Understanding the relationship between morphological traits and genetic diversity of *Vitellaria paradoxa* (Sapotaceae) in Cameroon

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Abstract

Vitellaria paradoxa C.F. Gaertn (Sapotaceae) is a keystone species of the parkland agroforestry system that extends across the wooded savannah of Cameroon, providing a range of environmental services at the landscape level and nutritional and livelihood resources for smallholder farming communities - particularly the rural women who gather its nutritious fruit, and process the kernel into shea butter. At the same time, the species is classified as vulnerable.

However, previous studies were limited to the phytochemical content of the shea butter, and they could not address the evident morphological diversity of the species, including fruit traits - identified as a significant driver for farmer selection and sustainable management of the species on farmed parkland. Of particular note is a provenance found only in the West region of Cameroon, which appears to be facing extinction. But other origins are also distinctive according to traits. The general objective of this study was to assess the morphological features in the characteristics of the shea tree and fruit in the selected sampling locations in Cameroon (western highlands, Guinean high savannah, Soudano-Sahelian). A total of 167 trees were randomly selected, and 2,211 kernels were collected at three agroecological sites. The trees sampled in the three populations were 60, 65, and 56, respectively. The measured fruit traits were kernel length, weight, width, DBH, crown diameter, and height. The data was analysed using Principal Component Analysis and hierarchical clustering. Preliminary results revealed three dominant clusters related to the tree and kernel traits. Kernel weight, width, and length are correlated, while DBH, crown diameter, and tree height are also positively correlated. Significant variation was observed in kernels parameters among and within sites ($p < 0.05$). The ongoing DNA genetic characterisation with single nucleotides polymorphisms molecular markers will help to explain this variation.

The results will improve (1) the understanding of tree and morphological diversity, (2) develop effective management strategies for sustainable use and conservation of this vulnerable underutilised species and (3) preserve the associated genetic biodiversity for breeding purposes.

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