

# Mapping race differentiation along the cultivated sorghum genome

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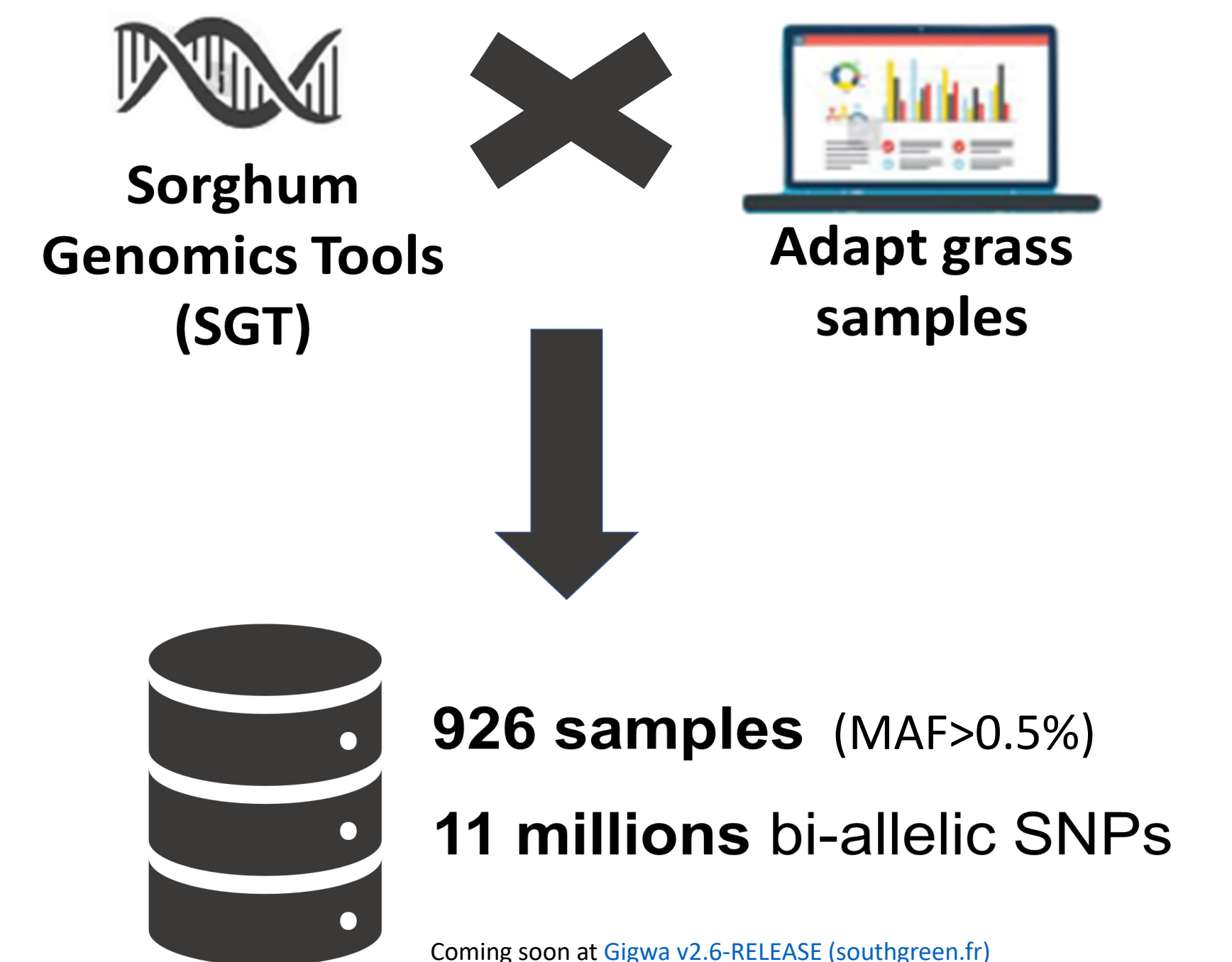
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## Key Points :

