

Which genetic diversity was brought to Vietnamese Robusta coffee (*Coffea canephora*)?

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Rationale:

As a consequence of climate change, Vietnam, the world's largest Robusta producer, is facing the risk of observing yield anomalies variation in Robusta production because of its sensitivity to weather in the producing regions (Dinh et al., 2022). To develop varieties that are better adapted to climate change, it is important to understand the genetic makeup and diversity of *Coffea canephora* cultivated in Vietnam. Robusta accessions from the WASI germplasm bank (in Dak Lak province) were collected for genomic evaluation.

Methods:

A total of 126 accessions were collected in WASI including 10 elite accessions (previously analyzed in Vi et al. 2023). A collection of African wild accessions of *C. canephora*, covering the wild diversity previously identified, were included as genetic references. 261 SNPs, selected from a 8.5K SNP array (Mérot-L'Anthoëne et al., 2019), were used to analyze the genetic diversity of the Vietnamese collection in relation to the wild African groups. A core set of representative individuals were selected to minimize genetic redundancy and maximize allelic diversity. Admixture segments of these individuals were further assigned at the chromosome level using whole-genome sequencing data, by a local ancestry inference method adapted in *C. canephora* (Vi et al., 2023).

Results:

Most of the Vietnamese genotypes were closely-related with accessions originating from the Democratic Republic of the Congo (DRC), corresponding to groups E and R (Mérot-L'Anthoëne et al., 2019), at high membership probability (> 90%). Few varieties including one elite accession presented introgressions, at different levels, from group A and G (Cameroon-Gabon and Angola groups, respectively), or group O (Uganda), or D (Guinean group). Contribution of each African source at the chromosome level, on the sequenced individuals of the core set, led to the identification of recent backcrosses and multi-way admixtures.

Conclusions & Perspectives:

The diffusion and hybridization of *C. canephora* in Vietnam were from multiple African sources of different geographical origins, but with a Congolese genomic background. Such an approach should contribute to the selection of elite parental genotypes necessary to further launch new Robusta breeding programs.

References:

1. Dinh TLA et al., Frontiers in Environmental Science, 2022, p.880.
2. Mérot-L'Anthoëne V et al., Plant Biotechnology Journal, 2019, 17(7): 1418–1430.
3. Vi T et al., Genome Biology and Evolution 15:5: evad065.