

# Comparison of homo(eo)logous regions containing clusters of duplicated RGAs within *Musa* species and with rice

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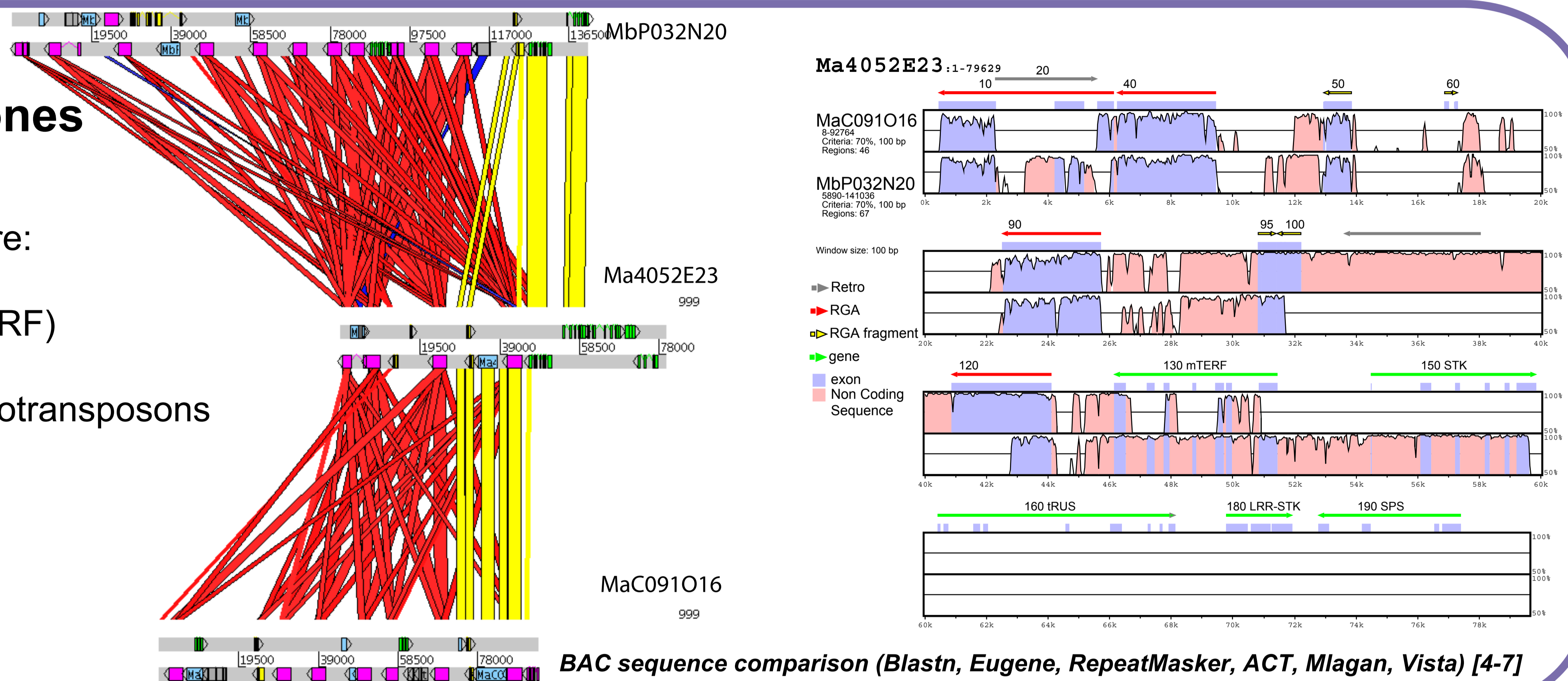
## Introduction

- Cultivated bananas are highly sterile, parthenocarpic, vegetatively propagated and very susceptible to diseases (e.g. fungi, virus).
- Two wild diploid species: *Musa acuminata* 'Calcutta 4' (AA, Ma4) and *Musa balbisiana* 'Pisang Klutuk Wulung' (BB, MbP) and one triploid cultivar *Musa acuminata* 'Cavendish – Grande naine' (AAA, MaC) are studied [1].
- The probe Musa Resistance Gene Analog MARGA08, corresponding to NBS-LRR type RGA [2], was used to screen high density filters from three banana BAC libraries. Fingerprint analysis revealed that MARGA08 is organized in clusters in the three banana clones [3].
- One BAC per banana clone containing the MARGA08 cluster has been sequenced and compared.