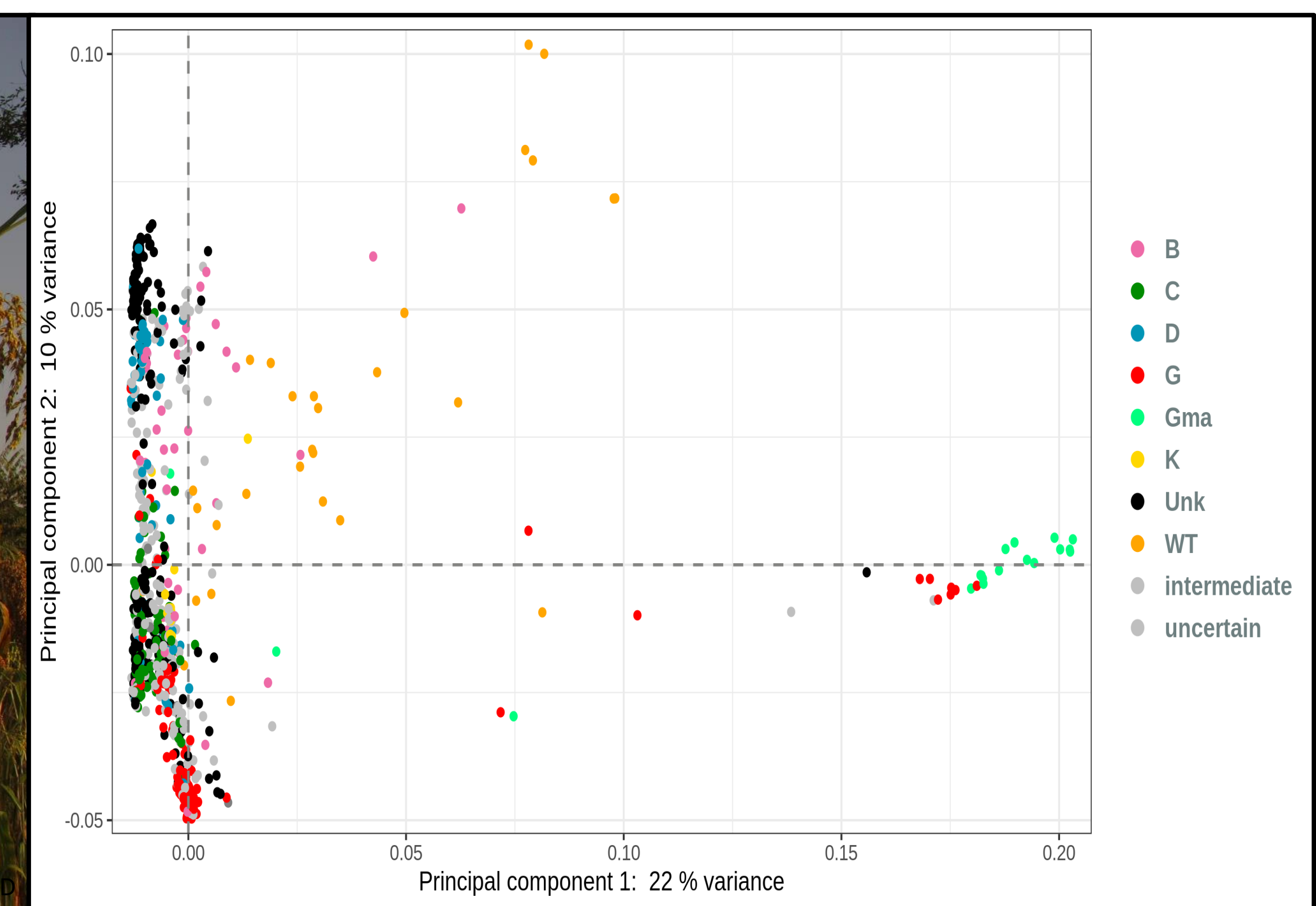
Cultivated sorghum has great genetic and phenotypic diversity. It is characterized by the existence of multiple races such as *bicolor*, *caudatum*, *durra*, *kafir* and *guinea*. Within this diversity there is a particular group called **guinea-margaritifera (Gma)**, which is markedly differentiated from the other groups. We use this group to **investigate genomic exchanges between races**. The genomic diversity of cultivated sorghum is analyzed and traces of introgressions between Gma and other components of sorghum diversity are identified.

