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ASSESSMENT OF GENETIC DIVERSITY IN WILD GERMPLASM OF RUBBER (*HEVEA BRASILIENSIS*) USING RAPD MARKERS

Saji T. Abraham, T. Saha*, J. Mathew, C.P. Reghu, Y. Annamma Varghese

Rubber Research Institute of India, Kottayam-686 009, Kerala, India

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The wild germplasm of the Para rubber tree (*Hevea brasiliensis*) was introduced to India primarily to expand the genetic base vital for enhancing crop improvement. Genetic diversity of 110 wild rubber germplasm (*Hevea brasiliensis*) accessions was assessed using random amplified polymorphic DNA (RAPD) markers. The polymorphism information content (PIC) ranged from 0.31 to 0.49 indicating their efficiency in revealing the polymorphism among wild accessions. A total of 126 loci were amplified using 16 primers, which revealed an overall polymorphism of 98 per cent. The accessions possessed a high variability as indicated by the wide range of similarity coefficients ranging from 0.16 to 0.81. Cluster analysis following unweighted pair-group method analysis (UPGMA) broadly classified the 110 wild accessions into nine distinct clusters. The clusters showed geographical distinctiveness to the three states of Brazil from where the accessions were originally collected. A few accessions, which were distinctly divergent in the clusters, were also identified. This finding can contribute to the conservation of wild *Hevea* germplasms and its utilization in future breeding programs.

Keywords: Genetic diversity, *Hevea brasiliensis*, RAPD markers, Wild germplasm

INTRODUCTION

The Para rubber tree *Hevea brasiliensis* (Willd. ex. Adr. de Juss.) Muell. Arg., produces about 99 per cent of world's natural rubber. Genetic improvement in rubber, despite being very elaborate and time consuming, has helped to achieve several fold increase in yield by evolving several high yielding clones. However, the genetic improvement of *Hevea* over the decades focused on yield, which resulted in the development of clones susceptible to several potential major and minor diseases.

Considering the urgent need for broadening the genetic base, fresh wild germplasm of *Hevea* was collected from its original center of diversity, in Brazil and introduced into the *Hevea* gene pool in India. India now maintains a total of 4548 wild accessions, which is a potential source for development of location-specific clones with resistance to biotic and abiotic stresses (Rao *et al.,* 2013; RRII, 2023). One of the serious constraints in the successful and quick utilization of the wild *Hevea* germplasm is the delay in characterization, evaluation and cataloguing of the same. Morphological characterization for evaluation of the germplasm accessions has the inherent limitation of being influenced by environmental factors and developmental

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Correspondence: Thakurdas Saha (Email: tdsaha58@gmail.com)