

# MOLECULAR AND CYTOGENETIC CHARACTERIZATION OF WILD *MUSA* SPECIES NEWLY INTRODUCED TO ITC COLLECTION



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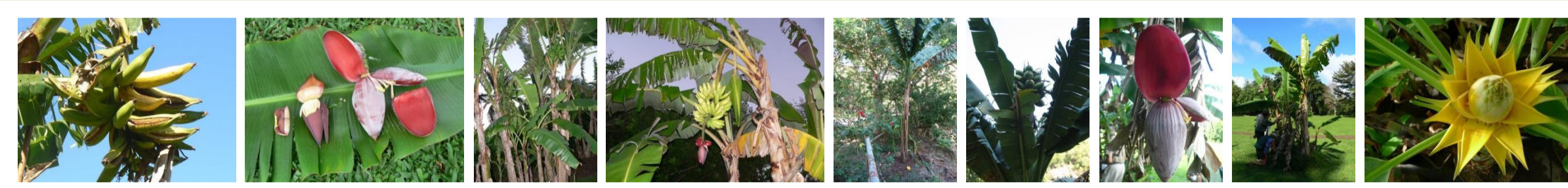
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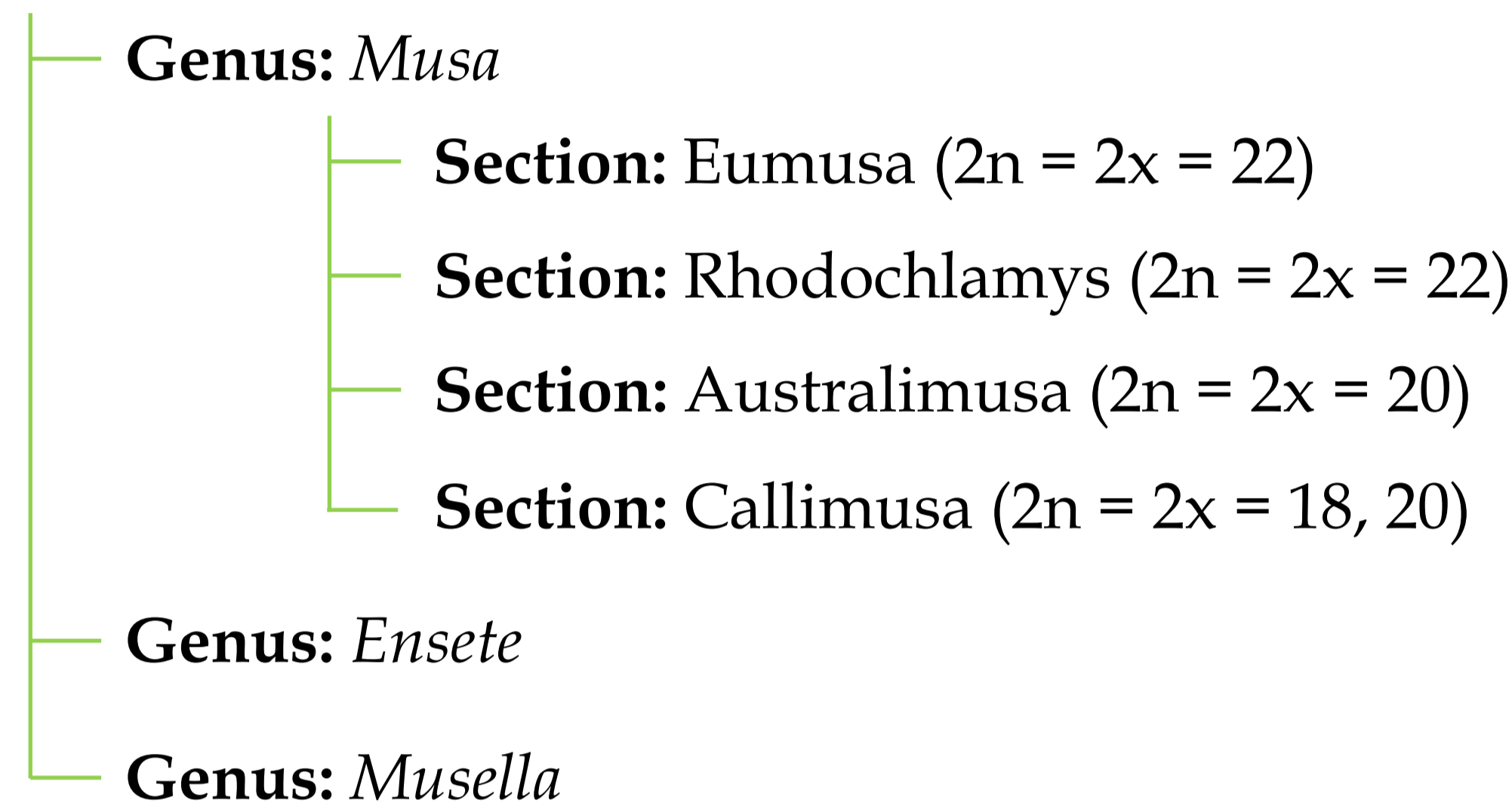
## INTRODUCTION