## Repeat and gene annotation of the same MARGA08 locus in 3 *Musa* clones

BAC Ma4052E23, MaC091O16 and MbP032N20 share:

- MARGA08 cluster
- Mitochondrial transcriptional termination factor (mTERF)
- Serine/threonine-protein kinase (STK)
- More than 30 Kb of genomic segments including retrotransposons



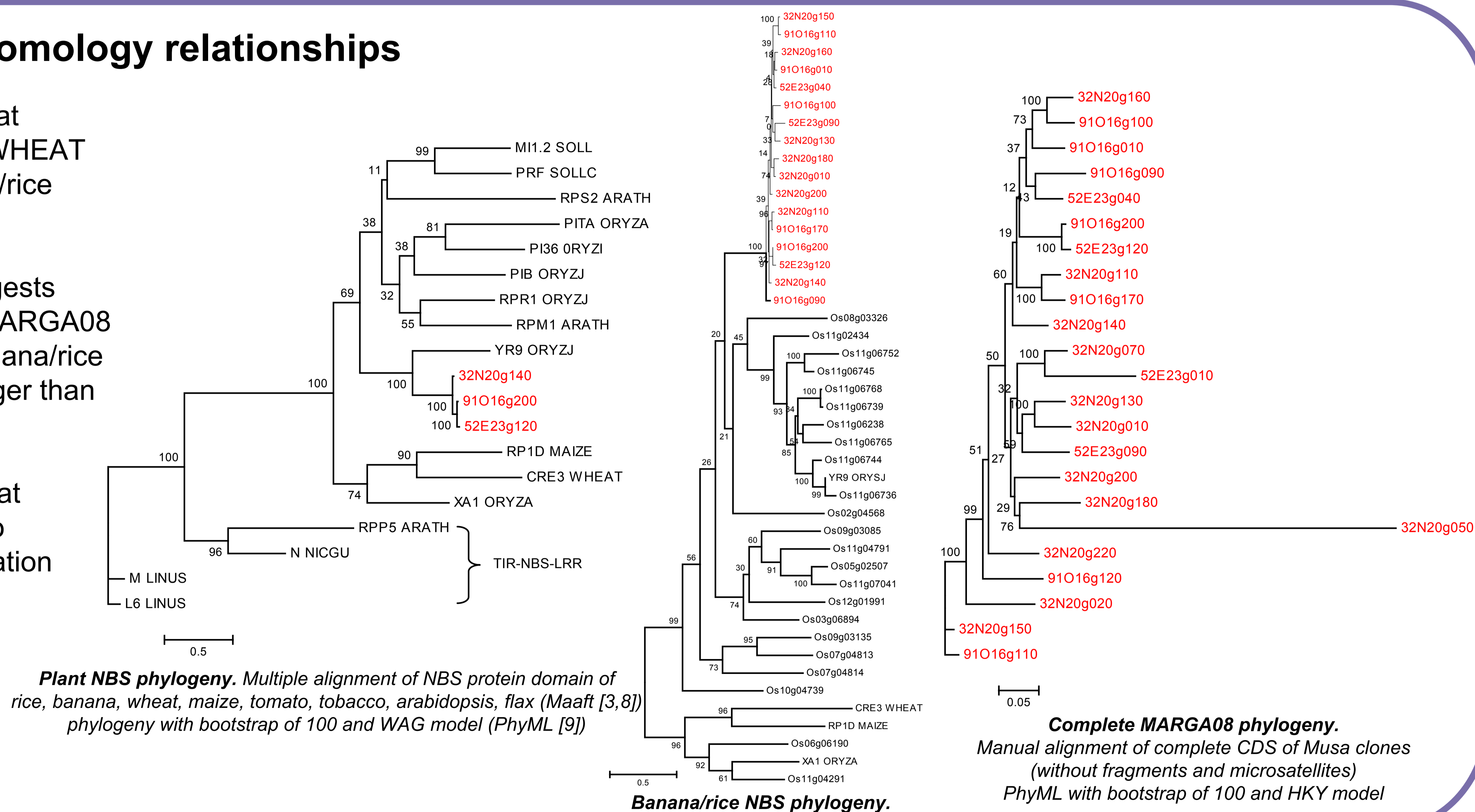
BAC sequence comparison (Blastn, Eugene, RepeatMasker, ACT, Mlagn, Vista) [4-7]

## Musa/Oryza NSB-LRR homology relationships

- **Plant NBS phylogeny** suggests that we can take RP1D\_MAIZE, CRE3\_WHEAT and XA1\_ORYZA to root the banana/rice NBS phylogeny.

- **Banana/rice NBS phylogeny** suggests the rice chromosome 11 RGA and MARGA08 tandem duplications occurs after banana/rice divergence (MARGA08 cluster younger than Os11RGA cluster).

- **MARGA08 phylogeny** suggests that duplications and mutations leading to pseudogenization or neofunctionalization occurred both before and after *Musa* speciation.



