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SHORT RESEARCH ARTICLE

Genetic relatedness study among the jack fruit (*Artocarpus heterophyllus* Lam.) genotypes of the North East India through molecular markers

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Abstract

Forty genotypes of jack fruit (*Artocarpus heterophyllus* L.) from six states, namely, Arunachal Pradesh, Mizoram, Manipur, Meghalaya, Assam and Tripura from of North East India were subjected to genetic diversity analysis using RAPD and SSR markers. Results obtained from the RAPD markers revealed that all the genotypes screened were closely related, i.e., 65 to 100% similar whereas 86 to 100%. The majority of the genotypes were observed similar to each other, indicating that the parental lines may have common parentage and hence showed adaptability to similar growing environmental conditions of the country's northeastern region.

Keywords: RAPD, SSR, genetic diversity, jackfruit

India is the second largest producer of the Jack fruit and is widely distributed in the states of Assam, Tripura, Bihar and Uttar Pradesh, the foothills of Himalayas, Kerala, Karnataka and Tamil Nadu in south India, Meghalaya, Sikkim, Manipur, Tripura, Nagaland and Assam (Singh et al. 2018). The tree is evergreen, medium-sized, typically reaching 8-25 m in height producing fruits weighing up to 35 kg (Shyamalamma et al. 2008). The fruits can be canned and processed into products like wine, ice cream, chips and jellies, dehydrated jackfruit bulbs and squash, vinegar, preserve, nectar and ready-to-serve beverages (Asquieri et al. 2008; Jagadeesh et al. 2009; Singh et al. 2001). However, there is not much systematic work had been done on the molecular characterization or screening of superior types found in India, particularly in North East India. Therefore, a study was conducted to assess genetic diversity in jack fruit at the molecular level.

A total of 40 tender leaves sample were collected from different trees from six states of North East, India distributed as 20 from Tripura State (T1 to T20), four of Manipur (T21-24), five of Assam (T25-T29), five of Arunachal Pradesh (T30-T34), two of Mizoram (T35-T36), and four of Meghalaya (T37-T40). For molecular characterization, DNA was isolated by using the Doyle and Doyle method (1987) with slight modifications. Genetic diversity of 40 samples of *Artocarpus heterophyllus* genotypes were investigated by using 10 RAPD markers and 30 Simple Sequence Repeat (SSR) markers. Ten RAPD and 30 SSR primers designed by Sigma-Aldrich were used in molecular analysis. The thermal cycling SSR primers had 36 cycles at 94°C for 3 minutes, 45–55°C for 1-minute, 72°C for 1-minute, a final elongation step of 4 min at 72°C.

Ten random oligo-nucleotide primers (Operon technologies) used in the study were able to amplify the genomic DNA successfully. Only three of them (OPA-01,

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OPC-07, OPG-03) were polymorphic and remaining seven (OPD-3, OPD-19, OPF-1, OPF-5, OPF-10, OPF-13, OPF-15) were monomorphic. The similarity coefficient determined the similarity among all the genotypes that ranged between 60 to 100%, with an average of 80% (Fig. 1). The dendrogram divided *Artocarpus heterophyllus* into two different clusters, A and B. Cluster A was further divided into two sub-clusters, T1, T2 and T5 consisting of genotypes from Tripura with similarity of 65 to 85%. Cluster B consisted of all the remaining genotypes i.e., T3-T4 and T6-T40, which belong to different jack fruit growing regions of North East India with similarity 76 to 100%. Within the sub-cluster of Cluster B, four genotypes i.e., T14 (Tripura), T37 (Meghalaya), T40 (Meghalaya), and T38 (Meghalaya) were recorded 100% similar. Similarly, in the other groups within sub cluster 100% similarity was noticed such as two genotypes, T30 and T33 from Arunachal Pradesh, nine genotypes (T35-T36) from Mizoram, T25-T28 from Assam; two genotype group i.e., T19 (Tripura) and T23 (Manipur) and similarly two genotype group each (T10 and T16) and (T13 and T15) from Tripura, respectively. The least similarity (65%) was found in genotypes, T5 (Tripura). These results were well supported by the finding of Singh et al. (2018) in which a good number of polymorphic bands were found with Primer OPC-07. Similar results were found in RAPD study of different genotypes of jackfruit by Schnell et al. (2001).