- Bananas (*Musa* spp.) are a major food crop and an important export commodity in many countries of humid tropics
- The production of banana is threatened by various diseases and adverse environmental conditions
- The preservation and characterization of banana diversity is essential for the purposes of crop improvement
- World's largest banana collection is maintained at the Bioversity International Transit Centre (ITC) in Belgium
- This reference collection is continuously extended by edible cultivars and wild species
- Efficient collection and conservation of *Musa* genetic diversity depends on unambiguous sample identification

## TAXONOMY OF THE FAMILY MUSACEAE



Family: Musaceae



Taxonomy of the family Musaceae is based on morphological characters and basic chromosome number

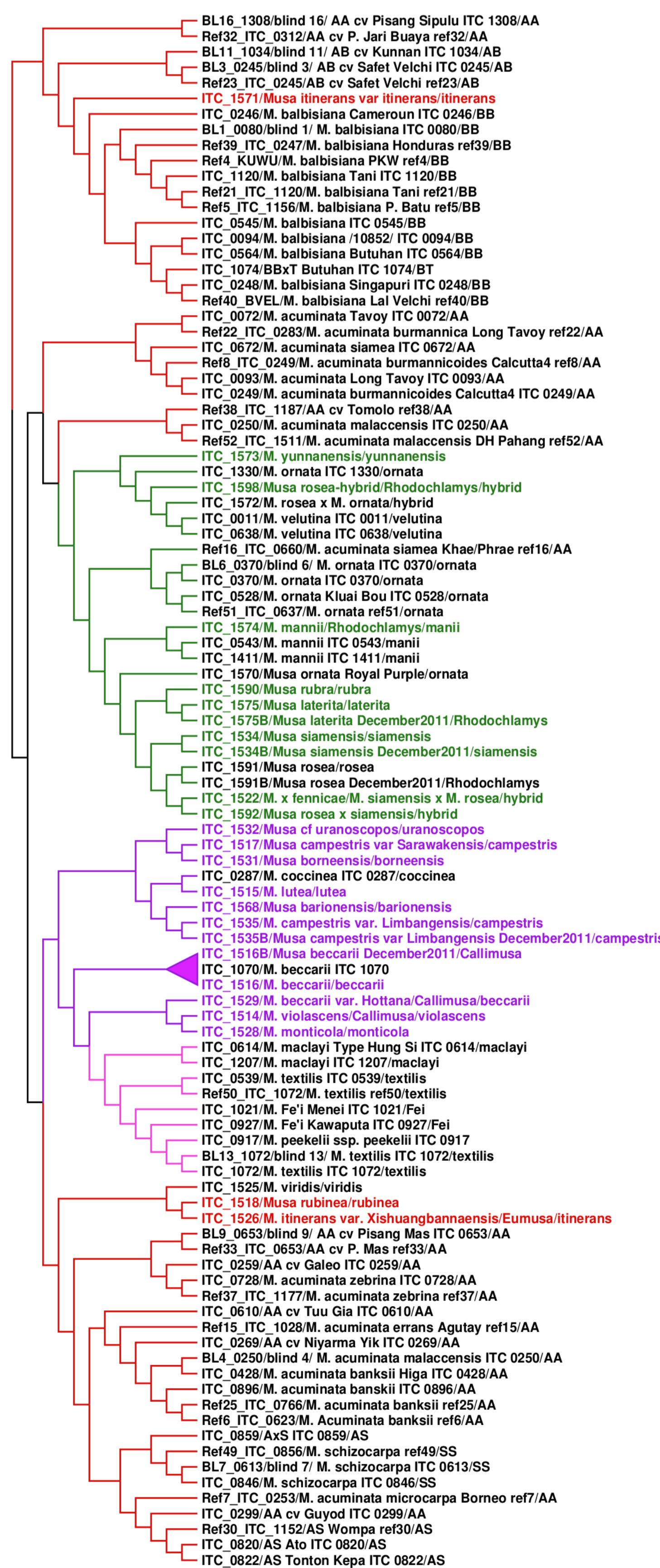
