

A genomic view of the banana (*Musa spp.*) diversification: the case of triploid ABB genome group

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Background

Bananas (*Musa spp.*) are a major staple food crop for hundreds of millions of people in developing countries. Most cultivated banana varieties are triploids with an AAA, AAB, or ABB genome constitution/group, where A and B genomes were provided by *M. acuminata* and *M. balbisiana*, respectively, both sequenced [1,2].

Prior to the availability of the genome sequence, it has been hypothesized that inter-genome translocation chromosomes are relatively common in banana and that cultivated banana hybrids are more likely to have passed through an intermediate hybrid [3] during the diversification step (Figure1). In our study, we explored those hypotheses at the chromosome structure level for the ABB group, taxonomically divided into 8 subgroups (each presumably corresponding to groups of clones): Bluggoe, Monthan, Ney Mannan, Klue Teparod, Peyan, Pisang Awak, Pelipita and Saba.

Materials & Methods

A panel of 25 ABB and 2 AAA genotypes spanning the different subgroups were sequenced using RADseq and RNAseq. Data were mapped on the genome of reference with BWA or STAR, and SNP positions were called with GATK software. To measure the B genome contribution, we developed a method to filter A genome polymorphisms identified shared by AAA and the reference genome (AA) (Figure 2).

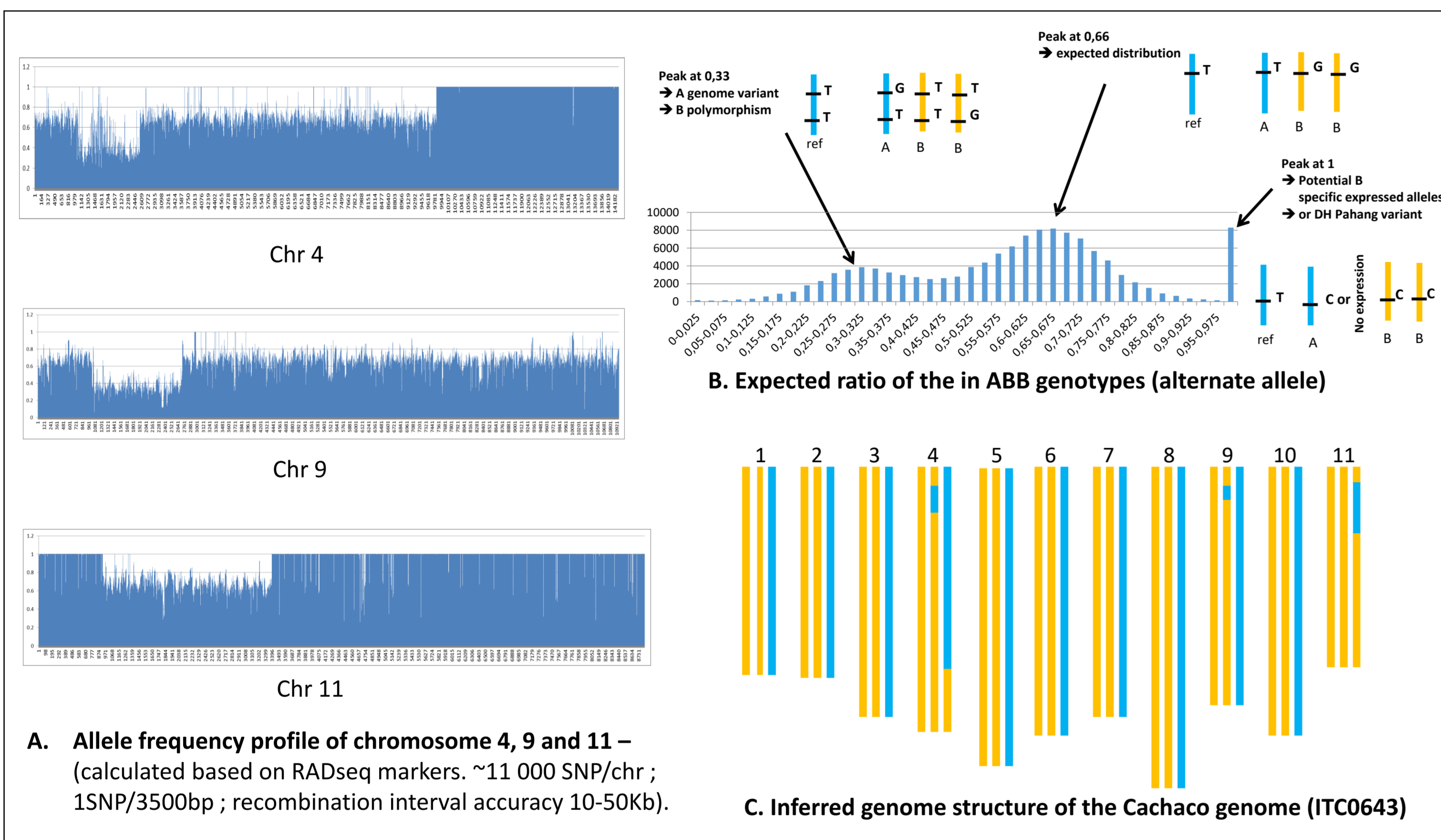


Figure 2. Interspecific recombinations in ABB Cachaco genome (Bluggoe)

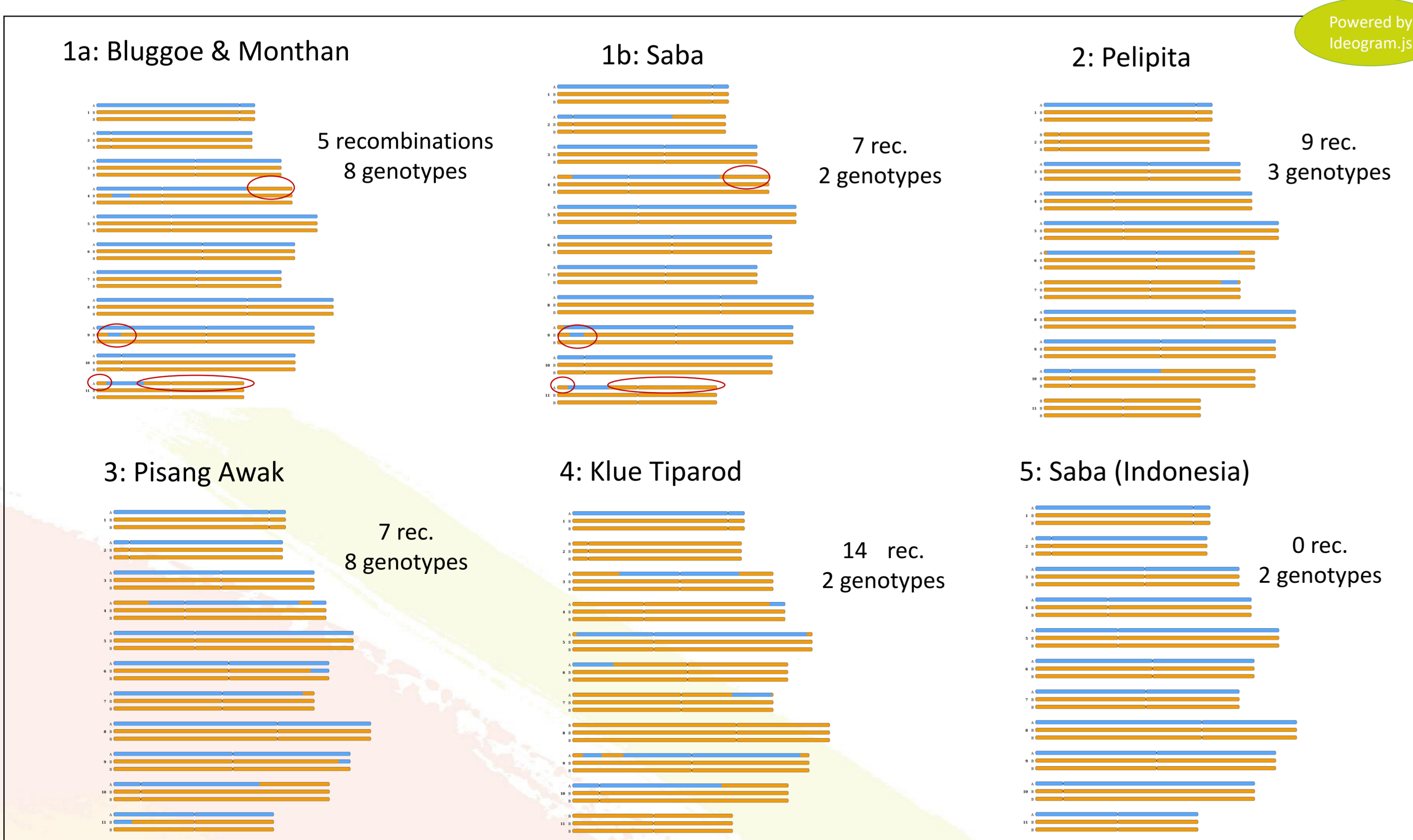


Figure 3. Different recombination patterns show 5 founding events in ABB subgroups

- References**
1. D'Hont et al. (2012) The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants. *Nature* 488,213-217.
 2. Davey et al. (2013) A draft *Musa balbisiana* genome sequence for molecular genetics in polyploid, inter- and intra-specific *Musa* hybrids. *BMC Genomics* 14:683.
 3. De Langhe E, Hribova E, Carpentier S, Dolezel J, Swennen R. 2010. Did backcrossing contribute to the origin of hybrid edible bananas? *Annals of Botany*. 106, 849-857.

