

Genomic characterization of 10 Vietnamese elite clones of Robusta (*Coffea canephora*)

Vi Bao Tram^{1,2} (baotram.vi@ird.fr), Cubry Philippe¹, Marraccini Pierre^{1,2,3}, Dinh Thi Tieu Oanh⁴, Phan Viet Ha⁴, Khong Ngan Giang², Poncet Valérie¹

¹UMR DIADE, Univ Montpellier, CIRAD, IRD, Montpellier, France ; ²AGI, Hanoi, Vietnam ; ³UMR DIADE, CIRAD, Montpellier, France ; ⁴WASI, Buon Ma Thuot, Vietnam

RATIONALE

As a consequence of climate change, Vietnam, the world's largest Robusta producer, is facing the risk of losing 50% suitable area for growing Robusta by 2050 (Bunn et al., 2015). To deal with the ongoing challenge, it is therefore important to understand the genetic makeup and diversity of *Coffea canephora* clones cultivated in Vietnam. As a preliminary work, the genetic diversity of 10 clones considered as elites (with high productivity and pest resistance over the years) was assessed using two sets of genetic markers, SSRs and SNPs.

METHODS

Leaves of the 10 clones were collected in Robusta germplasm bank of WASI (Buon Ma Thuot, Dak Lak province) and used to extract DNA for further population genetics analyses. A collection of 233 African wild accessions of *C. canephora* covering the eight genetic diversity groups previously identified (Mérot-L'Anthoene et al., 2019) were included in the analysis as genetic references. We performed Principal Component analysis (PCA), sparse nonnegative matrix factorization (sNMF) (Frichot et al., 2014), neighbor-joining (NJ) tree construction, and population genetics statistics on genotypic datasets of 19 microsatellites (SSRs) markers (moccadb.ird.fr) and 1.3M biallelic single nucleotide polymorphism (SNPs) detected on resequencing data.

RESULTS

The PCA results of both SSR and SNP data presented a close genetic relationship between all the 10 Vietnamese Robusta clones with the accessions originating from the Democratic Republic of the Congo (DRC), corresponding to groups E and R (Mérot-L'Anthoene et al., 2019). Indeed, sNMF results showed high membership probability of the Vietnamese clones with groups E and R (higher than 90%), except for one variety representing approximately 25% introgression of group A and G (Cameroon-Gabon and Angola groups, respectively). The results were also confirmed by the NJ trees as well as the low differentiation coefficient between the Vietnamese clones and the group of accessions from DRC (-0.0048 and 0.0028 in SSR data and SNP data, respectively).

CONCLUSIONS & PERSPECTIVES

The genomic characterization of the 10 elite clones in Vietnam showed the presence of clones belonging to the E and R groups of Robusta diversity, while one presented a different percentage of introgression with A and G groups. These results now open the way to perform an in depth characterization of the genetic diversity of Robusta plants presented in Vietnam by checking the whole collection available in the germplasm bank of WASI. Such an approach should contribute to the selection of elite parental genotypes necessary to further launch new Robusta breeding programs.

References:

- Bunn et al. 2015 Climatic Change 129(1): 89–101.
- Mérot-L'Anthoene et al. 2019 Plant Biotechnology Journal 17(7): 1418–1430.
- Frichot et al. 2014 Genetics 196(4): 973–983.