## Resources



## Objectives :

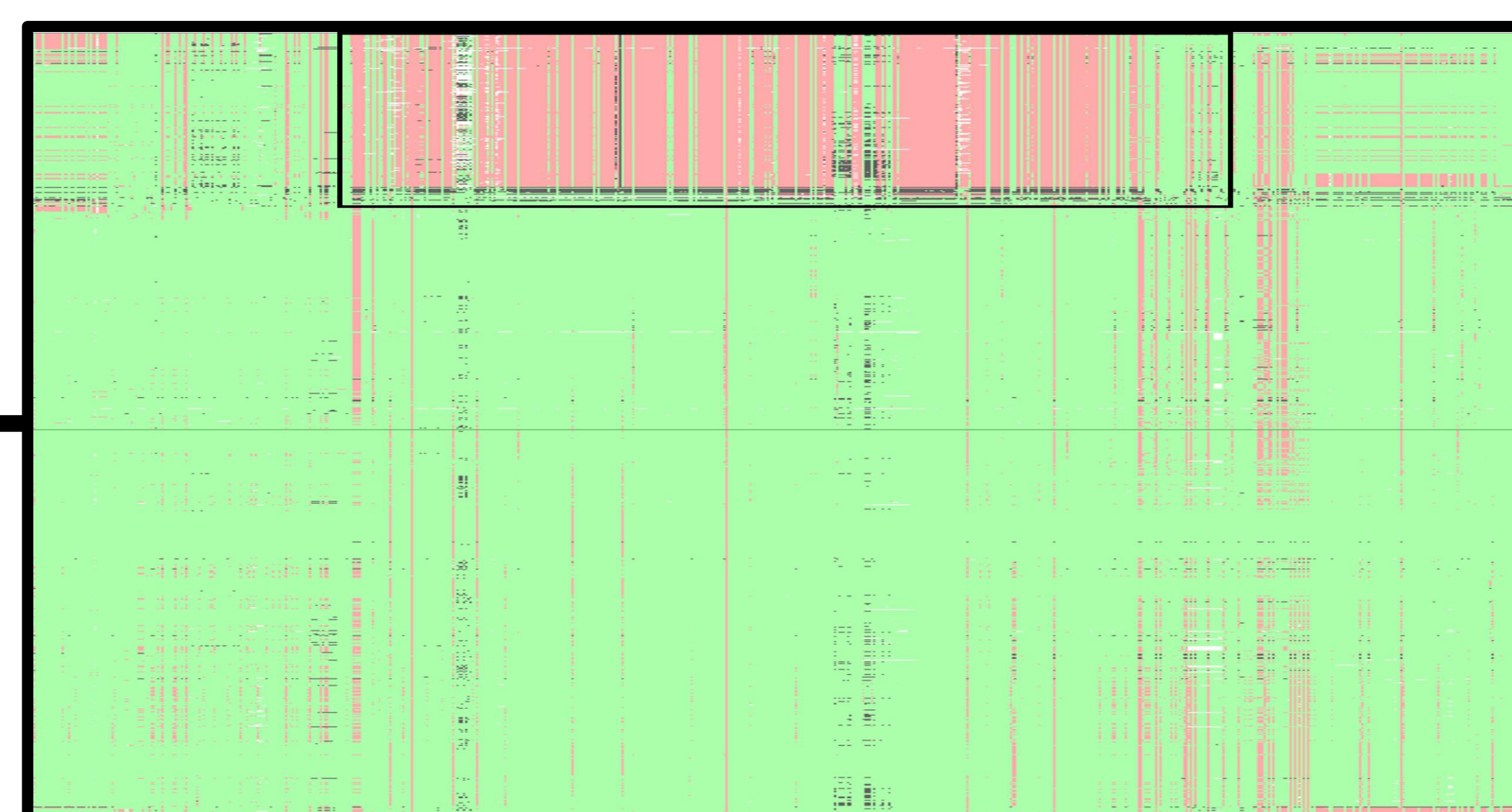
- ❖ Analyze genomic diversity of cultivated sorghum.
- ❖ Understand the importance of genomic exchanges between Gma and other groups.
- ❖ Characterize traces of local Gma introgressions in the genome of other cultivated sorghum.