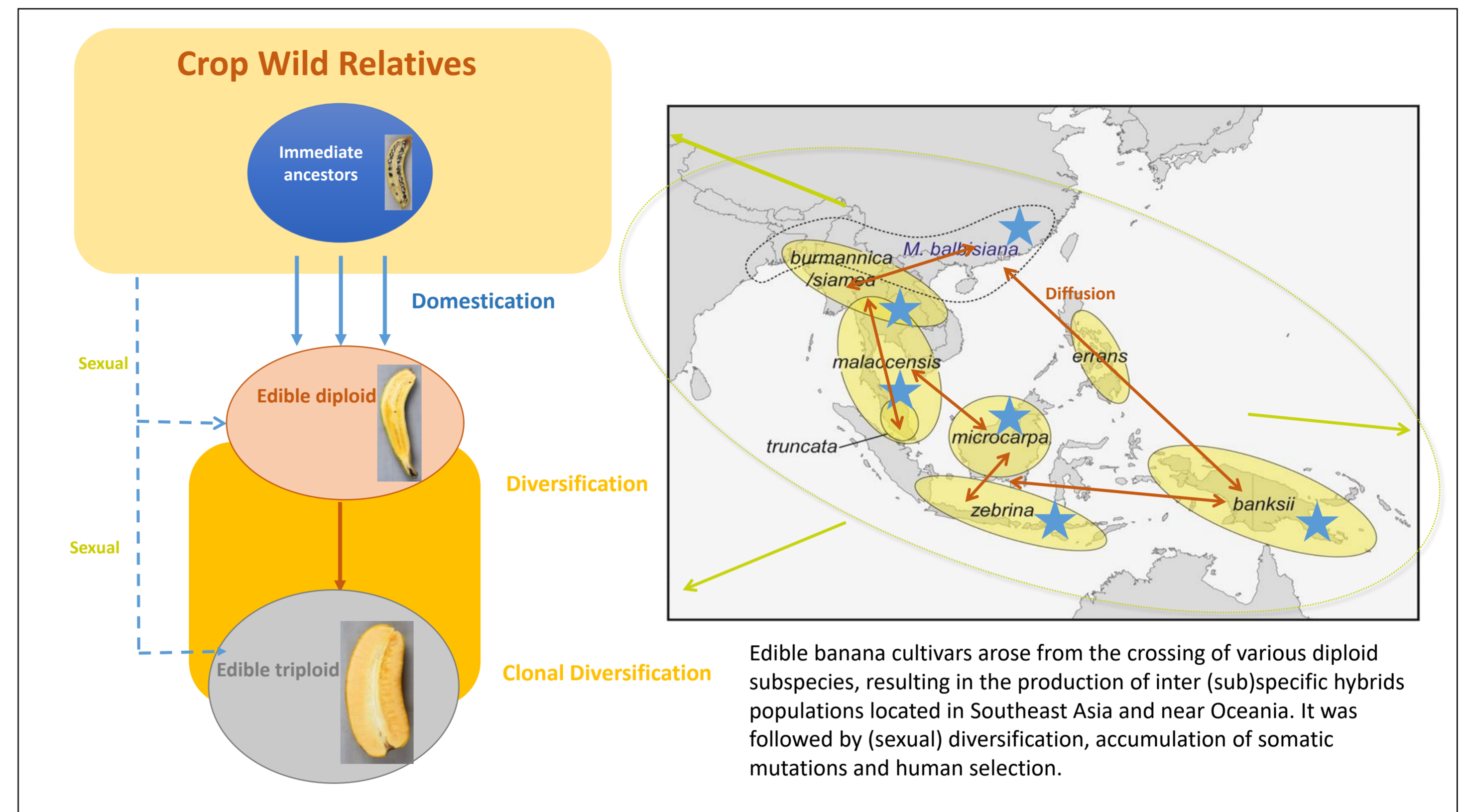


Figure 1. Domestication and diversification process of banana

Results

In the first genotype (ITC0643 - Cachaco, Bluggoe subgroup) two interstitial regions were detected with A genome homeoalleles replacing their respective homeoalleles in one chromosome B (on the first hybrid) and three terminal regions were detected having the B homeoalleles (on the first hybrid) replacing their respective A homeoalleles (Fig. 2). Same characterization was conducted in other subgroups (Fig. 3).

