Tropentag,
September 15-17, 2021
University of Hohenheim,
Germany

The population structure of *Garcinia kola* Heckel in Central region of Cameroon

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Introduction

Garcinia kola is a multipurpose fruit tree species indigenous to West African communities (Fig. 1). It is of significant ethnomedicinal, cultural and economic importance **[1]**. All plant parts have known medicinal uses (Figs. 2,3,4). Faced with the threat of declining population numbers **[2]**, the species was selected for conservation and participatory domestication programmes **[3,4]**. However, a lack of adequate information on genetic diversity is widely reported as a limiting factor in both processes **[2]**.

Figure 1: The distribution range of *G. kola* [2]

Figure 2: Tree crown with fruits

Figure 3: Fruit pulp and seed

Figure 4: Seeds at varying stages of maturity

Objective

The aim of this study was to assess the genetic diversity of *G. kola* individuals in the Central region of Cameroon, using Amplified Fragment Polymorphism (AFLP) markers.

Materials and Methods

Leaves were collected from 96 accessions, distributed across eight geographic populations. Genomic DNA was extracted and then digested with *Mse*I and *Eco*RI endonucleases. From initial 24 primers, four high-performing primer combinations were selected to assess genetic diversity within and among the eight provenances of *G. kola* with AFLP markers.

Acknowledgements

Various kinds of support were provided by the Faculty of Tropical AgriSciences, Department of Crop Sciences and Agroforestry and the World Agroforestry Centre (ICRAF).

References

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Results

A total of 1176 fragments were amplified with 98.6 % polymorphism at the species level. The computed values for Nei's gene diversity within populations (*Hj*), Total gene diversity (*Ht*), and the Wright's fixation index (F_{ST}) were 0.189, 0.192 and 0.0145 respectively (Table 1). The obtained results revealed a higher genetic diversity within the assessed populations than among them. Bayesian analysis of sampling groups revealed the existence of two differentiable but admixtured genetic clusters, implying a weak population structuring. The predominance of genetic cluster II (Green) increased from North towards the South, with increasing rainfall (Fig. 5). The existence of two genetic clusters is supported by recent studies of some Benin and Nigerian populations **[5,6]**. Prevalent seed kernel trade practices within the study area show expansive human-mediated seed dispersal **[7]**. This may be influencing genetic diversity through increased gene flow events.

Table 1: The genetic indices of the sampled population groups in Central region of Cameroon

Population	#loc_P	PLP	*Hj*
Akok	744	63.3	0.19504
Bokito	745	63.4	**0.21307**
Ebogo	631	53.7	**0.16851**
Lekiasi	661	56.2	0.19933
Bot-Makak	816	69.4	0.19223
Nkelikok	619	52.6	0.18360
Saa	433	36.8	0.19119
Ebolowa	723	61.5	0.17250
Mean Value	**671.5**	**57.11**	**0.18943**

Where*: #loc_P*= number of polymorphic loci at 5 % level; *PLP*= proportion of polymorphic loci at the 5 % level, expressed as a percentage; *Hj*=expected heterozygosity under the Hardy-Weinberg genotype proportions.

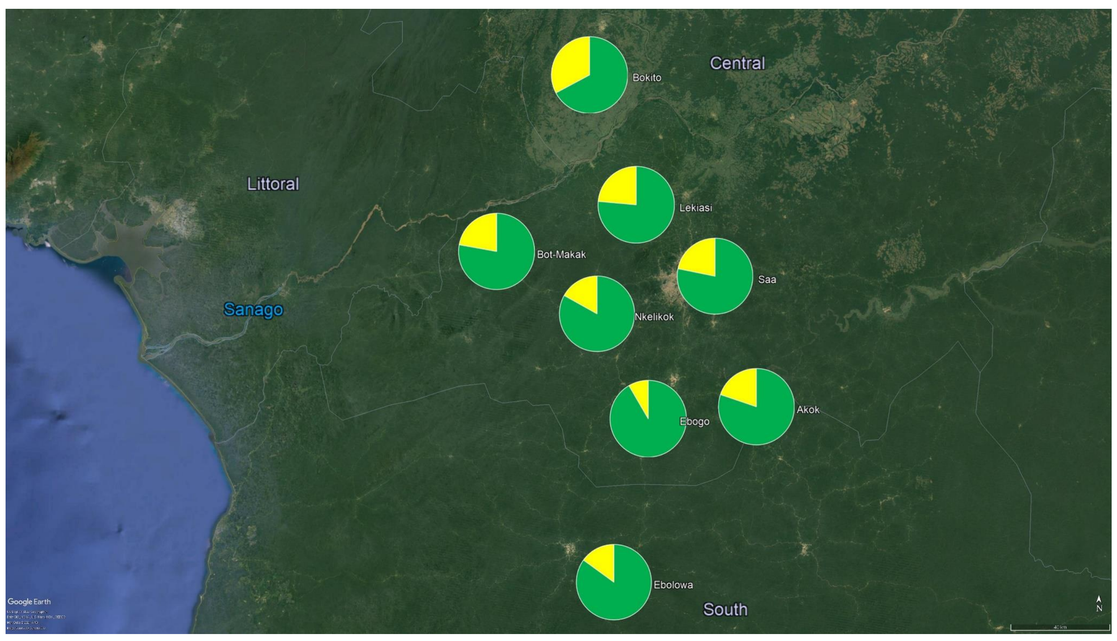

Figure 5: The Bayesian clustering of individuals among populations for a K value of 2. (Genetic cluster I-Yellow, Cluster II-Green)

Conclusion

The present results point to a potential existence of two diverging provenances within the study area. There exists a high level of genetic diversity within the studied *G. kola* populations with a relatively lower level of genetic diversity among the populations. Overall, the observed genetic diversity is viewed as a positive scenario for the conservation efforts within the study area. It is recommended that the existing genetic diversity is preserved through the use of gene banks. Assessments of the *G. kola* genetic diversity should be expanded to peripheral areas, which are not hotspots.

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