

Genetic Diversity of Garcinia kola (Heckel) in Southwest Cameroon

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Introduction

Garcinia kola (Clusiaceae) is an indigenous fruit tree, originating in Western and Central Africa. It is a highly valued medicinal plant with all its parts being useful in traditional medicine (treatment of inflammation, liver cirrhosis, hepatitis, diarrhoea, headaches, etc.)[1]. Despite the tree's frequent usage, its domestication process is at its beginning and seeds are still mostly harvested from the wild [2], which can lead to endangering of the species. Previous studies of *G. kola* have described the bioactive substances and nutritional content [3,4], however, information on genetic structure of existing populations which is crucial for domestication and conservation efforts of the species, is lacking.

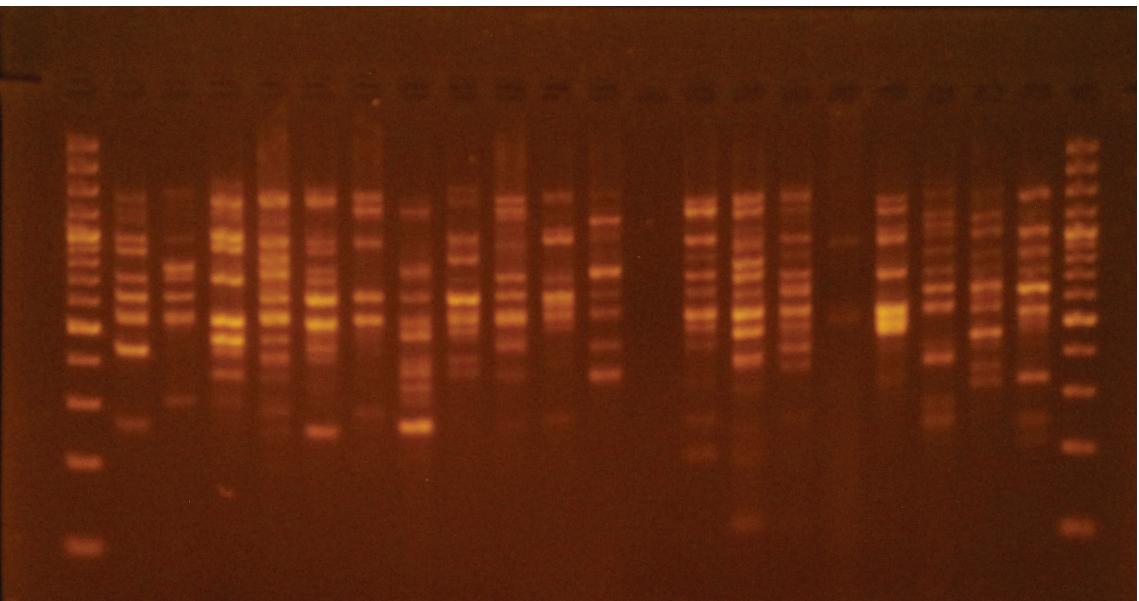
Materials and methods

75 individuals from 4 populations (Lebialem, Mamfe, Tombel and Kumba) (Figure 1) were sampled in the Southwest province of Cameroon and DNA was extracted from the seed coat. Twenty arbitrary RAPD primers were used for screening, and seven were chosen for final analysis based on polymorphism shown. PCR products were visualised on agarose gels and bands scored for presence or absence (Figure 3). The data was analyzed by POPGENE 1.32 [5] and Fig Tree 1.4.3.

Objectives

The main objective of this study was to assess the genetic diversity and population structure of farmer's accessions of *Garcinia kola* from Southwest region of Cameroon.





