



Tropentag 2024  
September 11-13, 2024

Conference on International Research on Food Security, Natural Resource  
Management and Rural Development  
organised by the University of Natural Resources and Life Sciences, Vienna (BOKU), Austria

---

## Exploring the Population Structure and Genetic Diversity of *Moringa Oleifera* Using DArTSeq Derived SNP Markers.

Jantor Ndalo<sup>1</sup> Prasad Hendre<sup>1</sup>, Alice Muchugi<sup>1</sup>, Steven Runo<sup>2</sup>, Robert Kariba<sup>1</sup>, Samuel Muthemba<sup>1</sup>

<sup>1</sup>CIFOR-ICRAF, Trees Genetic resources and Biodiversity, Kenya

<sup>2</sup>Kenyatta university, Department of Biochemistry, Microbiology and Biotechnology, Kenya

### Abstract

*Moringa oleifera* is a versatile tree native to the foothills of the Himalayas and now naturalized in the tropics. Moringa is nutritionally significant owing to its high nutrients and antioxidant content. The genetic diversity of Moringa across the tropics remains under investigated. 3968 SNP markers derived from DArTSeq technology were filtered to 1913 informative markers and used to investigate the genetic makeup of *Moringa oleifera*. Unweighted neighbour joining phylogeny and principal coordinate analysis revealed four distinct clusters related to the geographic origin: Caribbean (Haiti/Jamaica) and East African (Kenya/Tanzania) were identified to be a subset of the West African (Mali/Ghana) population while the South African (Malawi) segregated distinctly. Philippines samples clustered separately and farthest as expected. Analysis of molecular variance revealed high gene flow within populations (77%) compared to among populations (23%). Bayesian modelling in structure with best k being two still distinctly segregated the South African population from the other African regions suggesting a distinct introduction. The significant admixture of individuals noted in structure is typical of unnatural introductions possibly through human mediated events. This study highlights the power of SNP markers from DArTSeq technology in elucidating the genetic structure and molecular diversity of *Moringa oleifera*. The findings contribute to our understanding of the genetic resources of this important plant species and have implications for germplasm collection, improvement, conservation, utilisation strategies and policies. Further research utilising advanced genomic tools will enhance our knowledge of *Moringa oleifera* and support its sustainable utilisation for various applications.

**Keywords:** Diversity array technology, genetic structure, germplasm conservation, *Moringa oleifera*

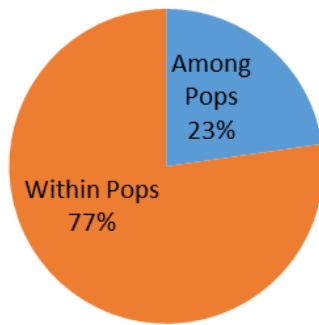
\*Corresponding author Email: J.ndalo@cifor-icraf.org

### Introduction

*Moringa oleifera*, a fast-growing deciduous tree in the Moringaceae family (Rajalakshmi et al., 2017), It thrives in tropical and subtropical regions across Asia, Africa, South and Central America, and the Caribbean (Saini et al., 2013). Known as “the natural nutrition of the tropics,” Moringa is valued for its nutrient-rich leaves, seeds, and pods, which contain higher levels of vitamins, minerals, and protein compared to common foods like carrots, oranges, and milk. This exceptional nutritional profile positions Moringa as a prime candidate for food fortification, particularly in developing countries with prevalent nutrient deficiencies (Shahzad et al., 2013). In agriculture, Moringa serves as nutritious fodder, while its pharmacological applications include treatments for diabetes, hypertension, and anaemia due to its antioxidant properties. Moreover, it shows promise in biotechnology as a source for biodiesel and water purification agents. Moringa’s resilience to harsh environments makes it particularly beneficial in arid regions facing food insecurity. Despite its advantages, Moringa remains underutilized and is recognized among the 101 neglected crops by the African Orphaned Crop Consortium (Dawson et al., 2018). Recent advances in genomic research, including the use of DArTSeq technology provides a platform for improved breeding and conservation efforts by enabling high-resolution genetic diversity assessments across the Moringa genome (Kilian et al., 2005). This study focused on the genetic diversity and



