

## ABSTRACT

Shea tree (*Vitellaria paradoxa* C. F. Gaertn.) is an important fruit tree known for its oil, used for producing valuable products in the food and cosmetic industries. Despite of its importance, Shea is considered an “orphan” due to limited research attention it receives especially in East Africa. In Uganda, the exploitation of the full potential of Shea is undermined by low nut/oil yield and genetic erosion. Shea tree breeding is key to increasing its productivity and utilization. However, to set up an effective and efficient Shea breeding and conservation program, it’s imperative to understand the status of its genetic and phenotypic diversity, farmers’ trait preferences and applicability of modern breeding tools. This study, therefore, sought to i) determine farmers’ Shea tree selection and retention criteria on farm, ii) determine the phenotypic and genetic diversity and population structure of Shea tree, iii) identify Single-Nucleotide Polymorphisms (SNP) markers significantly associated with oil yield traits in Shea tree and iv) determine the most suitable genomic models for Shea tree selection for oil yield in Uganda. Individual household interview, key informant interview and Focus group discussions were used to determine farmers’ criteria for selection and retention of Shea tree on farmer. Sampled fruits from the field were collected and taken to laboratory for physical (shape, size, color, weight) and chemical traits (oil content related) analysis. Seeds obtained from the field were planted at Ngetta Zonal Agricultural Research and Development Institute. DNA were extracted from the seedlings for generating molecular markers (SNPs) which were used to study genetic diversity, population structure and GWAS and genomic selection modeling. Results of this study indicate that farmers’ Shea tree selection and retention is influenced by oil content and fruit pulp traits. The study also revealed a medium (0.21) genetic diversity in Uganda’s shea tree population. Based on SNP markers, shea accessions collected clustered into two major groups (Eastern and West Nile populations). The marker-trait association analysis on a panel of 374 Shea tree accessions using 7,530 SNPs markers revealed 23 SNPs associated with studied traits. Four of these markers were significantly ( $LOD = 4.87$ ) associated with kernel percent oil content in Shea tree. The results of Genomic Selection revealed two genomic models (gblupRR and bglr\_RKHS) with high (0.5) prediction for oil yield in Shea tree, important for its breeding in Uganda. This study concludes that the farmers’ criteria for selection and retention of shea tree on farm vary from location to location; the variation in phenotypic and genetic characteristics are important for selection of promising parents for improvement and /or conservation; the shea tree has important marker traits that can be used for its breeding. The identified genomic regions associated with oil yield and the genomic models offer opportunities to furthering marker-assisted breeding in Uganda’s shea tree.