

African Mainland Baobab *Adansonia digitata* Suffers from Extremely Low Genetic Diversity and Genetic Erosion

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Abstract:
African mainland baobab (*Adansonia digitata*) is an iconic tree spread throughout the African continent. It occupies a special position across various cultures and societies in sub-Saharan Africa due to its wide-spread multiple uses including food, feed, and medicine. In this study, a total of 320 paired half sib individuals belonging to 17 different populations collected across four African countries (Kenya, Tanzania, Malawi and Mali) were genotyped using a total of 4,617 DArT-SNP (single nucleotide polymorphism, <https://www.diversityarrays.com/technology-and-resources/dartseq/>) markers. They were filtered to get a set of high quality 137 SNPs for diversity and population genetics analyses. Nei's genetic distance was estimated using MicroSatellite Analyzer v4.05 and replicated for 100 bootstraps. Further using 'neighbor' and 'cons' commands in PHYLIP v3.695 neighbour-joining (NJ) tree(s) and consensus tree for 100 bootstraps were built and viewed using FigTree v1.4.3 (<http://tree.bio.ed.ac.uk/software/figtree/>). This indicated five major groups; three Zambian (ZAM) and one each Malian (MAL), and Kenyan-Tanzania (KNTZ). The least diverse was the KNTZ followed by MAL and the most diverse was ZAM (Figure 1). Only 18 loci were in Hardy-Weinberg Equilibrium (HWE), whereas 16 were in heterozygosity excess and 66 were in heterozygosity deficiency as revealed by ARLEQUIN v3.5.3 and GenePop v 4.7.5.4. These tests indicated that the studied populations were under severe heterozygous deficiency and possibly indicate rapidly shrinking genepool and extremely low genetic diversity. Further genetic differentiation analyses indicated that majority of sub-populations have significant genetic differentiation from each other generally correlated with geographically distance by the FST (~95%) as well as by Exact G-test (~83%) analyses. This indicated genetic fragmentation of these sub-populations despite some of them being geographically closer e.g. Malindi and Taitaveta sub-populations from Kenya (physical distance of 188 Km). This calls for very urgent interventions to conserve genetic diversity and possible population collapse.

Introduction

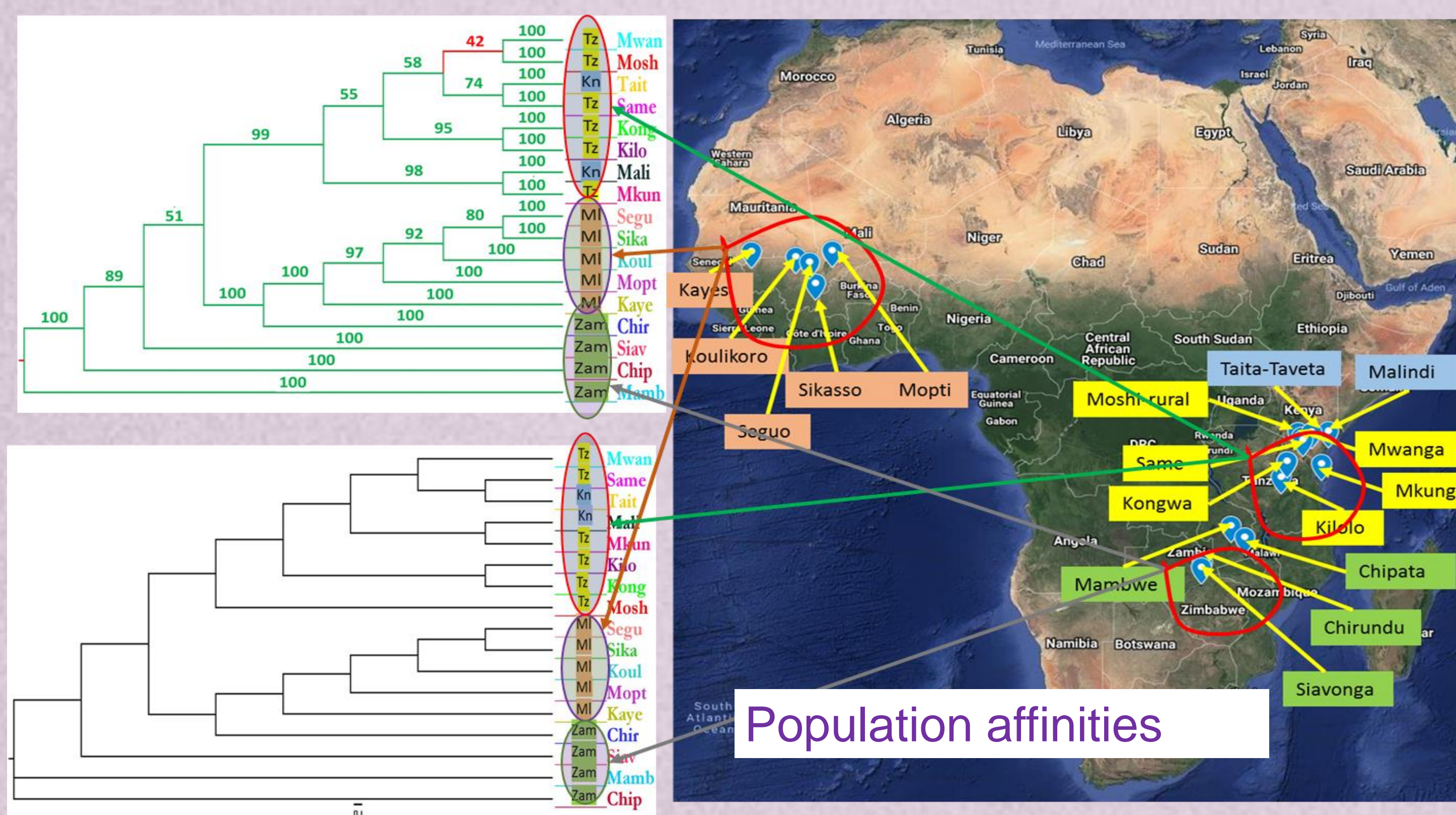
Baobab (*Adansonia digitata*) is a deciduous tropical tree which remains uncultivated and undomesticated due to its slow growth habit, large unmanageable size and shape, very long juvenile period, wide phenotypic variability for fruit size, shape, taste, acidity, yield etc., and lack of proper management practices. Thus, with an aim to domesticate and improve it, the World Agroforestry (CIFOR-ICRAF, Nairobi), is establishing a genebank representing African collections by developing a breeding and improvement program based on advanced genomics tools. This study was planned with objectives to-

