

GENETIC DIVERSITY AND POPULATION STRUCTURE OF SHEA TREES FOR ESTABLISHING A CORE COLLECTION IN CÔTE D'IVOIRE

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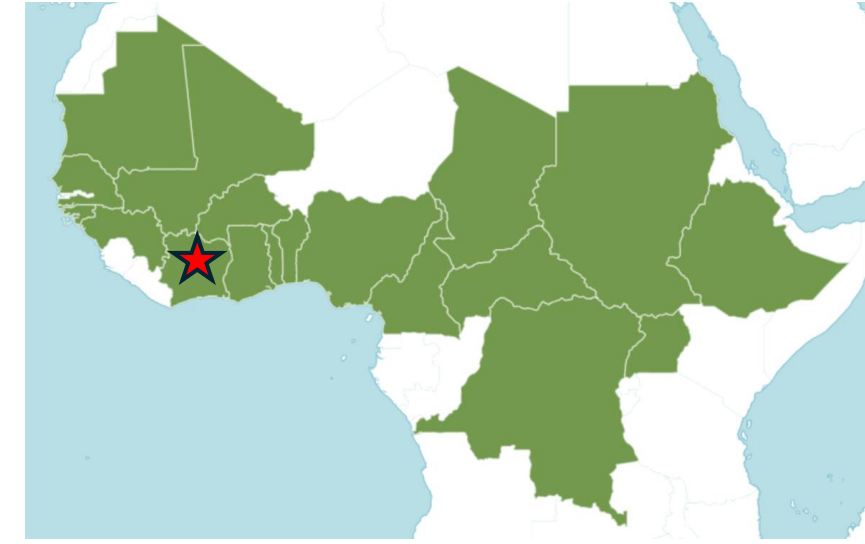
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Context and objectives

- ✓ *Vitellaria paradoxa*: African native plant species
- ✓ Global market of shea in 2020: \$30 billions
- ✓ Contribution to women autonomy in its natural range
- ✓ Carbon sequestration and substantial carbon reserve



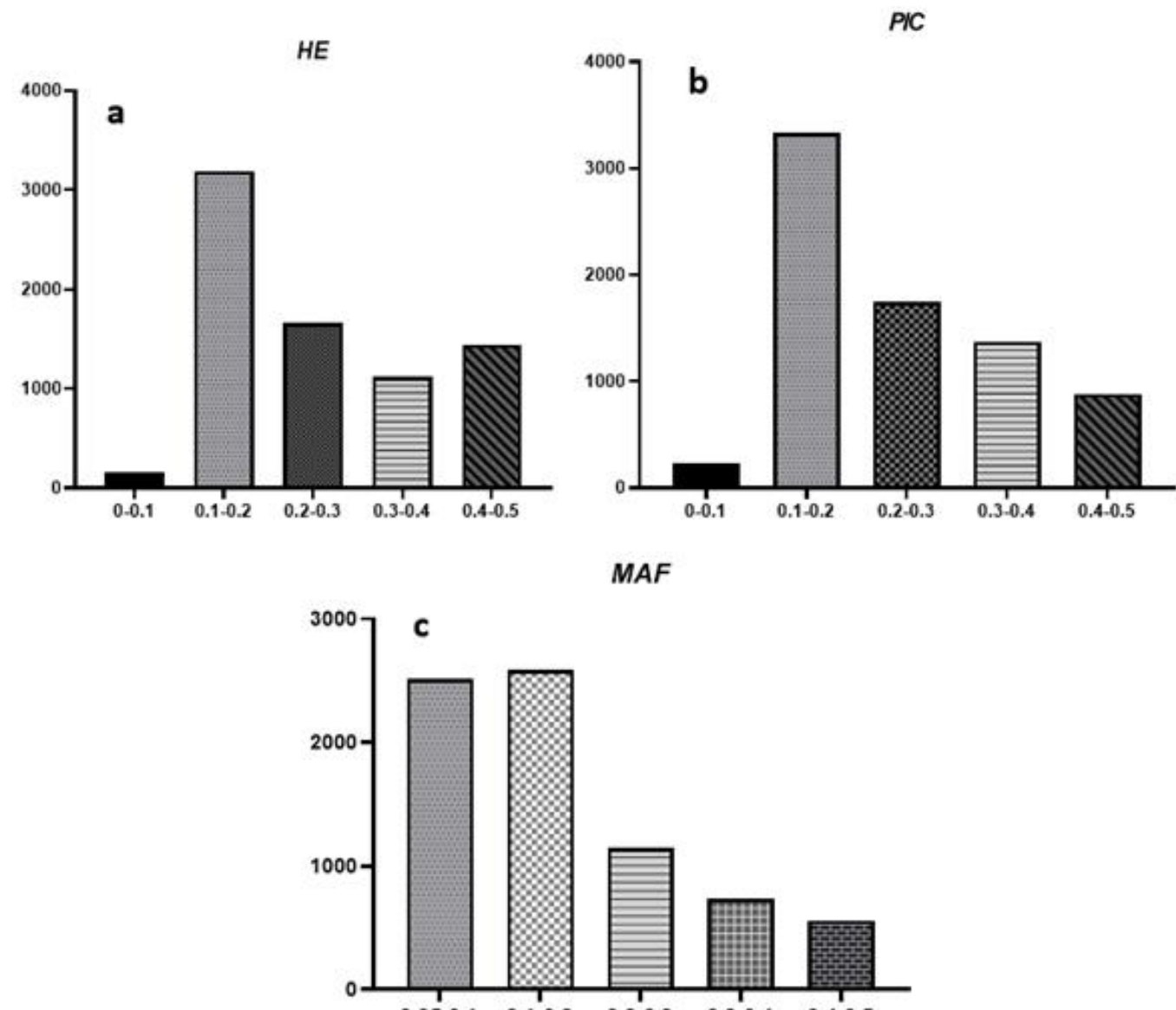
- ❖ **Threatened species**: abusive use of shea, lack of regeneration.
- ❖ **Consequence**: loss of important genotypes
- ❖ **Actions**: Identification and in situ collection
- ❖ **In situ collections challenges**: difficult and expensive to manage.