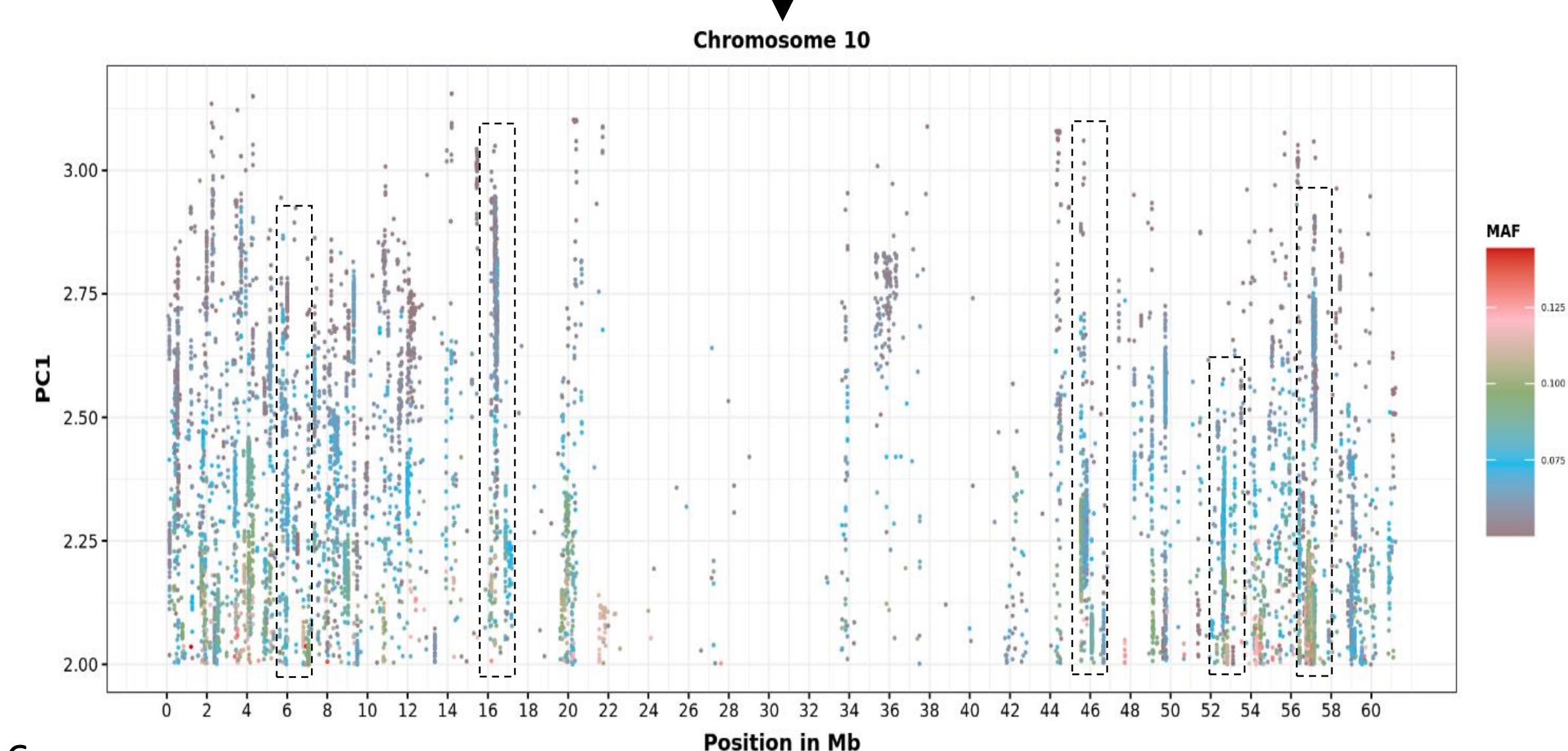
Plane (1,2) of the PCA identifies loci that highly contribute to the Gma differentiation along PC1.