## Analysis of Molecular Variance

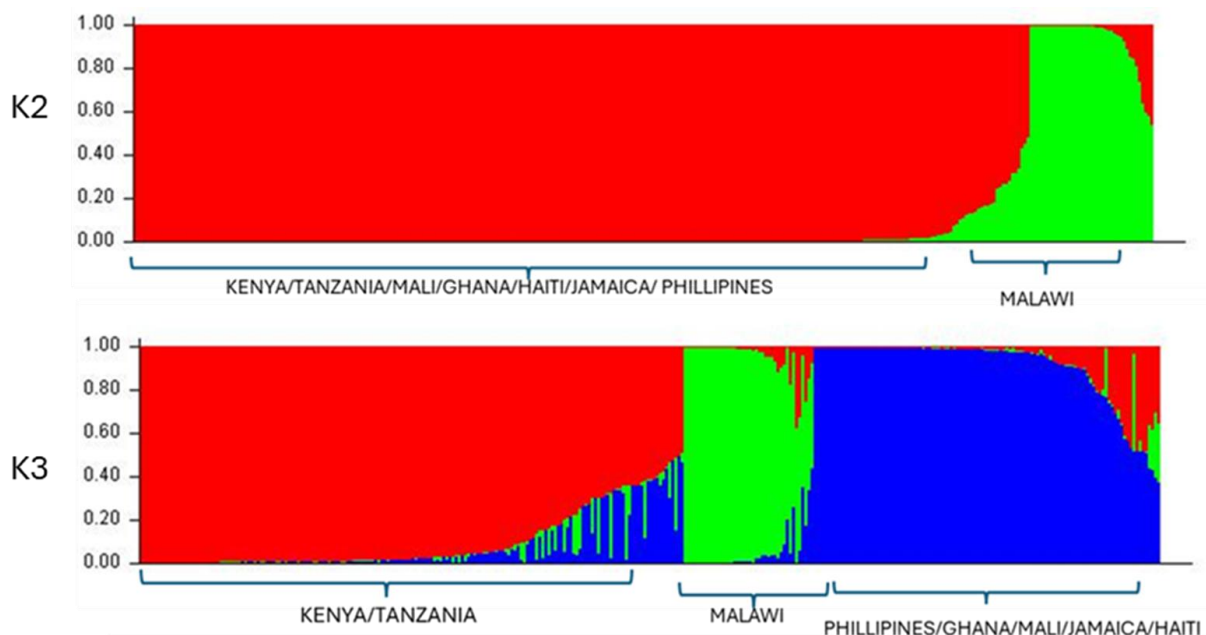


**Figure 2.** Pie chart illustrating the proportion of molecular variance among and within populations

From the AMOVA analysis, the diversity structuring was 77% within populations and 23% among populations. According to diversity structuring for outcrossing plant species gene flow is attributed to pollen movement (Sheng et al., 2005), and mating systems in plants contribute highly to patterns of genetic diversity within and among populations (Kithure et al., 2015).

### Genetic structure

Genetic structuring has important implications in ecological restoration exercises (Muchugi et al., 2008). Structure at K two hypothesize that Moringa was introduced in the African continent via two major events, Malawi population having been introduced by settlers from a specific region in India at a unique time point (Prasuna et al., 2009; Olsona 2017). unique introduction. At K four, west African and Caribbean population grouped together suggesting that the Caribbean and Eastern African populations are a subset of West African population. This supports the hypothesis that the Pacific slave trade introduced a Malian population to Jamaica and Haiti (Muluvi et al., 1999).



**Figure 3:** Population structure used to estimate the best K value using Bayesian-based population genetic structure analysis a) K=2 and B) K=4. Each solid bar represents an accession, with coloured areas corresponding to clusters. Admixed genomes of accessions are represented by bars with multiple colours.

### Conclusions and Outlook

These research findings identified Malawi and Philippines as the most unique and diverse populations among African and rest of the populations respectively hence should be the focus of conservation efforts. East African and Caribbean population were identified as subsets of the Western Africa population. A

notable admixture of entries not complying with geographical distribution is typical to unnatural mixing conceivably through anthropogenic events. Minimal genetic diversity noted among most of the African populations is presumed to be due to small number of *Moringa* accessions introduced from India to Africa serving as founder population. These findings have implications for *Moringa* germplasm collection, improvement, conservation, utilization strategies and policies.

