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

S1-PO-27

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VIETNAM is the world largest Robusta producer

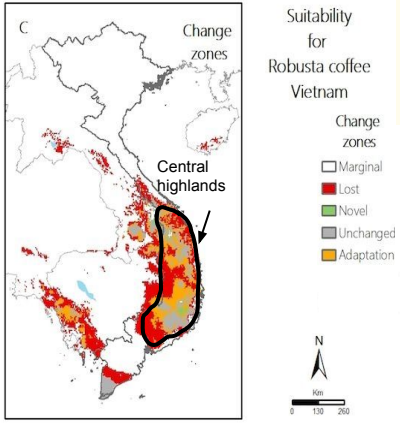


Chart courtesy of CIAT

Loss of areas suitable to coffee production by 2050

Objectives

1. Analyze the **genetic diversity**
2. Trace back to the **origins**

of **10 Vietnamese Robusta elite clones**

- Central highlands (WASI)
- High yield, good cup quality, drought tolerance, resistance to disease

Materials/Methods

- **Markers**: 19 SSRs and 1.2M genome-wide SNPs
- **Reference**: 233 African wild accessions - 8 genetic diversity groups
- **Methods**:
  - Principal component analysis (PCA)
  - Sparse nonnegative matrix factorization (sNMF)
  - Neighbor-joining (NJ) tree construction
  - Population genetics statistics

Results/Discussion

- 10 Vietnamese Robusta elite clones belong to the E and R groups (DRC).
- 1 clone presents ~25% introgression of group A and G (Cameroon-Gabon and Angola).

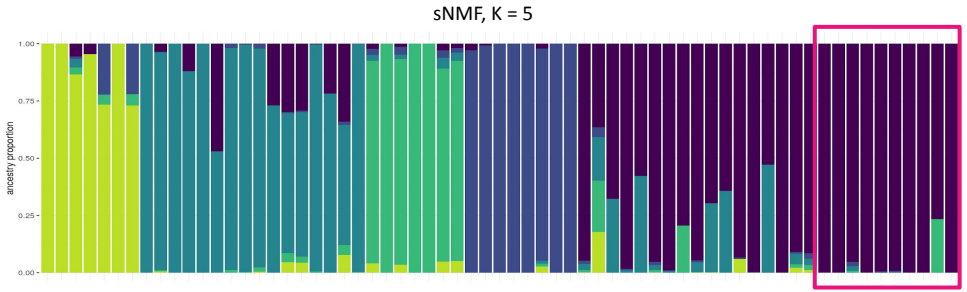


Figure 1. Ancestry proportion of 10 Vietnamese clone and 55 reference individuals detected by sNMF (K=5) using 1.2M genome-wide SNPs

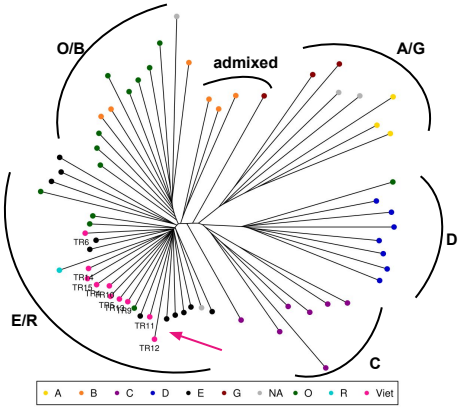
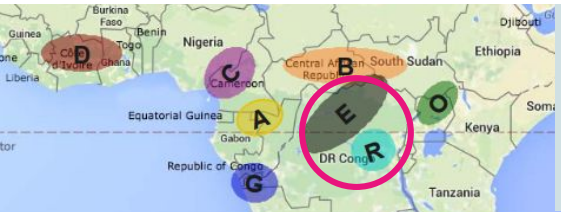


Figure 2. NJ tree based on Euclidean distance using 1.2M genome-wide SNPs



Conclusion

- 10 Vietnamese Robusta elite clones belong to the E and R groups (DRC).
- 1 clone presents ~25% introgression of group A and G (Cameroon-Gabon and Angola).

Perspectives

- Genetic characterization of large collection available in the germplasm bank of WASI
- ➔ Selection of elite parental genotypes for new breeding programs