



# Exploring the population structure and genetic diversity of *Moringa oleifera* using DArTSeq derived SNP markers.

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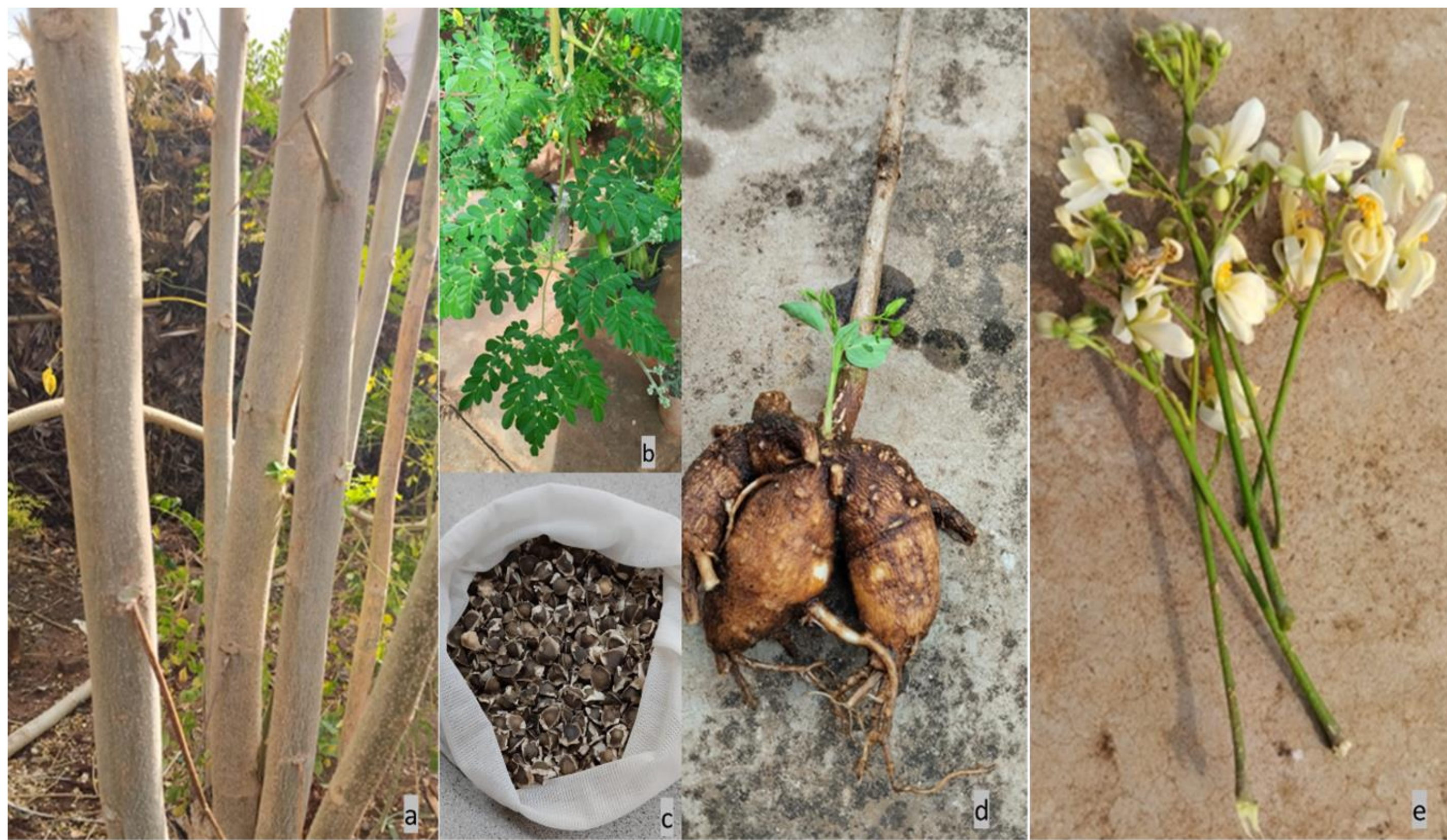
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## INTRODUCTION

- *Moringa oleifera* is a versatile tree native to the foothills of the Himalayas and now naturalized in the tropics.
- *Moringa* is nutritionally significant owing to its high nutrient and antioxidant content.
- Despite this and its increasing use as a fodder crop, wood fuel, medicine, an anticoagulant and a potential source of biofuel, the genetic diversity of *Moringa* across the tropics remains under investigated.



