

Assessment of the Diversity of Selected Jackfruit (*Artocarpus heterophyllus* Lam.) Accessions in Gannoruwa and Horana Field-Gene Banks

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Jackfruit (*Artocarpus heterophyllus* Lam.) is a tropical, evergreen tree that belongs to the family Moraceae. Mainly it is grown in Asian, African, and South American regions of the world. Jackfruit needs minimum inputs and thrives well in marginal environments making it an ideal crop to cater to the increasing demand for food with the population expansion, yet it is an underutilized crop in Sri Lanka. Identification of accessions with elite characters is important to select superior cultivars. Hence, this study was conducted to explore the diversity of selected jackfruit accessions in Gannoruwa and Horana field genebanks using morphological and molecular characters and to check the suitability of jackfruit across Sri Lanka. Morphological diversity was assessed by scoring seven traits. The Principal Component Analysis (PCA) of morphological data was conducted in R programming language. More than 40% variation existed between the first two principal components. A dendrogram with nine clusters was obtained for the selected 21 accessions. PCR primers for four genes (*adh1*, *AMY1*, *G3pdh*, and *PEPC*) were designed using the jackfruit genome sequence available in the Online Resource for Community Annotation of Eukaryotes (ORCAE) database. One accession from each cluster was then used for molecular characterization. The Polymerase Chain Reactions (PCR) were done to *adh1*, *rbcL*, and *matK* gene regions. But all the PCR failed thus, molecular characterization was discontinued. The suitability of the environment was tested using ENMTools implemented in the R program. This study showed the selected jackfruit accessions possess sufficient morphological diversity, hence, nine clusters were obtained. All of Sri Lanka seems fairly suitable for the cultivation of jackfruit. For future direction, it is suggested to carry out an analysis of genetic diversity by optimizing the DNA extraction protocol and using better molecular markers. The morphological dataset must be expanded by including more useful characters.

Keywords: Cluster dendrogram, Genetic diversity, Jackfruit, Molecular data, Morphological data

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