



# Identification by the DArTseq method of the genetic origin of the *Coffea canephora* cultivated in Vietnam and Mexico

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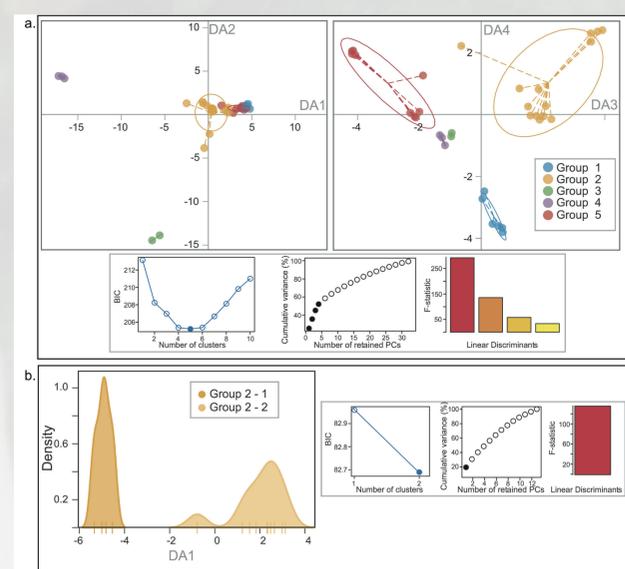
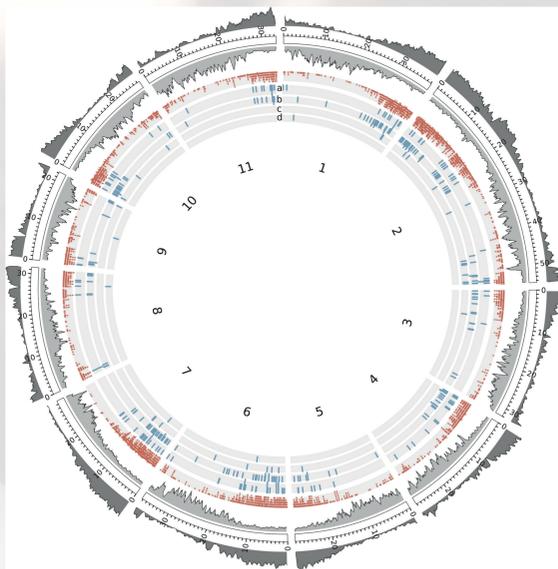
The coffee species *Coffea canephora* (Robusta) represents approximately 40% of coffee production worldwide. While the genetic diversity of wild *C. canephora* has been well studied in the past, only few studies have addressed the genetic diversity of currently cultivated varieties around the globe. Vietnam is the largest Robusta producer in the world, while Mexico is the only Latin American country, besides Brazil, that has a significant Robusta production. Knowledge of the genetic origin of Robusta cultivated varieties in countries as important as Vietnam and Mexico is therefore of high interest.

Through the use of the DArTseq method on a collection of *C. canephora* composed of known accessions and accessions cultivated in Vietnam and Mexico, 4,021 polymorphic SNPs were identified. We used a multivariate analysis using SNP data from reference accessions in order to confirm and further fine-tune the genetic diversity of *C. canephora*. Also, by interpolating the data obtained for the varieties from Vietnam and Mexico, we determined that they are closely related to each other, and identified their genetic origin. The genetic characterization based on SNP markers of the varieties grown throughout the world, increased our knowledge on the genetic diversity of *C. canephora*, and contributed to the understanding of the genetic background of varieties from very important coffee producers.