## AIMS OF THE STUDY

- Contribution to characterization of the genetic diversity of wild *Musa* species
- Determination of chromosome number, nuclear DNA content and genomic distribution of rRNA genes to shed light on the genome structure of evaluated accessions
- Verification of the classification of evaluated accessions based on SSR analysis
- Verification of the putative hybrid origin of evaluated *Musa* accessions

## RESULTS

### SSR ANALYSIS

- Standardized SSR genotyping platform (Christelová *et al.*, 2011, AoB PLANTS, doi: 10.1093/aobpla/plr024) was used to analyze genetic diversity of studied accessions
- Newly characterized *Musa* accessions are labeled in colors in the tree below



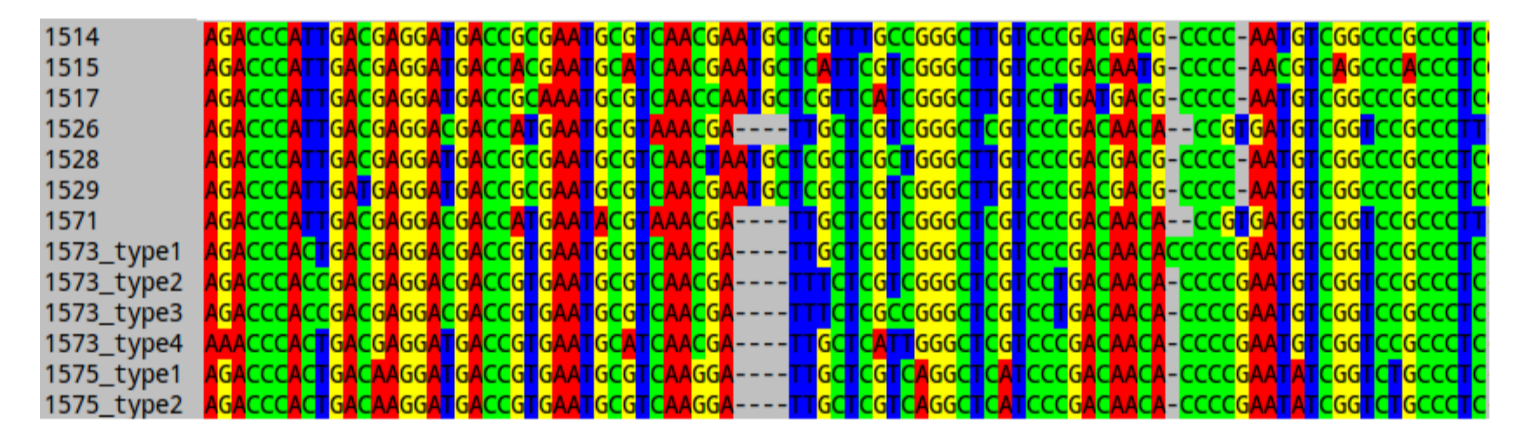
UPGMA cluster analysis of diploid accessions based on Nei (1973) genetic distance