## References

1. Dawson, I. K., Hendre, P., Powell, W., Sila, D., McMullin, S., Revoredo-, C., Odeny, D. A., Graudal, L., Roshetko, J. M., Hale, I. L., Deynze, A. Van, Prabhu, R., Cheng, S., Xu, X., Muchugi, A., Jamnadass, R., Buildings, K., Road, W. M., Africa, S., ... Bonington, S. (2018). Supporting human nutrition in Africa through the integration of new and orphan crops into food systems: placing the work of the African Orphan Crops Consortium in context. In *ICRAF Working Paper*. <https://doi.org/http://dx.doi.org/10.5716/WP18003.PDF>
2. Excoffier, L., Laval, G., & Schneider, S. (2005). Arlequin (version 3.0): An integrated software package for population genetics data analysis. *Evolutionary Bioinformatics*, 1(February), 117693430500100. <https://doi.org/10.1177/117693430500100003>
3. Felsenstein, J. (1989). {PHYLIP} -- Phylogeny Inference Package ({V}ersion 3.2). *Cladistics*.
4. Kilian, A., Huttner, E., Wenzl, P., Jaccoud, D., Carling, J., Caig, V., Evers, M., Heller-Uszynska, K., Uszynski, G., Cayla, C., Patararapuwadol, S., Xia, L., Yang, S., & Thomson, B. (2005). The fast and the cheap : SNP and DArT-based whole. "In the Wake of the Double Helix: From the Green Revolution to the Gene Revolution", May 2003, 443–461.
5. Kithure, R. K., Muchugi, A., Jamnadass, R., Njoka, F. M., & Mwaura, L. (2015). Genetic diversity of *Faidherbia albida* (Del.) A. Chev accessions held at the World Agroforestry Centre. *Forests Trees and Livelihoods*, 24(4), 219–230. <https://doi.org/10.1080/14728028.2015.1054439>
6. Muchugi, A., Muluvi, G. M., Kindt, R., Kadu, C. A. C., Simons, A. J., & Jamnadass, R. H. (2008). Genetic structuring of important medicinal species of genus *Warburgia* as revealed by AFLP analysis. *Tree Genetics and Genomes*, 4(4), 787–795. <https://doi.org/10.1007/s11295-008-0151-3>
7. Muluvi, G. M., Sprent, J. I., Soranzo, N., Provan, J., Odee, D., Folkard, G., McNicol, J. W., & Powell, W. (1999). Amplified fragment length polymorphism (AFLP) analysis of genetic variation in *Moringa oleifera* Lam. *Molecular Ecology*, 8(3), 463–470. <https://doi.org/10.1046/j.1365-294X.1999.00589.x>
8. Olson, M. E. (2017). *Moringa* frequently asked questions. *Acta Horticulturae*, 1158, 19–32. <https://doi.org/10.17660/ActaHortic.2017.1158.4>
9. Prasuna, C. P. L., Chakradhar, R. P. S., Rao, J. L., & Gopal, N. O. (2009). EPR and IR spectral investigations on some leafy vegetables of Indian origin. *Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy*. <https://doi.org/10.1016/j.saa.2009.05.020>
10. Pritchard, J. K., & Wen, W. (2002). Documentation for structure software: Version 2. *In Practice*, 29.
11. Rajalakshmi, R., Rajalakshmi, S., & Parida, A. (2017). Evaluation of the genetic diversity and population structure in drumstick (*Moringa oleifera* L.) using SSR markers. *Current Science*, 112(6), 1250–1256. <https://doi.org/10.18520/cs/v112/i06/1250-1256>
12. Saini, R. K., Saad, K. R., Ravishankar, G. A., Giridhar, P., & Shetty, N. P. (2013). Genetic diversity of commercially grown *Moringa oleifera* Lam. cultivars from India by RAPD, ISSR and cytochrome P450-based markers. *Plant Systematics and Evolution*, 299(7), 1205–1213. <https://doi.org/10.1007/s00606-013-0789-7>
13. Shahzad, U., Khan, M. A., Jaskani, M. J., Khan, I. A., & Korban, S. S. (2013). Genetic diversity and population structure of *Moringa oleifera*. *Conservation Genetics*, 14(6), 1161–1172. <https://doi.org/10.1007/s10592-013-0503-x>
14. Sheng, Y., Zheng, W., Pei, K., & Ma, K. (2005). Genetic variation within and among populations of a dominant desert tree *Haloxylon ammodendron* (Amaranthaceae) in China. *Annals of Botany*, 96(2), 245–252. <https://doi.org/10.1093/aob/mci171>