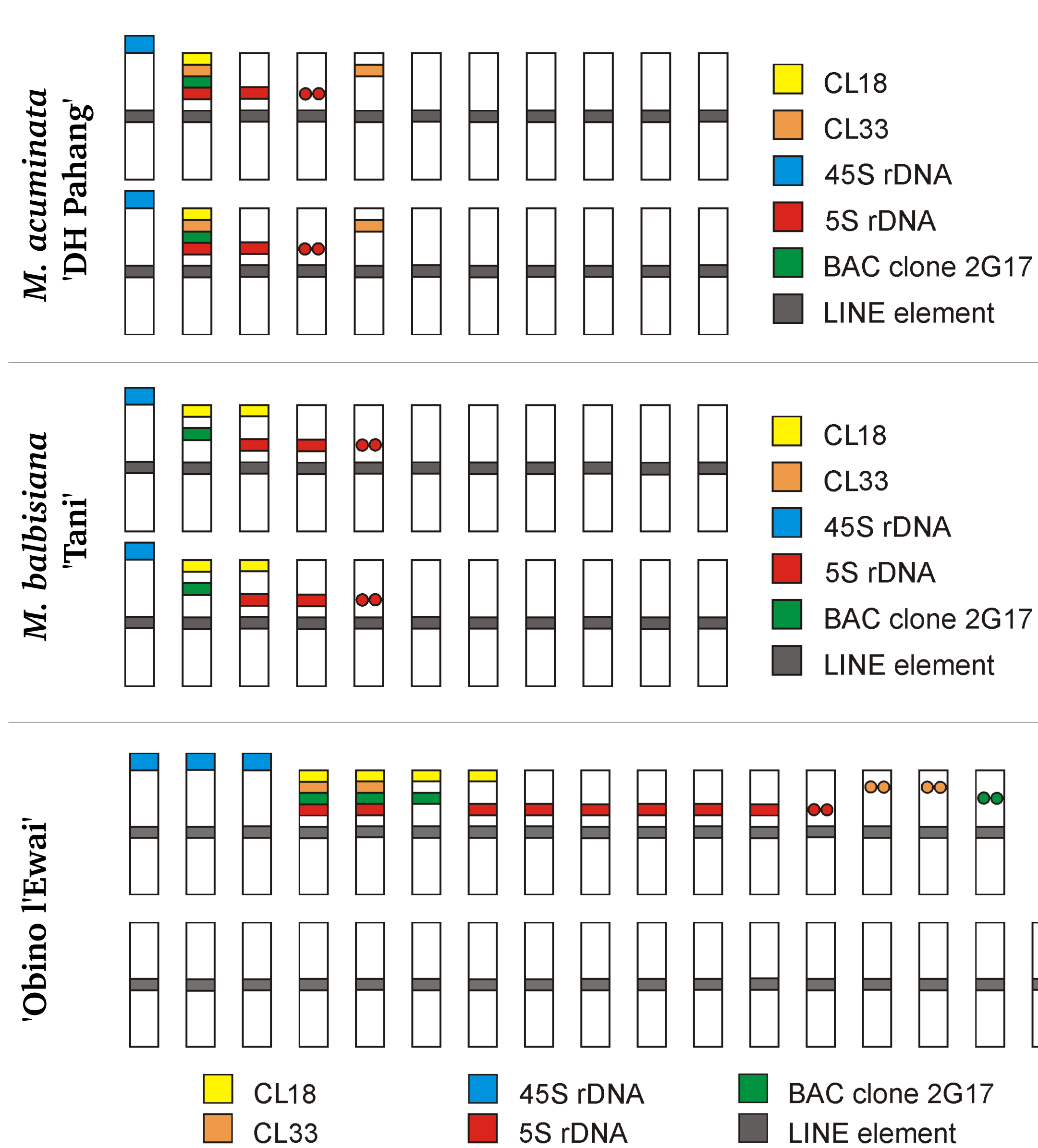
#### DIPLOID ACCESSIONS

(A) Localization of CL18 (red) and CL33 (green) on chromosomes of 'Long Tavoy'. (B) Localization of 5S rDNA (red) and CL18 (green) on chromosomes of 'Maia Oa'. (C) Localization of 5S rDNA (red) and CL33 (green) on chromosomes of 'Long Tavoy'. (D) Localization of CL18 (red) and LINE element (green) on chromosomes of 'Tuu Gia'. (E) Localization of 5S rDNA (red) and CL18 (green) on chromosomes of 'Pisang Klutug Wulung'. (F) Localization of BAC clone 2G17 (red) and 5S rDNA (green) on chromosomes of 'Cameroun'. (G) Localization of BAC clone 2G17 (red) and CL18 (green) on chromosomes of 'Tani'. (H) Localization of 45S rDNA (red) and 5S rDNA (green) on chromosomes of *M. schizocarpa*. (I) Localization of 5S rDNA (red) and CL33 (green) on chromosomes of *M. schizocarpa*. (J) Localization of CL18 (red) and CL33 (green) on chromosomes of *M. schizocarpa*. (K) Localization of CL18 (red) and 5S rDNA (green) on chromosomes of *M. schizocarpa*. Chromosomes were counterstained with DAPI (blue). Bar = 5 µm. CL18 is marked by long arrow, CL33 is marked by short arrow.