1. Analyze extant genetic diversity in baobab collections of ICRAF genebank using DArT-seq based SNP markers.
2. Study population behavior of the sampled populations

Materials and methods

- A total of 4,617 DArT-SNPs were generated, over 320 accessions (Kenya= 12, Tanzania (with Zanzibar)= 159 (4 from Zanzibar), Zambia= 56, Mali= 93) with 138 high quality SNP markers for the final analysis.
- The data was analyzed to estimate Nei's genetic distance (1983) using MicroSatelliteAnalyzer (MSA4.05, Dieringer, 2003), Neighbour Joining (NJ) tree drawn for 100 bootstraps using PHYLIP3.695 followed by consensus tree.
- Hardy Weinberg Equilibrium (HWE) analysis was performed in Arlequin ver 3.5.2.2 (Excoffier & Schneider 2005) and Structure ver 2.3.4 analysis (Pritchard et al. 2000).
- Other population genetic analyses were performed using GenePop v4.7.5.4 (Rousset F (2008)).

Results & Discussion



- There are five major groups; three Zambian (ZAM) and one each Malian (MAL), and Kenyan-Tanzania (KNTZ). The least diverse was the KNTZ followed by MAL and the most diverse was ZAM (Figure 1).
- Only 18 loci were in Hardy-Weinberg Equilibrium (HWE), whereas 16 were in heterozygosity excess and 66 were in heterozygosity deficiency as revealed by ARLEQUIN v3.5.3 and GenePop v 4.7.5.4. These tests indicated that the studied populations were under severe heterozygous deficiency
- Genetic differentiation analyses indicated that majority of sub-populations have significant genetic differentiation from each other generally correlated with geographically distance by the FST (~95%) as well as by Exact G-test (~83%) analyses.
- Majority of the Kenyan-Tanzania and Zambian populations and half of the Malian populations have undergone significant bottlenecks.
- Thus, all these parameters possibly indicate rapidly shrinking genepool and low genetic diversity in the populations.

Conclusions

- The results indicated fragile nature of *Adansonia digitata* populations in Africa due to habitat loss, population fragmentation and genetic erosion.
- This calls for immediate conservation measures for African mainland baobabs.

References

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