Images showing *Moringa* a) trunks b) leaves c) seeds d) roots and e) flowers

## OBJECTIVE

- This study was carried out to genotype 330 *Moringa* samples using Diversity array Technology (DArTSeq) generated Single Nucleotide polymorphisms.

## METHODOLOGY

- *Moringa* seeds samples collected from Africa, Caribbean and South-East Asia comprising 19 provenances from eight countries were planted at ICRAF tree nursery.
- Genomic DNA was isolated from 330 of the samples
- Quality analysis was done by nanodrop, qubit and gel electrophoresis.

- Complexity reduction
- Sequencing (HiSeq 2500 sequencer)
- Scanning to segregate poor quality markers
- Collapsing identical sequences into Fastqcoll files

- 3968 SNPs were filtered to a final set of 1913 markers
- Hardy Weinberg Equilibrium tests in Arlequin ver 3.5.2.2
- Genetic distance calculations in MSA ver. 4.05
- Constructed Neighbor Joining and bootstrap tree in PHYLIP ver. 3.695
- Genetic structure in STRUCTURE ver 2.3.
- PCA and AMOVA in GenAlex ver. 6.503

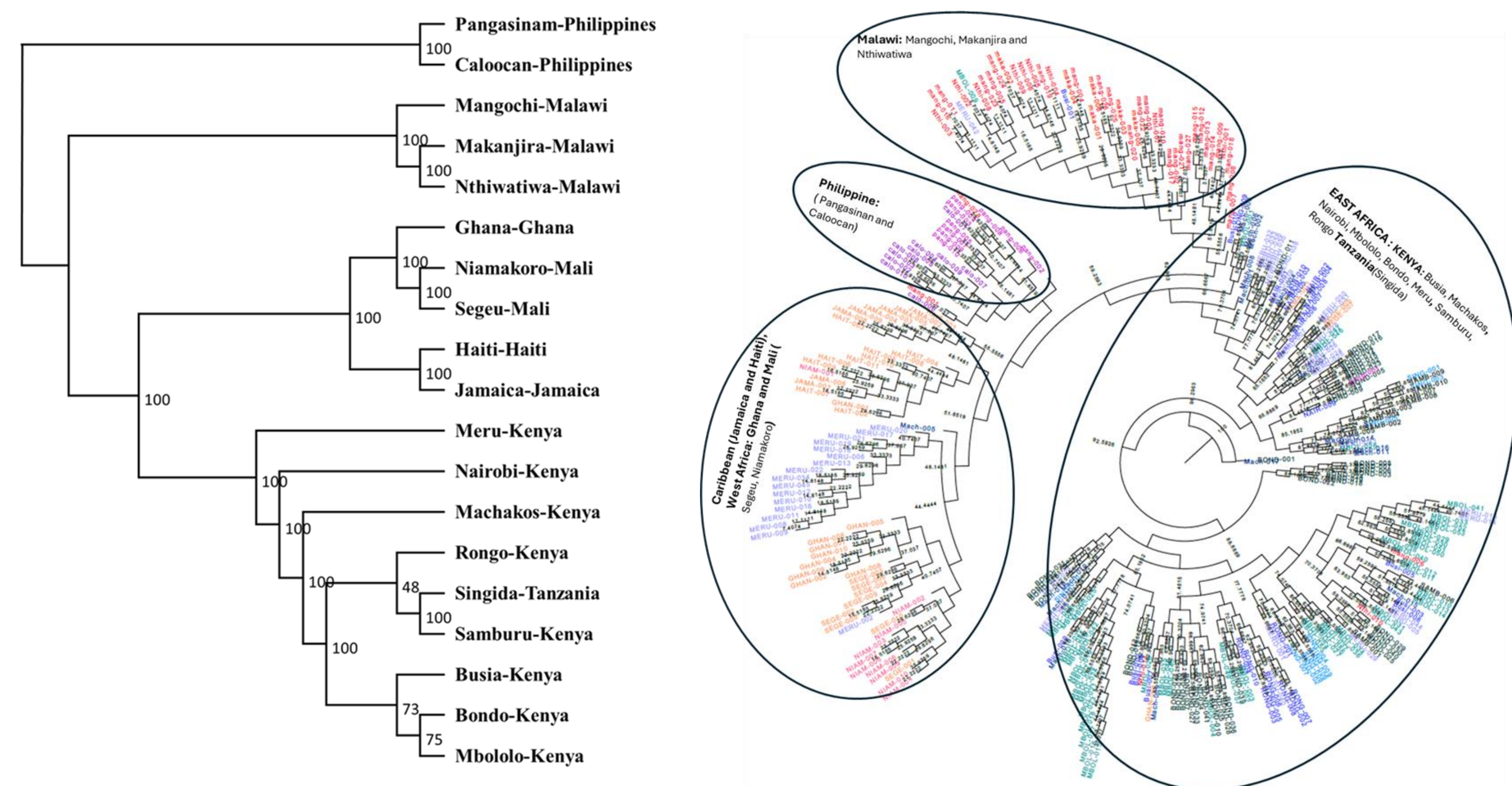
DNA ISOLATION

Genotyping by sequencing

Data analysis

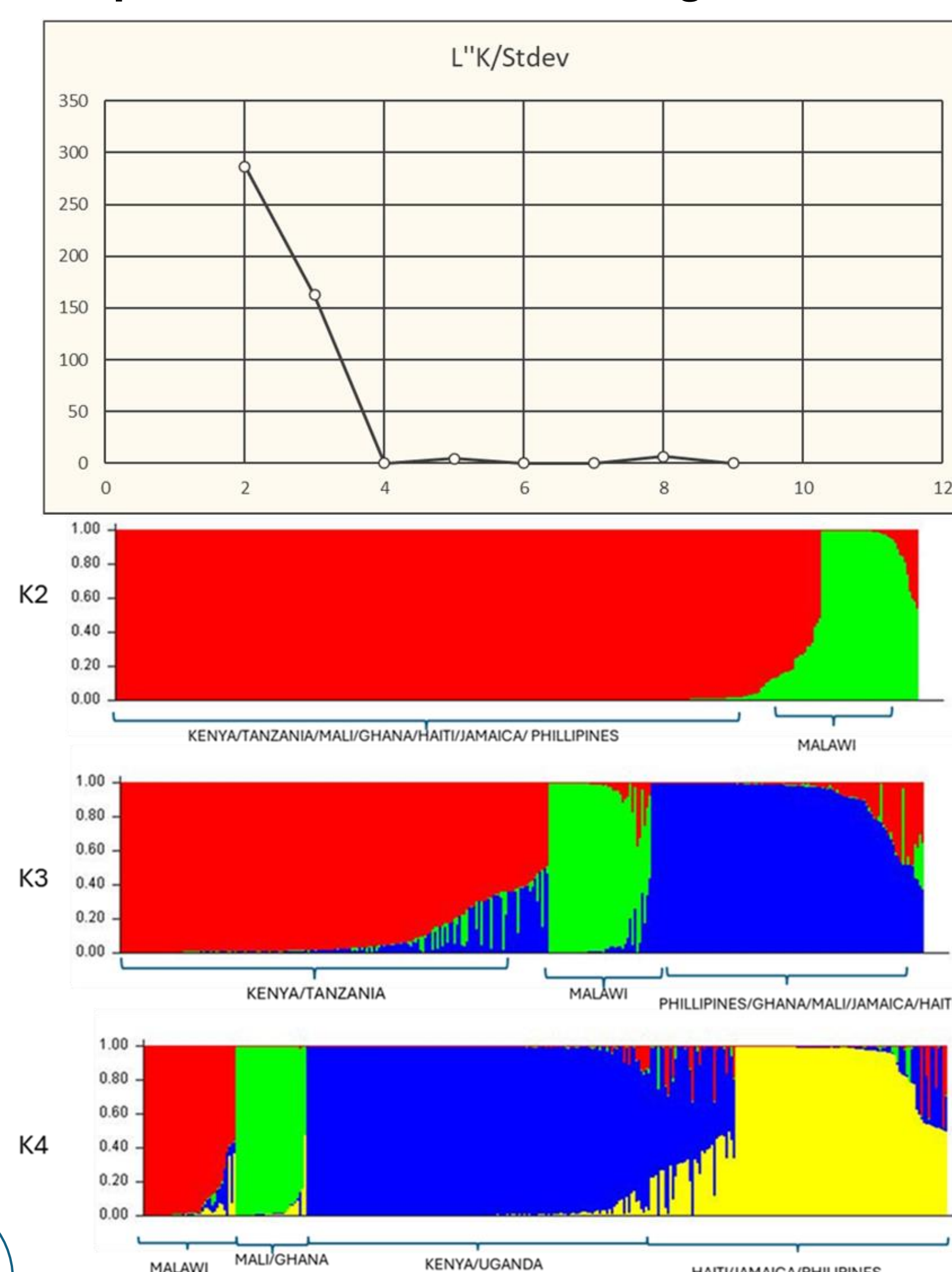
## RESULTS

### Genetic Diversity of *Moringa Oleifera*



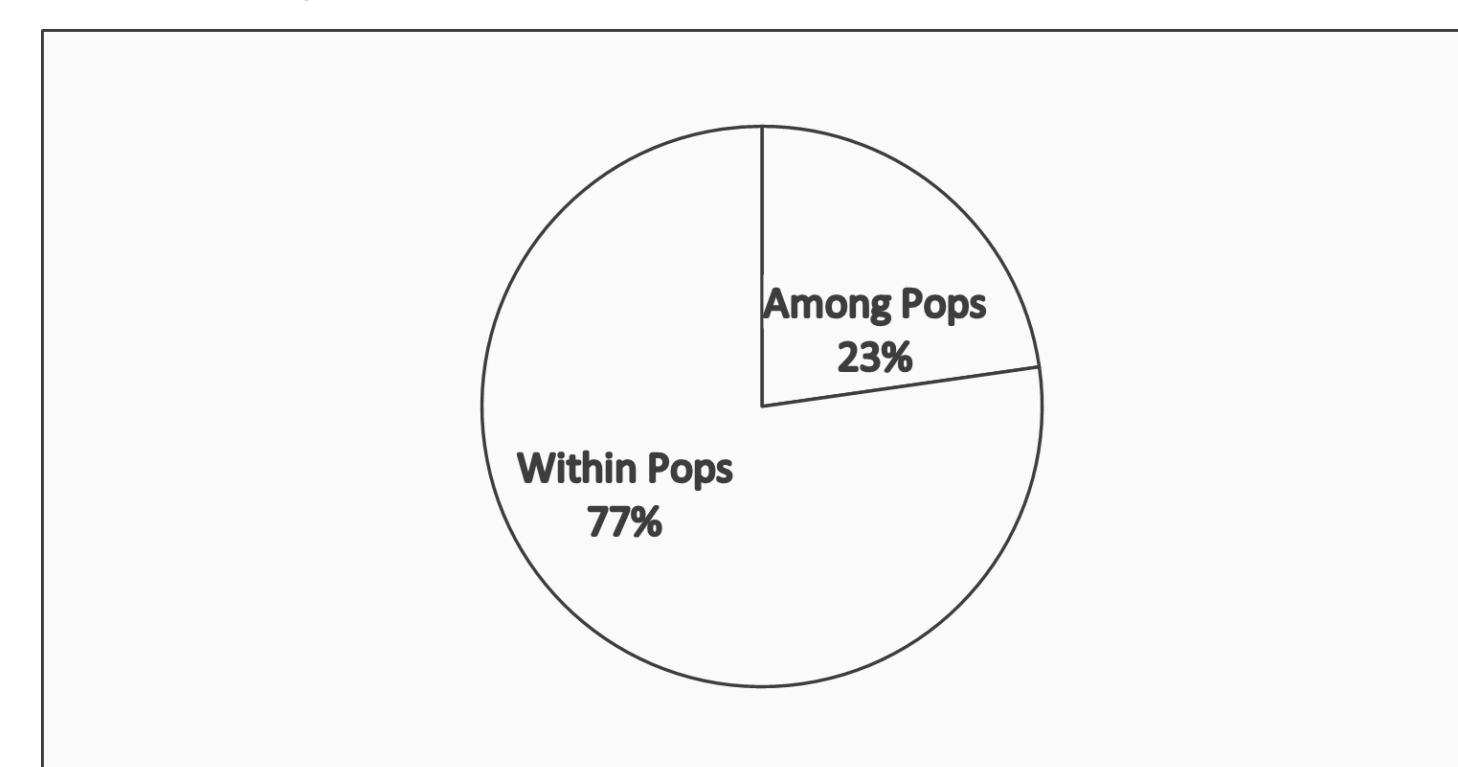
Neighbor joining population and individual sample trees showing genetic relationships among the 19 provenances and 330 accessions respectively using Nei's chord genetic distance.

