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# Conservation to use: Genetic characterization of the National Ugandan *C. canephora* collection

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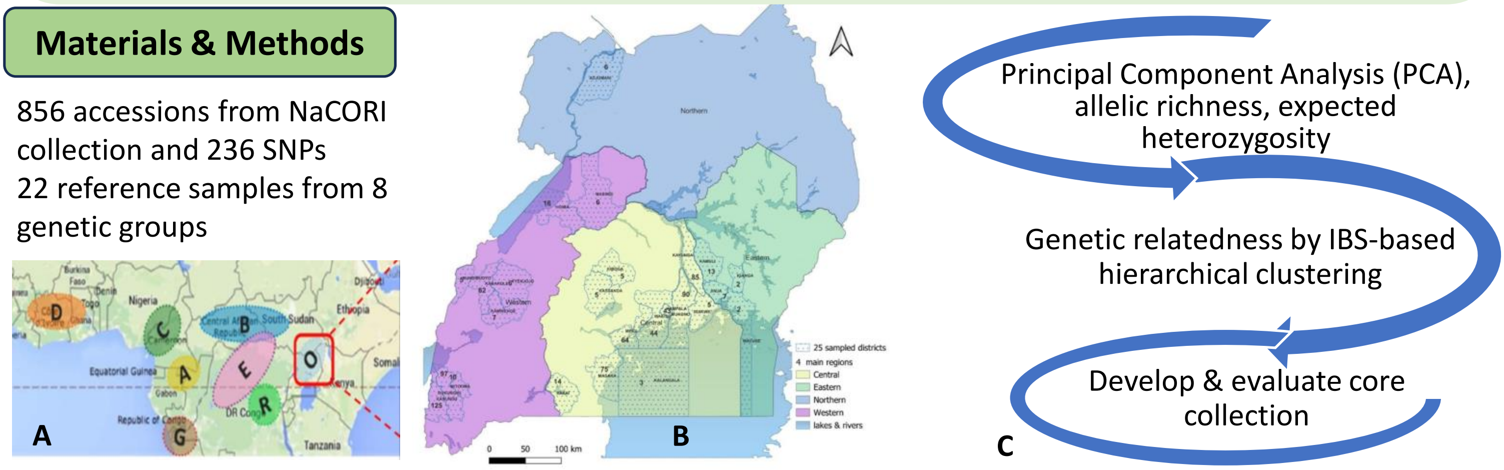
## Introduction

- Ex-situ collections play a key role in the conservation and sustainable use of plant genetic resources. Therefore, fundamental studies in genetics of these collections must be thoroughly conducted.
- Despite the importance of *C.canephora* globally, the genetic diversity and structure of many national collections remain insufficiently documented. This is also true for Uganda, Africa's largest coffee producer and known centre of diversity with a longstanding culture history of germplasm collection from diverse ecozones.
- The Ugandan collection (at NaCORI), which includes landraces and elite wild accessions offers a unique opportunity to investigate these aspects. This study aims to prove a comprehensive genetic assessment of the collection, identify potential gaps/redundancies, and inform its future use in breeding and research.

## Materials & Methods

856 accessions from NaCORI collection and 236 SNPs
22 reference samples from 8 genetic groups



Principal Component Analysis (PCA), allelic richness, expected heterozygosity

Genetic relatedness by IBS-based hierarchical clustering

Develop & evaluate core collection

**Figure1: Distribution of the global genetic groups (A – [1]); sampling sites for the cultivated Ugandan coffee (B) and the analysis conducted for this study (C)**

## Results/ Discussions

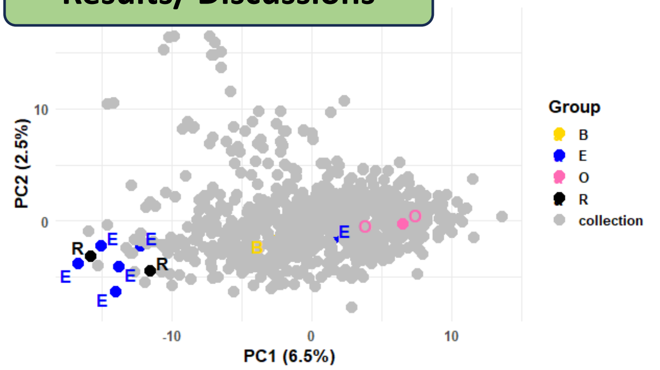


**Figure 2: Genetic positioning of NaCORI collection relative to the East African genetic groups**

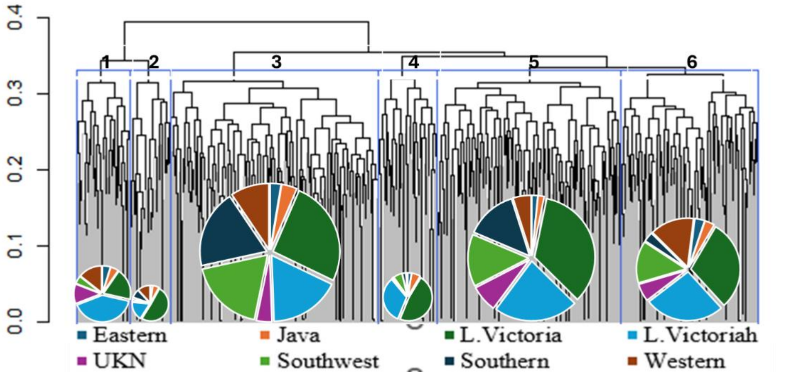


**Figure 3: Dendrogram revealing six clusters with individuals from diverse origins reflecting high admixture and weak population structuring (low fst)**

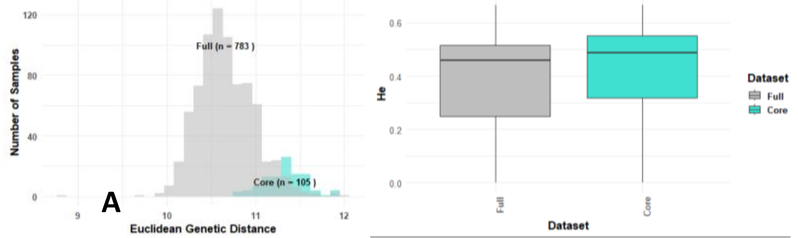


**Figure 4: Evaluation of the core collection (109) designed using corehunter3 [2] based on pairwise Euclidean distances (A) and expected heterozygosity (B).**
**It captured > 75% of the genetic variation**

## Conclusion/Perspectives

- NaCORI collection show a major affiliation to the to East African genetic groups and more specifically to "O" (from Uganda).
- Clustering does not reflect the sources of origin due to admixtures resulting from the long diffusion history.
- A core collection of 109 accessions captured over 75% of genetic variation, enabling efficient diversity conservation.

**References:**; [1] Kiwuka et al., 2021. https://doi.org/10.1371/journal.pone.0245965 **[2]** Beukelaer et al.,2018. https://doi.org/10.1186/1471-2105-13-312