- **Objectives**: In this study, we used SNP markers to assess the genetic diversity and the structure of the *in situ* collection of shea trees to design a core collection. This core will contribute to the sustainable conservation of the species.

Results

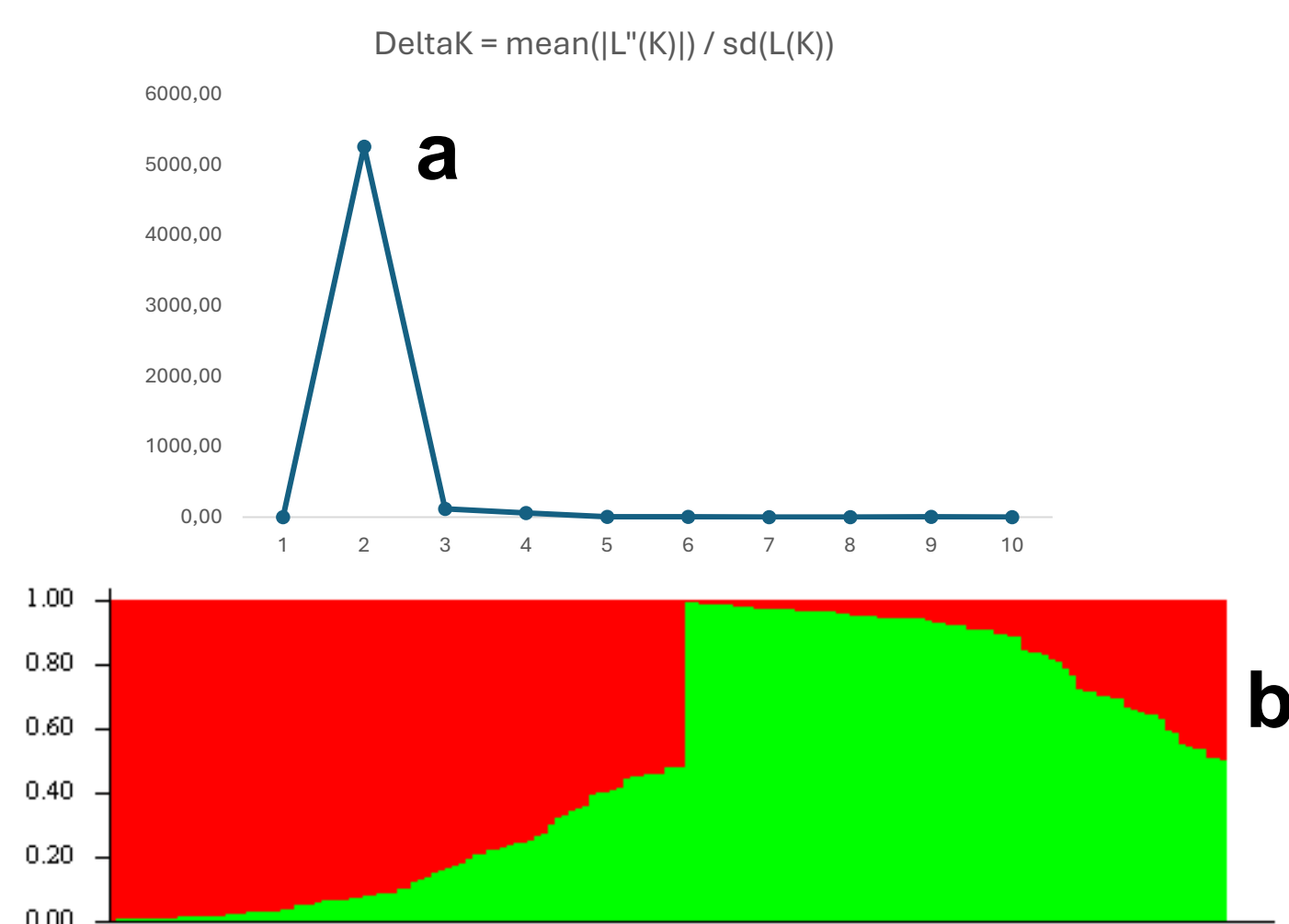
Genetic diversity of Shea Tree using SNP markers