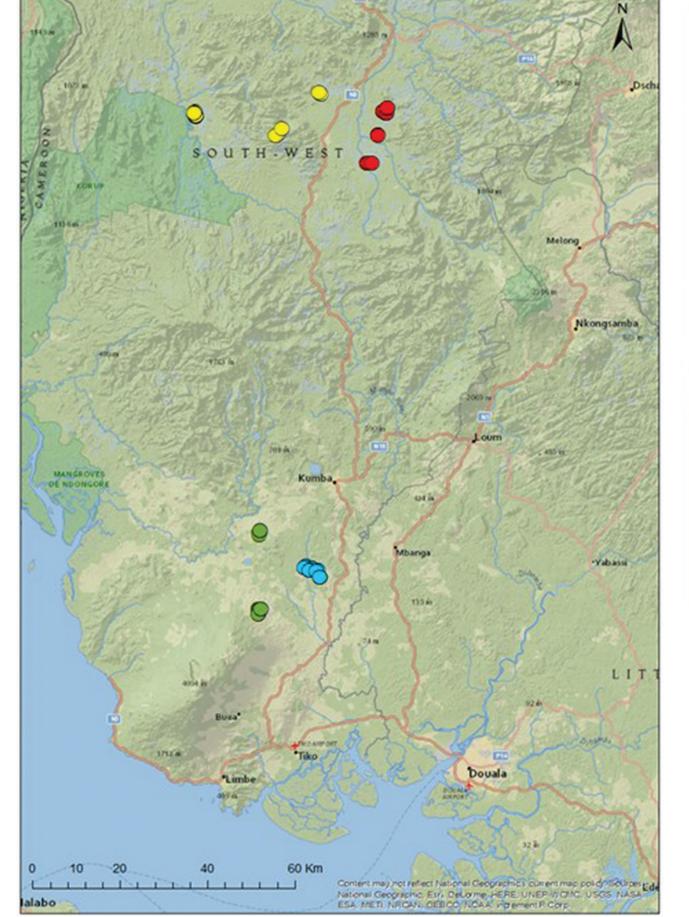


Figure 1. Locations of sampled trees

Populations • Lebialem • Mamfe

Tombel

Kumba

• Kumba



Figure 3. Example of a RAPD profile for analyzed individuals of *G. kola* (primer OPAI6)

Results

A total number of 135 loci were obtained, showing 100% polymorphism (Table 1). The overall values of Nei's gene diversity and Shannon's diversity index (h=0.20, I=0.34) indicate high levels of genetic diversity in the sampled individuals (Table 2). However, the index of Nei's genetic distance between populations reached very low values, showing lack of population structuring. The division of populations by UPGMA dendrogram reflected their geographical and altitudinal distances (Figure 2).



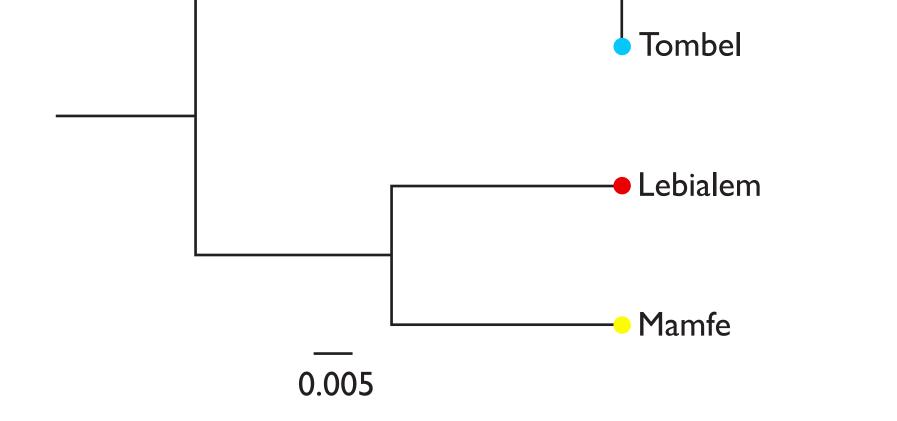


Figure 2. UPGMA dendrogram based on Nei's genetic distance showing relationships between populations of *G. kola*

Table 1. Genet	tic diversity in analysed po	pulations of G. kola		
Population	nr polymorphic loci	%polymorphic loci	h	Ι
Kumba	121	89.63%	0.1940	0.3239
Lebialem	129	95.56%	0.1889	0.3372
Mamfe	122	90.37%	0.2037	0.3355
Tombel	128	94.81%	0.1868	0.3184
Overall	135	100%	0.2028	0.3431

h: Nei's gene diversity index, I: Shannon's information index

Table 2. Nei's genetic identity (above diagonal)and genetic distance (below diagonal) between pairs of populations of *G. Kola*

pop ID	Kumba	Lebialem	Mamfe	Tombel
Kumba	****	0.9929	0.9922	0.9945
Lebialem	0.0072	***	0.9923	0.9926
Mamfe	0.0078	0.0077	****	0.9918
Tombel	0.0055	0.0075	0.0082	* * * *



Conclusions

Results obtained in this study present values that are quite typical for natural populations with low selection and domestication pressure. This study represents the first report to describe population genetics of *G. kola*. The results, together with morphological and biochemical data, can lead to better management and utilisation of *G. kola* genepool.

References

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