



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

Vi Tram^{1,2}, Cubry Philippe¹, Marraccini Pierre^{1,3}, Dinh Thi Tieu Oanh⁴, Phan Viet Ha⁴, Zhang Dapeng⁵, Stoffelen Piet⁶, Vigouroux Yves¹, Poncet Valérie¹, Khong Ngan Giang²
¹ DIADE, Univ Montpellier, CIRAD, IRD, Montpellier, France ; ² AGI, Hanoi, Vietnam ; ³ CIRAD, UMR DIADE, Montpellier, France ; ⁴ WASI, Buon Ma Thuot, Vietnam ; ⁵ Sustainable Perennial Crops Laboratory, USDA-ARS, Beltsville, Maryland, United States ; ⁶ Meise Botanic Garden, Meise, Belgium



BACKGROUND

- Vietnam is the world's largest Robusta producer and exporter
- Challenges: Climate change, aging tree, abiotic and biotic stress
- Sustainable coffee improvement: new varieties with better adaptability

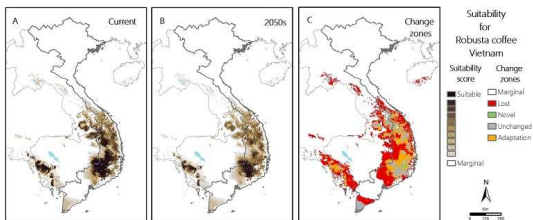


Fig 1: Suitability of Robusta in Vietnam in the present and future (CIAT)

It is important to understand the genetic diversity of Robusta coffee cultivated in Vietnam.

METHODS

- 126 Vietnamese accessions
- 127 African wild accessions (reference)
- Population structure analysis using 261 genome-wide SNPs
- Selection of a core set (45 accessions) by maximizing genetic diversity
- Detection of admixture segments in the core set accessions, using whole-genome SNPs

RESULTS

- Most of Vietnamese accessions are closely-related to group in **DRC (ER)**, and some are admixed with groups in **west Africa (D)**, **Cameroon-Gabon (A)**, and **CAR-Uganda (OB)**

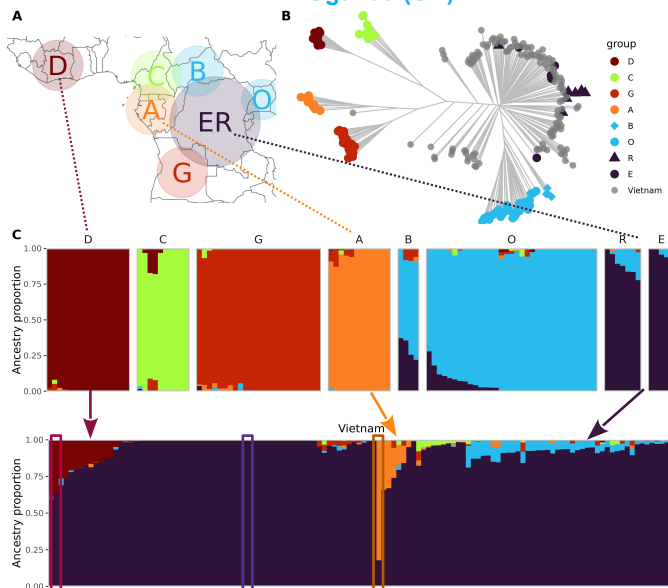


Fig 2: Population structure analysis of Vietnamese and wild accessions, using 261 genome-wide SNPs

CONCLUSIONS & PERSPECTIVES

- Diffusion and hybridization of multiple African sources
- Useful for selection of breeding materials

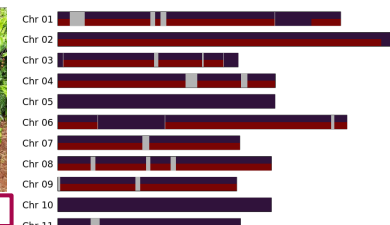
- A core set of 10 elite, 4 pure ER, and 31 admixed individuals with different backcross patterns were selected



TR15 (99% ER) – elite var.



S-75 (62.6% ER - 33.7% D)



S-122 (75.8% A - 16.4% ER - 3.3% OB)

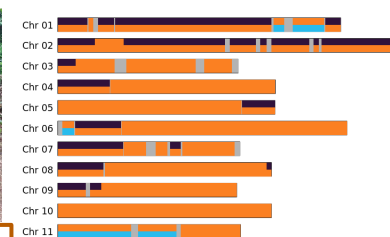


Fig 3: Three representative accessions in the core set, and their ancestral segments on the genome detected by using whole-genome SNPs