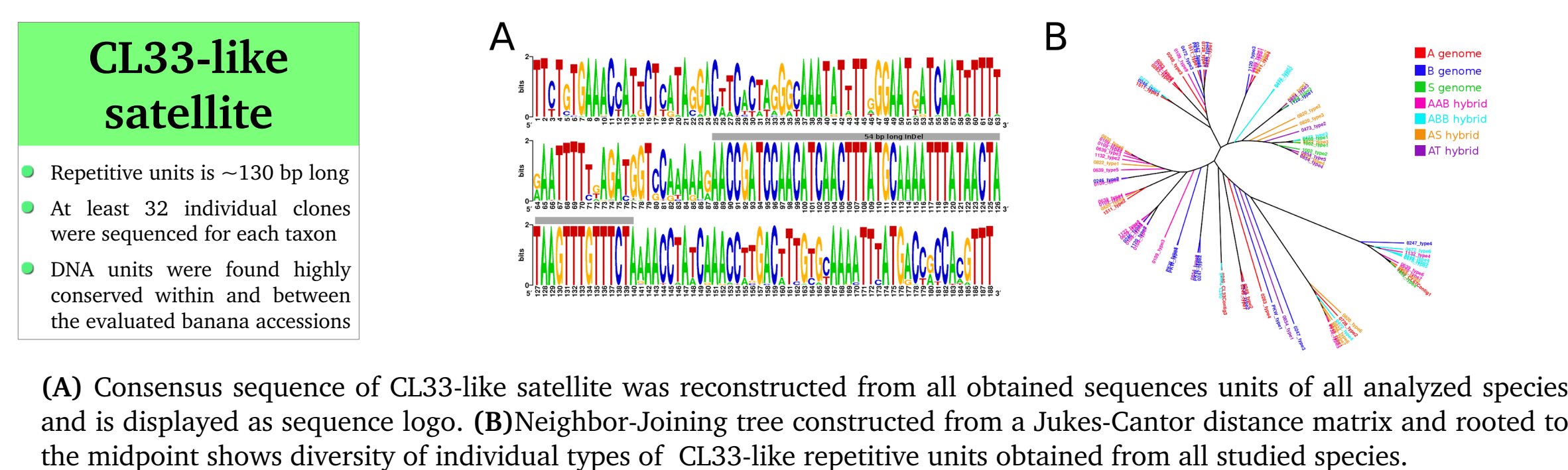
#### HYBRID ACCESSIONS

(A) Localization of CL18 (red) and CL33 (green) on chromosomes of 'Maritú'. (B) Localization of CL18 (red) and 5S rDNA (green) on chromosomes of 'Maritú'. (C) Localization of 5S rDNA (red) and CL33 (green) on chromosomes of 'Maritú'. (D) Localization of CL18 (red) and BAC clone 2G17 (green) on chromosomes of 'Pelipita'. (E) Localization of CL18 (red) and 5S rDNA on chromosomes of 'Pelipita'. (F) Localization of CL18 (red) and CL33 (green) on chromosomes of 'Ato'. (G) Localization of CL18 (red) and 5S rDNA (green) on chromosomes of 'Tonton Kepa'. (H) Localization of CL18 (red) and CL33 (green) on chromosomes of 'Umbubu'. (I) Localization of 5S rDNA (red) and CL33 (green) on chromosomes of 'Ato'. (J) Localization of CL18 (red) and CL33 (green) on chromosomes of 'Tonton Kepa'. (K) Localization of 5S rDNA (red) and CL18 (green) on chromosomes of 'Umbubu'. Chromosomes were counterstained with DAPI (blue). Bar = 5 µm. CL18 is marked by long arrow, CL33 is marked by short arrow.

### Examples of Idiograms



### Sequence analysis of DNA satellites



## Conclusions

- Genomic distribution of satellite sequences CL18 and CL33, 5S rDNA, 45S rDNA and BAC clone 2G17 was established in a set of *Musa* species and cultivated clones
- The use of CL18, CL33, 5S rDNA, 45S rDNA and BAC clone 2G17 as probes for FISH increased the number of chromosomes which could be identified in *Musa*
- Different patterns of probe co-localization in *M. acuminata* sp. and *M. balbisiana* sp. enabled determination of genomic constitution in their interspecific hybrids
- For the first time, diversity of satellite sequences CL18 and CL33 was analyzed at molecular level
- Sanger sequencing of both satellites revealed extensive conservation within and between the evaluated accessions
- No genome-specific sub-types of satellite repetitive unit were found in A and B *Musa* genomes

#### CL18-like satellite

- Repetitive units is ~2 kb long
- Two parts of the sequence unit were sequenced
- Sequencing of *M. acuminata* 'Tuu Gia' and *M. schizocarpa* did not result in the sequences similar to part 1
- Sequences of AS hybrid banana clones homologous to part 1 of CL18-like repeat contained a long deletion
- Sequences homologous to part 2 of CL18-like repetitive units were not identified in hybrid banana clone '3 Hands Planty'

Consensus sequences of both parts of CL18-like satellite were reconstructed from all analyzed species and are displayed as sequence logo (Part1 - A; Part2 - C). Neighbor-Joining trees constructed from a Jukes-Cantor distance matrix and rooted to the midpoint show diversity of reconstructed parts of CL18-like satellite units obtained from all studied species (Part1 - B; Part2 - D).

