(ID 232)

Genotypic Variation of Native Sweet Potato (*Ipomea batatas* L.) Accessions Compared to Improved Varieties in Sri Lanka

Safwa, M.F.Z.¹, Shyamalee, H.A.P.A.², Ranawake, A.L.¹*

¹Department of Agricultural Biology, University of Ruhuna, Matara, Sri Lanka ²Agricultural Research Station, Matara, Sri Lanka *<u>lankaranawake@hotmail.com</u>

Abstract

Genetic diversity of native *Ipomea batatas* accessions provides a valuable resource for breeding programs, enabling the development of new cultivars with improved traits, nutritional content, and overall crop resilience. This study examined the significance of diversity among seventeen native *I*. batatas accessions compared to five improved varieties. The experiment was carried out at the field of Agriculture research station, Thelijjawila, according to a randomized complete block design with three replicates. Twenty-one qualitative and twelve quantitative characters were measured according to the recommendation of International Potato Center. Twelve quantitative agromorphological characteristics were analyzed using IBM SPSS 25 statistical software. Principal component (PC) analysis and cluster analysis and correlation analysis were performed to evaluate the accessions' morphological diversity and yield components. According to Duncan's Multiple Range Test (DMRT) grouping, all the evaluated characteristics were significantly different among accessions. The PC analysis revealed four PCs representing 76.55% of total variance among accessions exceeded the eigen value one. PC1, PC2, PC3 and PC4 explained 31.92%, 20.88%, 13.81% and 9.94% variability, respectively. PC1 was positively contributed with total yield, best four storage root yield, storage root width, root cortex thickness and vine diameter. Mature leaf length, petiole length, vine internode length and main vine length contributed for PC2 and number of leaves per plant contributed for PC3 while storage root length contributed for PC4. According to hierarchical agglomerative clustering using Ward linkage, four distinct clusters were identified at cluster distance ten. Cluster II comprised accessions with the highest storage root diameter and root cortex thickness. The 2D scatter plot diagram suggested a moderate variation among evaluated accessions distributed in three quadrants of the diagram. This genetic variation can be utilized in breeding programs to enhance resilience to changing environment conditions and contributes to improve yield, quality, and adaptability to diverse environments. Moreover, understanding and conserving the genetic diversity of *I. batatas* ensures a sustainable foundation for future breeding efforts, supporting long-term food security.

Keywords: Agro-morphological characteristic, Ipomea batatas, PCA, Sri Lanka