

Evaluation of genetic diversity in jackfruit (*Artocarpus heterophyllus* Lam.) based on amplified fragment length polymorphism markers

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ABSTRACT. *Artocarpus heterophyllus* Lam., commonly called jackfruit, is a medium-sized evergreen tree that bears high yields of the largest known edible fruit. Yet, it has been little explored commercially due to wide variation in fruit quality. The genetic diversity and genetic relatedness of 50 jackfruit accessions were studied using amplified fragment length polymorphism markers. Of 16 primer pairs evaluated, eight were selected for screening of genotypes based on the number and quality of polymorphic fragments produced. These primer combinations produced 5976 bands, 1267 (22%) of which were polymorphic. Among the jackfruit accessions, the similarity coefficient ranged from 0.137 to 0.978; the accessions also shared a large number of monomorphic fragments (78%). Cluster analysis and principal component analysis grouped all jackfruit genotypes into three major clusters. Cluster I included the genotypes grown in a jackfruit region of Karnataka, called Tamaka, with very dry conditions; cluster II contained the genotypes collected from

locations having medium to heavy rainfall in Karnataka; cluster III grouped the genotypes in distant locations with different environmental conditions. Strong coincidence of these amplified fragment length polymorphism-based groupings with geographical localities as well as morphological characters was observed. We found moderate genetic diversity in these jackfruit accessions. This information should be useful for tree breeding programs, as part of our effort to popularize jackfruit as a commercial crop.

Key words: Jackfruit; Genetic diversity; Markers; Polymorphism; Amplified fragment length polymorphism