Assessing Genetic Diversity in Nine Kenyan Populations of *Strychnoshenningsii* (Gilg.) as revealed by RAPD and ISSR Markers.

Kuria, M.W.
Kirinyaga University, Kenya.
Correspondence: *marykuria2012@gmail.com*

Abstract

Strychnos henningsii (Gilg.) is an endangered medicinal plant in Kenya due to over exploitation for medicinal purposes. To understand the levels of genetic variation across populations and geographical regions of this species, we assessed the genetic diversity in nine Kenyan populations of *Strychnos henningsii* using Random amplified polymorphic DNA (RAPD) and inter-simple sequence repeat (ISSR) Markers.

A total of 270 samples from nine (9) populations of *S. henningsii* were collected. Genetic variation within and among populations were evaluated using inter-simple sequence repeat (ISSR) and randomly amplified DNA polymorphism (RAPD) markers. 10 primers of both RAPD and 10 ISSR were used.

A total of 136 loci and 96 loci were revealed by RAPD and ISSR primers respectively, all of which were polymorphic. Kitui population was the most polymorphic with 75 (55.15%) and baringo the least polymorphic with 35 (25.75%) loci detected using by RAPD primers. ISSR markers showed Ngong population as the most polymorphic with 51 (53.12%) and Baringo as the least polymorphic with 28 (29.17%) loci detected. Population specific loci 25 and 13 were also revealed by RAPD and ISSR markers respectively which might have contributed to specific population traits. A higher molecular variance was revealed among populations ($p>0.001$) than within populations RAPD analysis showed 54%polymorphism among populations and 46% within populations while ISSR markers showed 58% among populations and 41% within populations. According to Nei's unbiased genetic distance matrix, the most genetically close populations were Jilore and Baringo with the highest genetic identity (0.9796) and the lowest genetic distance (0.0206) as revealed by RAPD primers. ISSR markers indicated that Taveta and Marsabit were the most genetically close with the highest genetic identity (0.8803) and the lowest genetic distance (0.1275). Clustering analysis based on Nei's similarity matrix grouped the nine population into two groups; Cluster I included Kitui, Taveta, Karura, Marsabit, Ngong, Nyeri, and Narok) while Cluster II

included Baringo and Jilore. These results were also supported by principal coordinate analysis.
These findings indicate that both markers can be used in determining the genetic diversity of *S. henningsii*. We suggest an urgent need for conservation of existing natural populations along with extensive domestication of this species for commercial purpose.
Keywords: *S. Henningsii, RAPD, ISSR, Genetic Diversity, Polymorphism.*