- Ho: 0.17
- He: 0.26
- PIC: 0.24
- MAF: 5,104 SNPs (67.5%) > 0.1
- ✓ Moderate genetic diversity

Figure 1: Distribution of genetic diversity

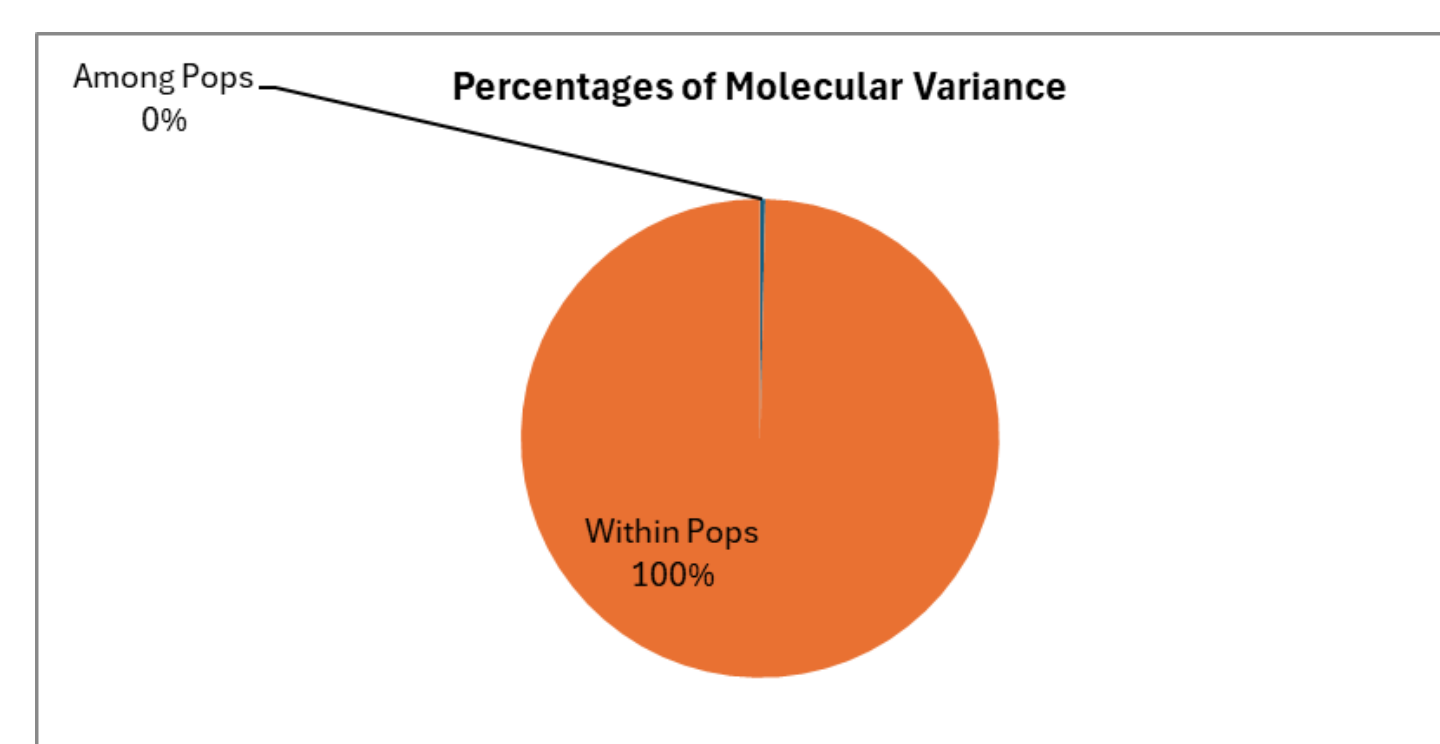
Population structure and Genetic relationships