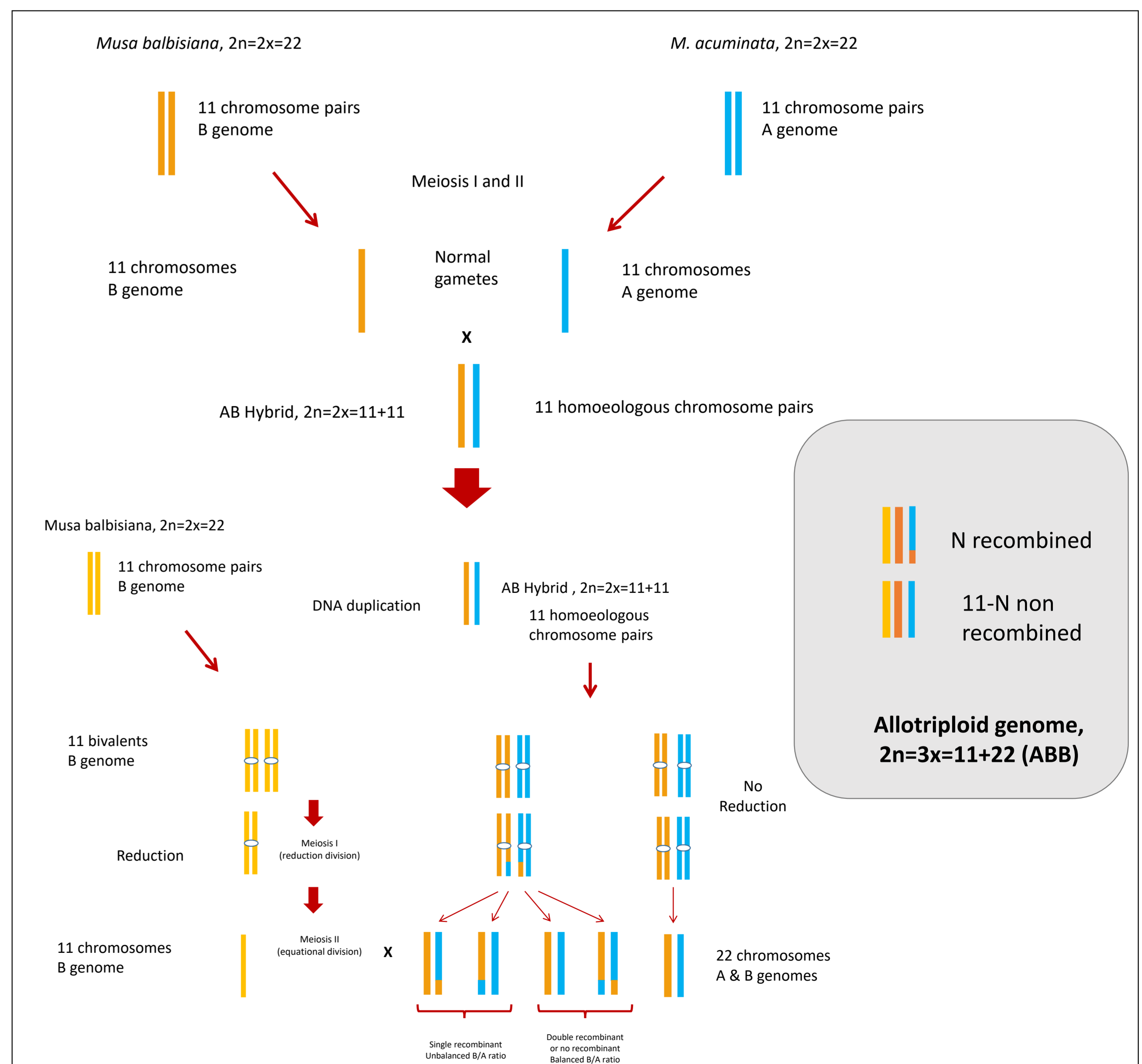


Figure 4. Inferred recombination route via AB genome

Conclusions

- Recombination events between A and B homoeologous chromosomes are common. Some subgroups show no recombination or very unbalance A/B genome ratio.
- 5 founding events in the ABB genome group followed by diversification events.
- Hypotheses can be done on the routes at the origin of the diversification such as 1a and 1b (Figu 3 & 4).
- Highly unbalanced A/B genome ratio can explain hypothesis and debate on BBB group existence.