### NUCLEAR DNA CONTENT

Accession name	ITC code	Section	Chromosome number	2C nuclear DNA content [pg]
<i>M. itinerans</i> var. <i>xishuangbannaensis</i>	1526	Eumusa	22	1.311
<i>M. itinerans</i> var. <i>itinerans</i>	1571	Eumusa	22	1.217
<i>M. yunnanensis</i>	1573	Eumusa	22	1.306
<i>M. rubinea</i>	1518	Rhodochlamys	22	1.310
<i>M. x fennicae</i> ( <i>M. siamensis</i> x <i>M. rosea</i> )	1522	Rhodochlamys	22	1.261
<i>M. siamensis</i>	1534	Rhodochlamys	22	1.280
<i>M. mannii</i>	1574	Rhodochlamys	22	1.282
<i>M. laterita</i>	1575	Rhodochlamys	22	1.315
<i>M. rubra</i>	1590	Rhodochlamys	22	1.306
<i>M. rosea</i> x <i>siamensis</i>	1592	Rhodochlamys	22	1.279
<i>M. rosea</i> (hybrid)	1598	Rhodochlamys	22	1.285
<i>M. cf. uranoscopus</i>	1532	Australimusa	20	1.442
<i>M. violascens</i>	1514	Callimusa	20	1.428
<i>M. lutea</i>	1515	Callimusa	20	1.432
<i>M. beccarii</i> var. <i>beccarii</i>	1516	Callimusa	18	1.537
<i>M. campestris</i> var. <i>sarawakensis</i>	1517	Callimusa	20	1.417
<i>M. monticola</i>	1528	Callimusa	20	1.390
<i>M. beccarii</i> var. <i>hottana</i>	1529	Callimusa	18	1.673
<i>M. borneensis</i>	1531	Callimusa	20	1.772
<i>M. campestris</i> var. <i>limbangensis</i>	1535	Callimusa	20	1.454
<i>M. barioensis</i>	1568	Callimusa	20	1.480