Plant NBS phylogeny. Multiple alignment of NBS protein domain of rice, banana, wheat, maize, tomato, tobacco, arabidopsis, flax (Maafft [3,8]) phylogeny with bootstrap of 100 and WAG model (PhyML [9])

Banana/rice NBS phylogeny.

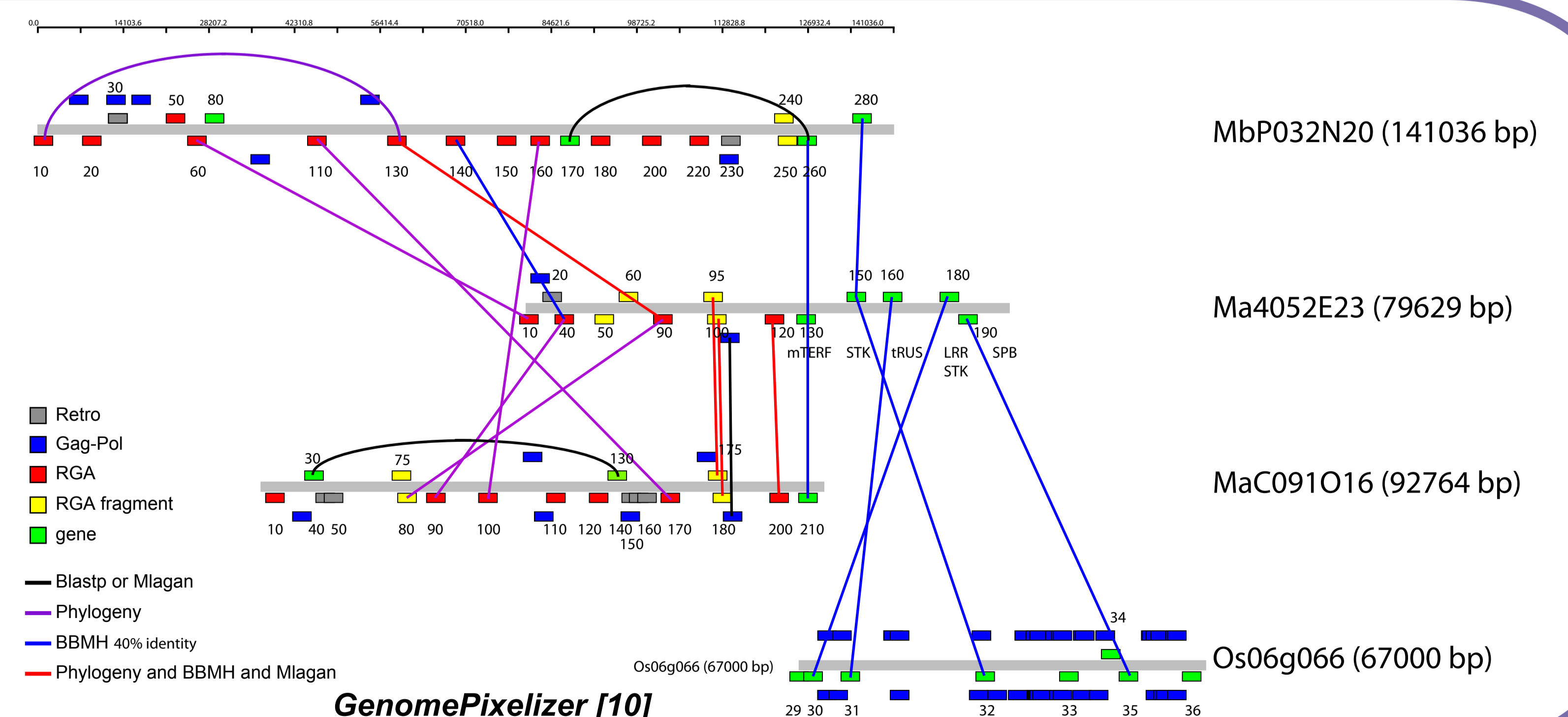
Complete MARGA08 phylogeny. Manual alignment of complete CDS of *Musa* clones (without fragments and microsatellites) PhyML with bootstrap of 100 and HKY model

## Comparative Genomics

The history of MARGA08 clusters between the 3 *Musa* clones is complex.

Microsynteny between Ma4052E23 and a region of the rice chromosome 6:

- Serine/threonine-protein kinase (STK)
- tRNA pseudouridine synthase (tRUS)
- LRR-STK
- Squamosa promoter-binding-like protein (SBP)



GenomePixelizer [10]

## Conclusion & Prospects

- The MARGA08 ancestor seems to be mono-exonic.
- Microsatellites seems to bring biodiversity.
- Compute Ka/Ks to define which MARGA08 are pseudogenes and which are functional.
- Compute Ks to estimate the degree of MARGA08 divergence within *Musa* clones.
- Complete the entire MARGA08 locus in banana including haplotypes.

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