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Morphological and molecular characterization of Sapota (*Achras zapota* L.) using RAPD markers A. Harshavardhan, M. Rajasekhar and R. Rajyalakshmi

Dr. Y. S. R. Horticultural University, India

A n investigation was carried out on morphological and molecular characterization of sapota using RAPD markers during 2012-2013 at Horticultural Research Station, Venkataramannagudem. Among the different cultivars evaluated cv. CO-1 recorded maximum plant height (6.80 m), whereas, maximum stem circumference (88.67 cm) and shoot girth (4.17 cm), were observed with cv. DHS-1. Significantly maximum plant spread and shoot length was obtained with cv. DHS-2 (8.73 north-south), Cricket Ball (25.60 cm) respectively. More number of flowers per shoot was noticed in cv. CO-1 (15.33). Cultivars pala and Cricket Ball (ARSA) took minimum days for flower opening (34.13 days) and fruit set (24.00), respectively. The cultivar PKM-1 recorded significantly maximum per cent fruit set (29.50%) and number of fruits per tree (2450). Significantly maximum fruit diameter (5.96 cm) was observed with cv. CO-2, while, maximum fruit length (6.64 cm) and fruit weight (133.41 g) was recorded with cv. CO-1. Significantly higher content of total soluble solids was observed with DHS-1 (23.90 ° B), whereas, cv. CO-1 recorded lower content of acidity (0.126%). Maximum number of seeds per fruit was noticed with cv. DHS-2 (4.14).

The study was also conducted to find out the genetic diversity among 31 accessions (comprising of 19 cultivars, 6 landraces and 6 hybrids) of sapota using PCR based randomly amplified polymorphic DNA (RAPD) markers. Among 20 random decamer primers screened, seven gave consistent banding patterns. These primers yielded 48 markers which were selected for the estimation of genetic diversity using UPGMA (Unweighted Pair Group Method with Arithmetical Averages) cluster analysis having Jaccard's Co-efficient of similarity matrix. Results indicated a moderate to high genetic diversity among 31 genotypes, which are distributed between the ranges of 35 to 100 per cent. Genotypes are categorized into two distinctive groups based on fruit characteristics (shape) and canopy shape and hybrids are distributed based on fruit shape, growth habit, parentage and bearing habit, which made two distinctive groups. The cluster analysis revealed that all round and oval shape fruit bearing genotypes are genetically closely related, while, oblong shape fruit bearing genotypes are genetically more diverse from them as they grouped together in different cluster.

harsha.arjaneni@gmail.com