Genetic diversity of baobab (*Adansonia digitata* L.) accessions along an elevation transect in Kenya

Anna Chládová¹, Bohdan Lojka¹, Marie Kalousová¹, Bohumil Mandák², Jakub Houška³, Katja Kehlenbeck^{4,5}

 ¹ Czech University of Life Sciences Prague, Faculty of Tropical AgriSciences, Prague, Czech Republic
² Czech University of Life Sciences Prague, Faculty of Environmental Science, Prague, Czech Republic
³ Czech University of Life Sciences Prague, Faculty of Agrobiology, Food and Natural Resources, Prague, Czech Republic

⁴ Rhine-Waal University of Applied Sciences, Fac. of Life Sciences, Kleve, Germany

⁵ Tree Diversity, Domestication and Delivery, World Agroforestry Centre (ICRAF), Nairobi, Kenya

Adansonia digitata L. (Malvaceae) is a huge multipurpose tree of the savannahs of sub-Saharan Africa, with high economic potential for local communities. The edible fruits and leaves are known for their high nutritional values and can be used fresh or processed. However, a high intra-specific variability regarding morphology, genetics and nutritional content of baobab and its products is documented for several African regions, while data for Kenya is largely lacking. This study aimed at documenting the genetic and morphological variability of baobab accessions in Kenya and at checking the presence of the newly described diploid baobab species *Adansonia kilima*. Samples were collected from 204 baobab trees from seven populations defined by geographical distance in South-eastern and Coastal Kenya at altitudes of 6-1,058 m asl. Leaf or bark samples for genetic diversity assessment were collected from all 204 trees, while leaves only from 65 and fruits from 76 trees (all in inland locations) for morphological analyses based on the publication 'Descriptors for Baobab'. Nine microsatellite loci were used to assess genetic variation and results analysed with specific software because of the tetraploid nature of baobab.

Overall genetic diversity was high and all loci were polymorphic. The mean gene diversity was 0.803 and observed heterozygosity was 0.907. Analysis of molecular variance (AMOVA) revealed low variation among populations (12.4%) and high variation within populations (87.6%). Bayesian clustering and Principal Coordinate Analysis (PCA) divided the accessions into two clusters, one with only inland and one with coastal accessions. Although the presence of *Adansonia kilima* was previously postulated for Kenya, flow cytometry did not detect any among the analysed samples as only tetraploids were observed.

Regarding morphological characteristics, no differences among the accession from inland populations were found (no fruits were collected in coastal areas). Leaf morphological data showed significant differences between inland and coastal populations with longest leaflets and leaf petioles in accession from the Coast, thus confirming the results obtained for genetic analysis. This study contributes to the overall knowledge of the genetic diversity of baobab in Kenya and can contribute to the development of germplasm conservation strategies and domestication programs for baobab.

Keywords: conservation, domestication, genetic markers, microsatellites (SSR), morphological diversity