Out of 30 SSR primers, 10 produced strong polymorphic bands and the remaining primers produced weak and monomorphic bands. The jackfruit genotypes were grouped into two major clusters viz., A and B (Fig. 2). Cluster A consisted of 32 genotypes having 88 to 100% similarity, whereas in cluster B only 8 genotypes were included having 86 to 100% similarity. Highest similarity (100%) was found in sub-cluster having four genotypes, T1, T3, T4 (Tripura) and T38 (Meghalaya); two genotypes T8 and T10 (Tripura); three genotypes T12, T15, T18 (Tripura); three genotypes T5, T9, T11 (Tripura); three genotypes T6, T7, T19 (Tripura); four genotypes T22 (Manipur), T39-T40 (Meghalaya), T28 (Assam) and T24 (Manipur), T25-T26 (Assam). In cluster B 100% similarity was found in sub-clusters i.e., four genotypes of T31, T32, T34 (Arunachal Pradesh), T35 (Mizoram). Least similarity i.e., 86 per cent was found in T30 (Arunachal Pradesh), T37 (Meghalaya). Similar findings were reported by Kavya et al. (2019), who used 22 SSR markers in 20 diverse genotypes of jack fruits. However, only six out of 22 primers showed polymorphisms. In another study, Nakintu et al., (2019) analysed genetic diversity in 200 genotypes of jackfruit from Uganda and found that genetic variation was high within the population than among the population.

It has been concluded from the present study that all the genotypes collected from different states of North East India had genetic similarity as per the molecular analysis.

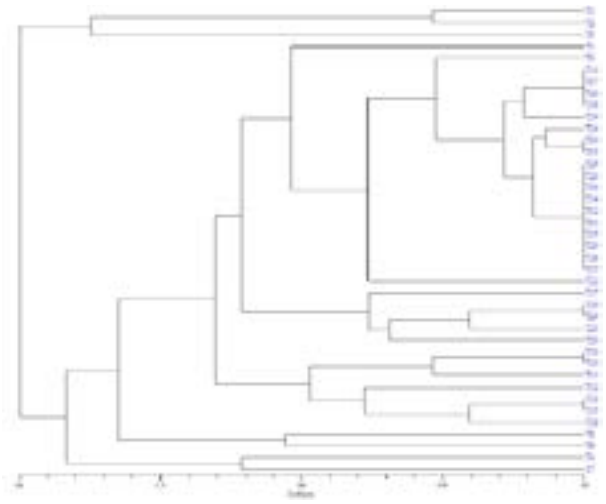

Fig. 1. UPGMA-based dendrogram generated by RAPD molecular data

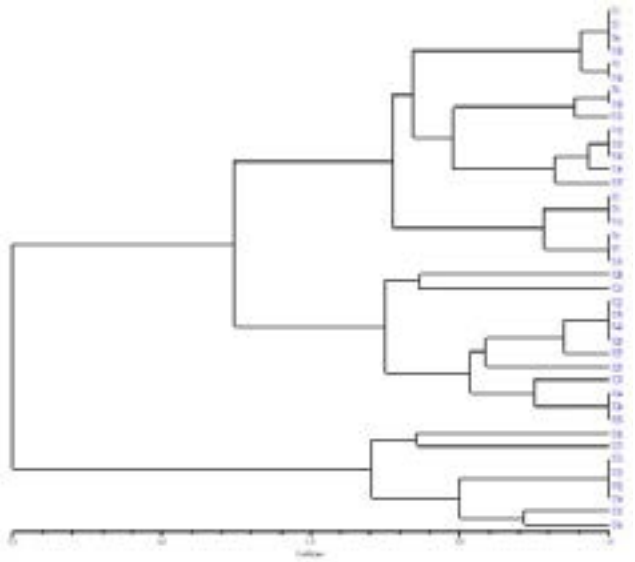

Fig. 2. UPGMA-based dendrogram generated by SSR molecular data

The lack of genetic diversity in jack fruit population in this region may be ascribed to common parentage in their evolution. These genotypes adapted to similar growing environmental conditions. In order to enrich the genetic diversity, breeders need to follow modern techniques of tree breeding to encourage higher production of jack fruit.

Authors' contribution

Conceptualization of research (AC, BNH); Designing of the experiments (AC, BNH, SS, LW); Contribution of experimental materials (AC, SS, LW); Execution of field/lab experiments and data collection (AC, SS); Analysis of data and interpretation (AC, VK); Preparation of the manuscript (AC, VK).

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