GENE ID	Type	Orthologs	Species	Location
Sobic.010G077700	C2H2, Zinc finger	LOC_Os02g53530.1	<i>O. sativa</i>	Chr2: 32751400..32750101
		Zm00001d037136	<i>Z. mays</i>	Chr6: 113639620..113643420
Sobic.010G077800	Kinesin-like protein	LOC_Os02g53520.1	<i>O. sativa</i>	Chr2: 32740500..32731189
		Zm00001d044982	<i>Z. mays</i>	Chr9: 9199609..9212969

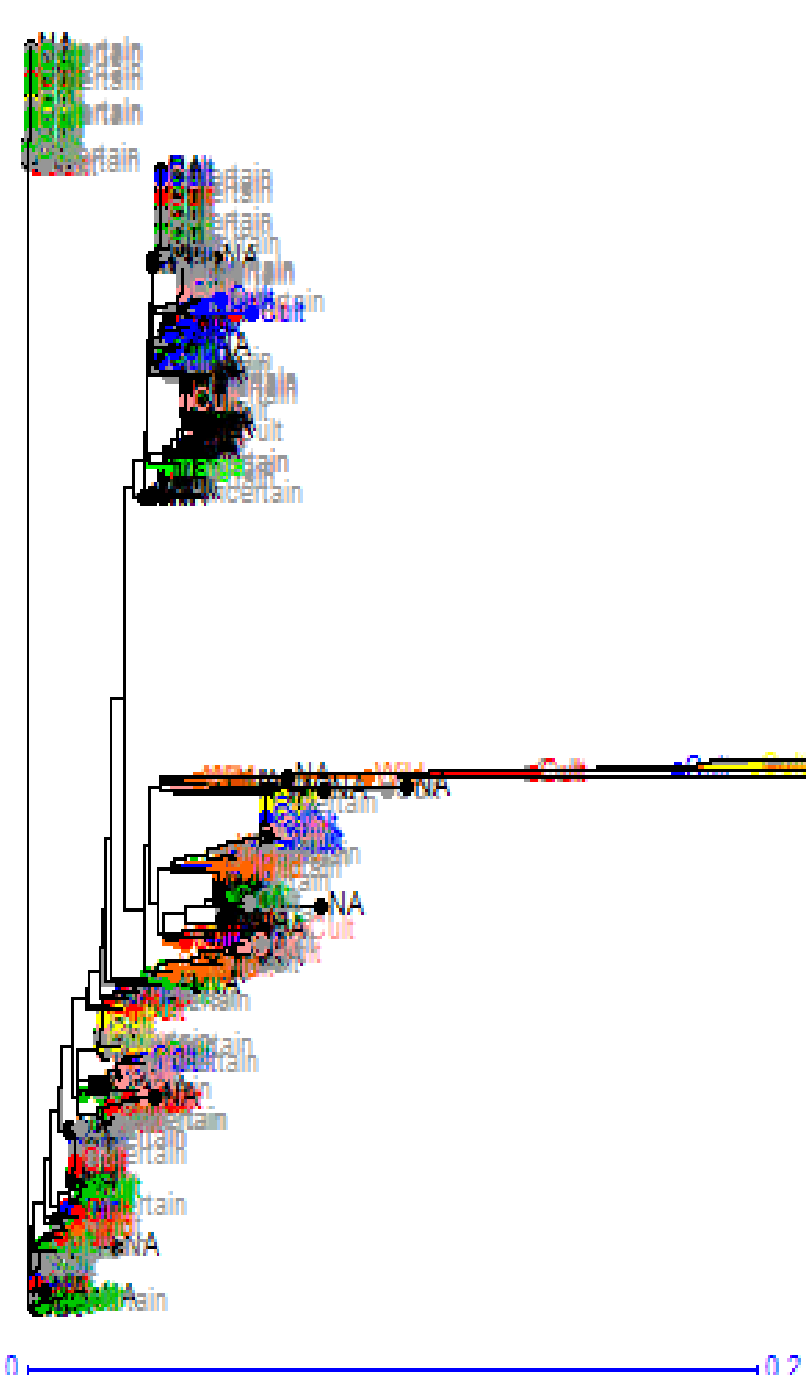
Genes identified in introgression region and their orthologs.