- Two genetic groups
- Presence of admixtures
- ✓ Extensive gene flow

Figure 2: Genetic structure of the 163 shea trees

Genetic Differentiation of Populations



- Fixation index (Fst): 0.003
- Nm (Haploid): 71.6
- ✓ Low genetic pop. Differentiation
- Semi-domestication
- Out-crossing

Figure 3: Analysis of molecular variance Among genetic groups

Construction of a Core Collection

- 51 Superior shea trees, representing 31%

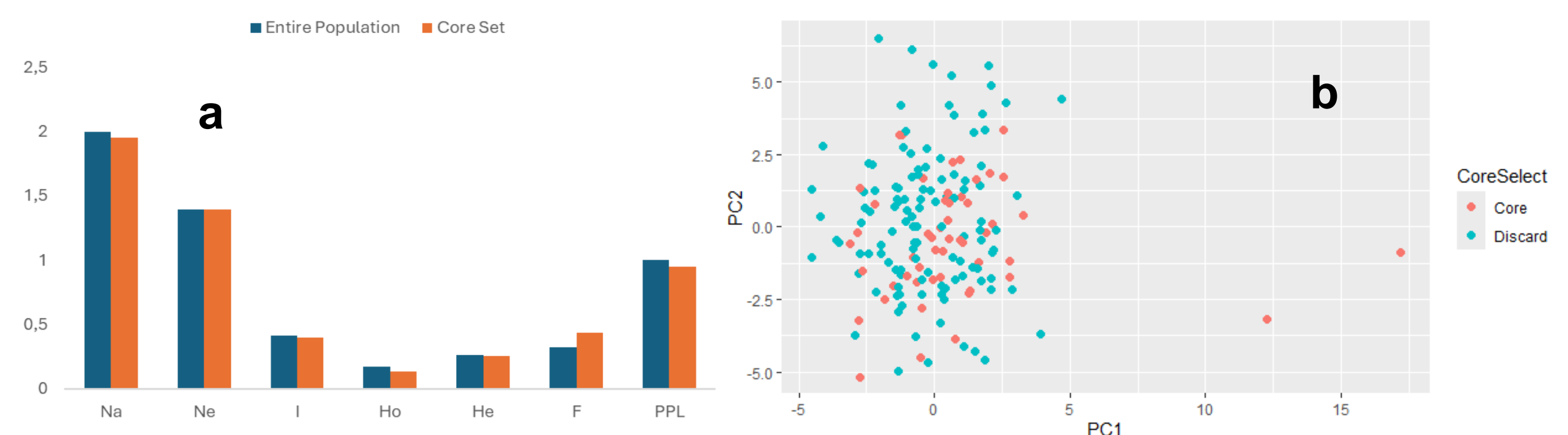


Figure 4: a) Means of genetic parameters in the core set and full panel; b) Distribution of the core set

- ✓ Core set captures the full genetic diversity
- ✓ Robust subset for: conservation, genetic studies and breeding

Methods

- ❑ DNA extraction: NucleoMag Plant kit
- ❑ Genotyping: **DARtseq**
- ❑ Markers: **7559 SNPs**
- ❑ Clustering: **Structure Software (2.3.4)**
- ❑ AMOVA: **GeneAlex version 6.503**
- ❑ Core construction: of **DARwin software version 6.0.21** "Maximum length sub-tree function"
- ❑ PCA: **R version 4.3.3.**

Conclusion

- ✓ Moderate Genetic Diversity of the superior shea trees
- ✓ Two genetic groups
- ✓ Low populations differentiation
- ✓ High-quality core set for suitable conservation and future breeding programs

Perspectives

- ✓ Creation of ex-situ collection for appropriate conservation
- ✓ Perform GWAS to identify quantitative trait nucleotides associated with important agronomic traits

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