## Results

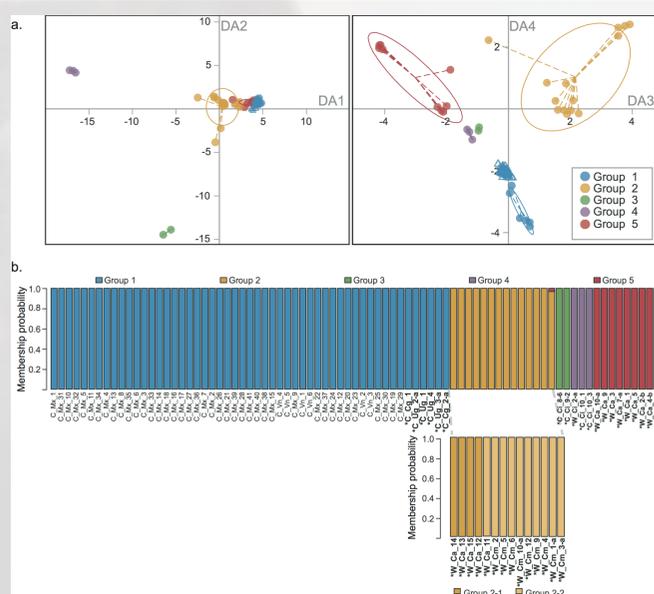
**Figure 1.** The DArTseq-derived SNP markers showed a tendency towards gene-rich regions when mapped on the recently sequenced *C. canephora* genome.

Gene density (dark gray), Transposable elements (light gray), the location of the 4,021 DArTseq SNPs used for the analysis (red), and the markers with the highest contribution (blue) to the four discriminant axes (see Figure 2) are shown.



**Figure 2.** The genetic structure revealed by the DArTseq-derived SNP markers confirms the genetic diversity previously revealed by RFLPs and SSRs, as five genetic clusters were identified.

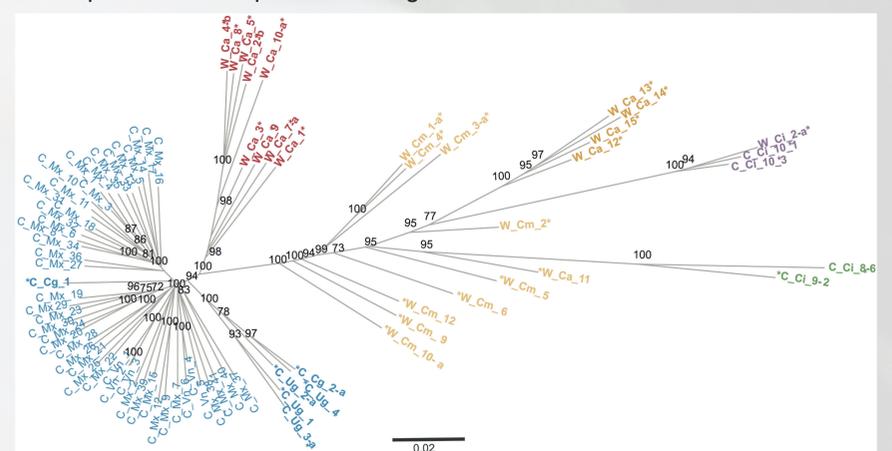
Discriminant axes from a DAPC analysis carried out with 34 *C. canephora* reference accessions (a) and with individuals from group 2 (b).



**Figure 3.** Accessions from Vietnam and Mexico collocated closely with individuals from Group 2. Membership probabilities for each accession were close to 100%

Circles represent reference accessions used to identify genetic groups, while triangles represent interpolated individuals from Vietnam and Mexico.

**Figure 4.** The constructed unrooted Neighbor-joining tree comprises at least eight well-defined branches, all in agreement with the DAPC results. The color patterns are equivalent to Figures 2 and 3.



## Conclusions

- Markers derived from NGS approaches are easily exploitable in coffee, with an error rate similar to what has been observed for other crops.
- The genetic characterization of the varieties grown throughout the world using SNP markers increased our knowledge on the genetic diversity of *C. canephora*, and contributed to the understanding of the genetic background of varieties cultivated in very important Robusta producing countries.
- The discriminant SNP markers identified in our work represent a valuable tool that could be used by breeders to discriminate between *C. canephora* genetic groups, in Robusta germplasm.
- Given the similar characteristics of the climatic areas and relatively high altitude where Robusta is grown in Uganda, Mexico and Vietnam, and their common genetic origin, we can state that the Vietnamese and Mexican accessions have the genetic potential to increase the quality of coffee they produce.