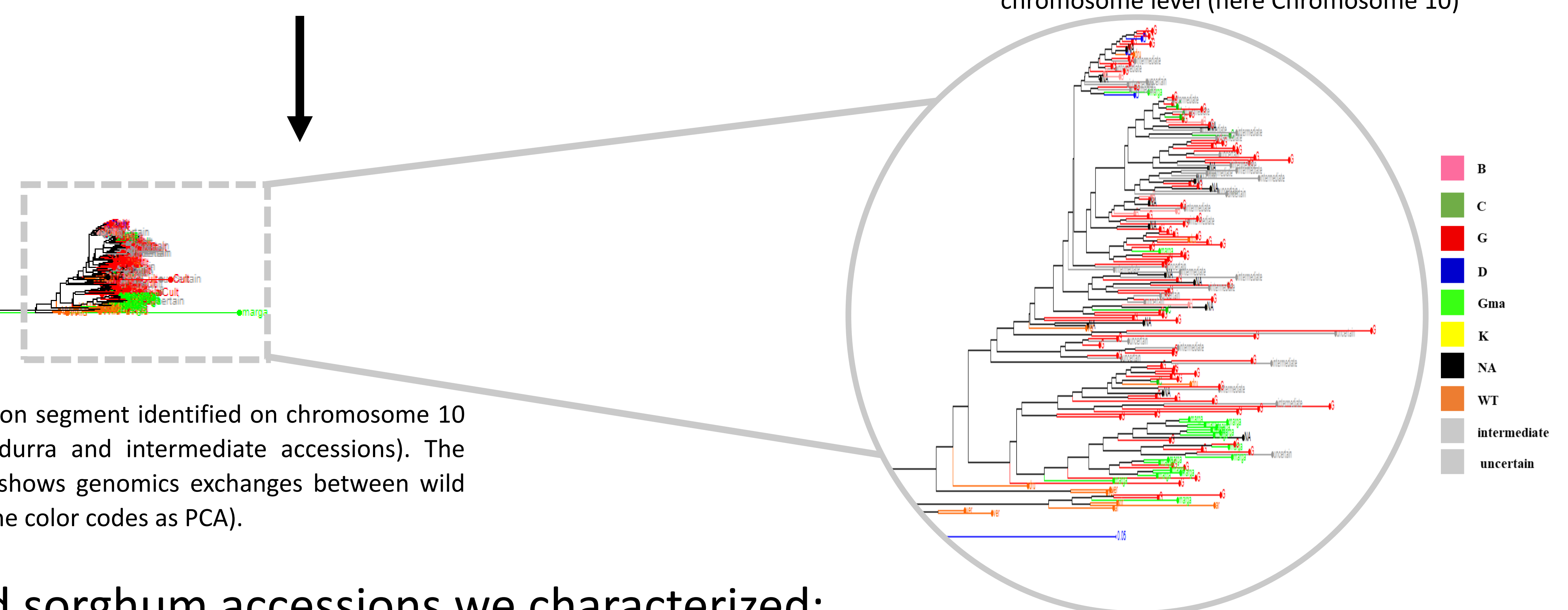
Each peak makes it possible to test for introgression of Gma using Gigwa v2.6 and Flapjack view for visualization.



Locate peaks with high contribution of loci to PC1 (more than 2) at whole chromosome level (here Chromosome 10)



Neighbor joining tree of the introgression segment identified on chromosome 10 (Gma introgression in some guinea, durra and intermediate accessions). The presence of wild sorghum accessions shows genomic exchanges between wild and cultivated sorghum accessions (same color codes as PCA).



**Results:** In whole genome of cultivated sorghum accessions we characterized:

- Genomics exchanges between guinea-margaritifera and other cultivated sorghum.
- Local introgressions between groups in different genomic region of several sorghum accessions.
- Several genes highlighting the importance of guinea-margaritifera in sorghum accessions adaptation.