### Population structure of *Moringa oleifera*



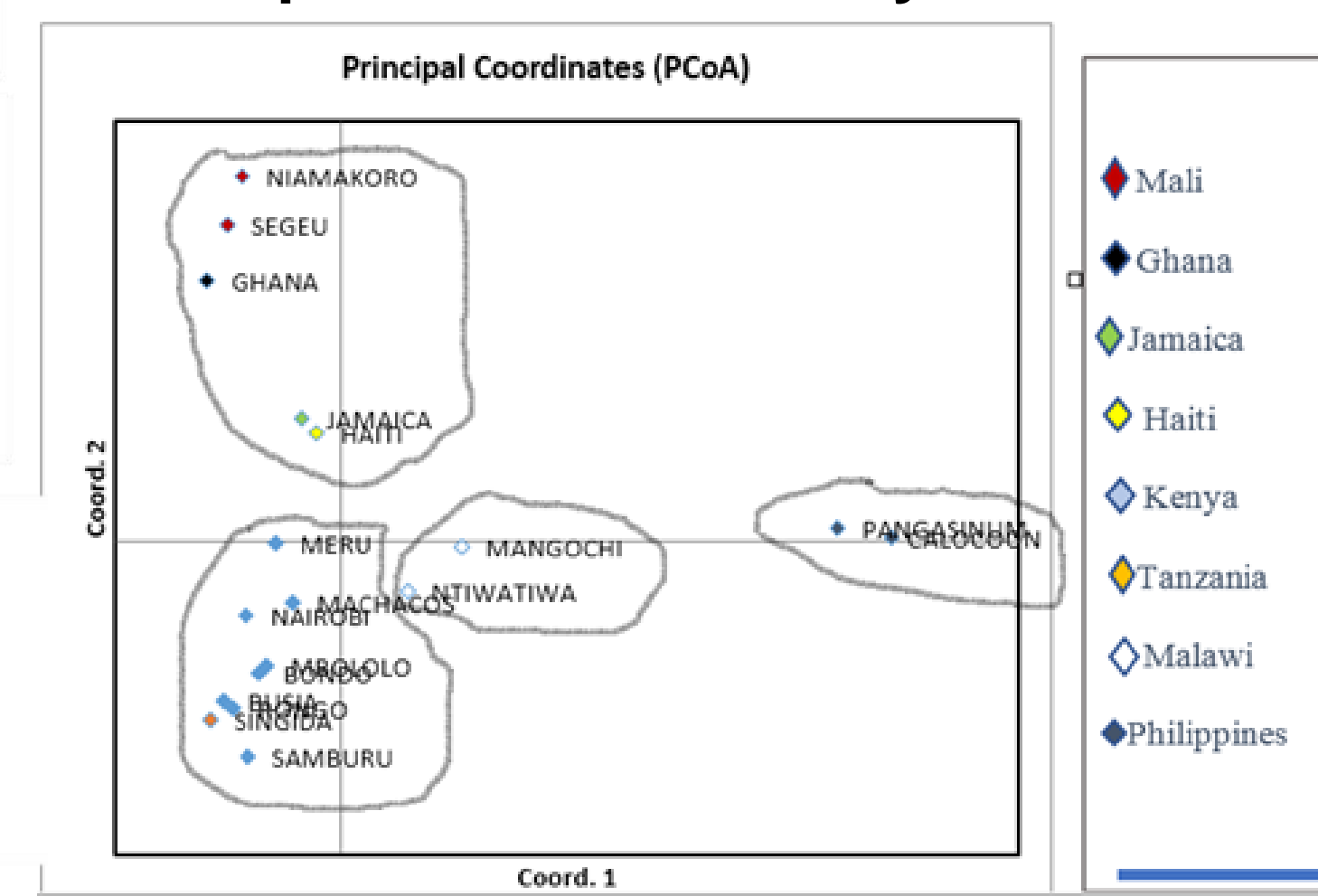
The maximum value in structure harvester was obtained at k=2 whereas k=3 and k=4 corroborates with neighbor joining dendrograms and PCA output

### Analysis of molecular variance



Indicates high intraspecific divergence within the populations ( 77% ) and a low divergence among the populations (23%).

### Principal coordinate analysis



Four cluster groups of the PCoA by provenance in GeneAlix.

## CONCLUSIONS

- Findings confirm Malawi and Philippines most diverse among African and rest of the populations respectively.
- East African and Caribbean population are subsets of the Western Africa population.
- A notable admixture of entries not complying with geographical distribution is typical to unnatural mixing conceivably through anthropogenic events.
- minimal genetic diversity among most of the African populations; small number of *Moringa* accessions introduced from India to Africa served as founder population.
- These findings have implications for *Moringa* germplasm collection, improvement, conservation, utilization strategies and policies.