### ANALYSIS OF ITS REGION

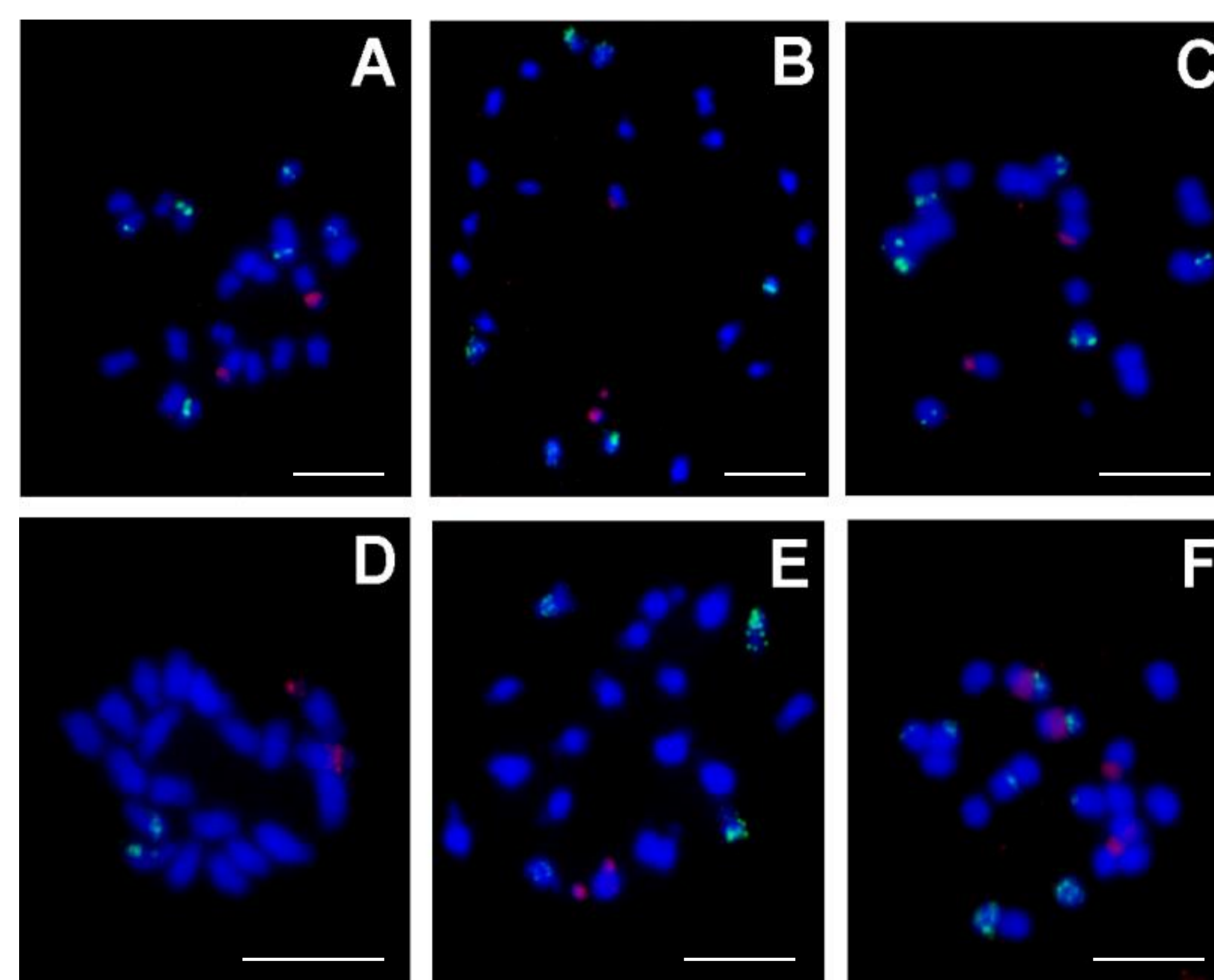
- Clone based sequencing strategy was used to analyze the ITS1-5.8S-ITS2 sequence region of 45S rDNA locus
- Analysis of ITS region was used with the aim to verify hybrid origin of evaluated *Musa* accessions



Multiple alignment of a part of ITS1 sequence region created using mafft

- Except for 10 accessions (ITC 1514; 1515; 1517; 1526; 1528; 1534; 1529; 1571 and 1598) all others contained three or more ITS types which support their hybrid origin
- Hybrid origin was observed also for *M. beccarii* var. *hottana* (ITC 1529) which did not cluster together with other *beccarii* species analysed in this as well as in previous study using SSR genotyping

### CYTOGENETIC MAPPING OF rDNA



Localization of 45S rDNA (red) and 5S rDNA (green) on mitotic metaphase chromosomes. (A) *M. yunnanensis*, (B) *M. rubra*, (C) *M. rosea* x *siamensis*, (D) *M. campestris* var. *sarawakensis*, (E) *M. monticola*, (F) *M. borneensis*. Bar = 5 µm.

## CONCLUSIONS

- Nuclear DNA content, chromosome number and genomic distribution of 45S and 5S rDNA were estimated in studied accessions showing higher variability in these characters in comparison with previous studies
- For *M. borneensis* (ITC 1531), the highest nuclear DNA content known for diploid *Musa* species was estimated
- SSR analysis did not confirm genetic origin of several accessions (ITC 1518, ITC 1532 and ITC 1573)
- Classification of these accessions should be re-evaluated
- Analysis of ITS region suggested hybrid origin of most of studied accessions