



Genetic divergence in jackfruit (*Artocarpus heterophyllus* Lamk.)

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The jackfruit (*Artocarpus heterophyllus* Lamk.) is highly heterozygous and cross pollinated tree and as such seedlings exhibits a wide range of variations which aid in the selection of superior desirable types. Due to cross pollination and predominance of seed propagation over long period of time, there is high degree of genetic diversity within the species. Improvement in yield and quality of highly cross-pollinated crops like jackfruit is generally achieved by selecting genotypes with desirable character combinations existing in nature. Mahalanobis [1] D^2 statistic which is based on multivariate analysis of quantitative traits is a powerful tool for measuring the divergence among a set populations. Therefore, an attempt was made to study the multivariate analysis of genetic divergence in jackfruit.

The experimental material comprised of 44 selected genotypes of jackfruit belonging to different geographical regions of West Bengal. The mean data of each quantitative trait for 18 economic characters in each year were replicated three times for statistical analysis and year was considered as a replication (entries). The analysis of genetic divergence was carried out by using Mahalanobis D^2 statistics. The grouping of the genotypes into clusters was made as per Tochar's method [2].

The analysis of variance for 18 quantitative characters showed significant differences among 44 genotypes indicating the existence of genetic diversity. These 44 genotypes were grouped into 13 clusters as embodied in Table 1. It was apparent that eight genotypes were in cluster VI, 7 genotypes were in cluster III, 5 genotypes were in clusters VII, VIII and X while rest of the clusters had one genotype each. The clustering pattern of genotypes showed that genotypes from the same area did not necessarily belong to the same cluster. From the study of genetic divergence among 44 genotypes, it appears that genetic drift and natural selection under different environmental conditions could cause considerable diversity than

Table 1. Clustering pattern of 44 genotypes of jackfruit based on 18 characters of economic importance

Cluster	No. of genotypes	Name of genotypes	Source of genotypes
I	2	T ₆	24-Pargana (S)
		T ₃₀	24-Pargana (S)
II	3	T ₃₄	Nadia
		T ₃₃	24-Pargana (S)
		T ₄₀	Coochbehar
III	7	T ₇	24-Pargana (N)
		T ₈	Nadia
		T ₁₁	24-Pargana (N)
		T ₃₁	24-Pargana (S)
		T ₂₀	Nadia
		T ₁₂	Nadia
		T ₉	Nadia
IV	2	T ₃₂	24-Pargana (S)
		T ₃₈	Coochbehar
V	2	T ₃₆	Coochbehar
		T ₂₆	Nadia
VI	8	T ₄₂	Midnapore
		T ₃	Nadia
		T ₂	Nadia
		T ₁₆	24-Pargana (N)
		T ₁₇	24-Pargana (N)
		T ₄₄	24-Pargana (N)
		T ₂₅	Nadia
		T ₂₃	Nadia
VII	5	T ₂₇	Puruilia
		T ₄	Nadia
		T ₂₉	Nadia
		T ₂₄	Nadia
		T ₁	Nadia
VIII	5	T ₃₉	Coochbehar
		T ₄₃	24-Pargana (N)
		T ₁₅	24-Pargana (N)
		T ₃₇	Coochbehar
		T ₁₃	Nadia
IX	2	T ₁₈	Nadia
		T ₁₀	Nadia
X	5	T ₅	Nadia
		T ₂₈	Nadia
		T ₁₉	Nadia
		T ₂₁	Nadia
		T ₁₄	24-Pargana (N)
XI	1	T ₃₅	Nadia
XII	1	T ₂₂	Nadia
XIII	1	T ₄₁	Coochbehar

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geographical distance. It is apparent that genotypes coming from different ecogeographic areas were grouped into same cluster and genotypes belonging to same geographic origin were included in different clusters suggesting that geographic diversity does not necessarily represent genetic diversity [3].

Average intra and inter cluster distance analysis (Table 2) showed that the intra cluster distance was

obviously genetically more divergent. Hence, it would be logical to incorporate genotypes from these clusters in breeding programme or selection for new genotypes.

An overview of clusters in context with mean of different quantitative characters indicated that cluster XIII possesses genotypes of economic importance as means for TSS, total sugar and TSS/acid ratio than that of other clusters (Table 3). With regard to weight

Table 2. Average intra and inter cluster distances (D^2) in 44 genotypes of jackfruit

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	0.0												
II	153.5	140.3											
III	1996.6	1643.8	128.2										
IV	10355.6	11744.3	14319.1	0.0									
V	1606.4	1677.5	1655.4	2550.7	0.0								
VI	2025.6	1909.4	1441.1	1927.2	1788.8	95.5							
VII	5923.8	5033.1	2212.3	6653.7	2085.6	1094.0	117.6						
VIII	1753.8	1508.0	588.7	1941.9	1488.1	549.5	1633.0	84.8					
IX	1827.6	1534.7	374.0	2086.1	1528.1	767.4	1853.5	240.3	71.7				
X	1785.4	1815.2	1668.4	1534.1	1746.2	559.3	563.4	1090.5	1311.0	172.7			
XI	1810.0	1848.3	1727.8	1538.6	1781.5	631.3	532.7	1149.8	1370.2	218.1	0.0		
XII	1723.5	1705.2	1455.7	1559.9	1641.7	344.1	764.1	877.9	1098.3	249.7	345.0	0.0	
XIII	1703.8	18512.7	804.7	1813.8	1479.7	334.2	1414.8	231.9	449.9	874.5	938.3	658.6	0.0

Table 3. Cluster means for 18 characters in 44 genotypes of jackfruit

Characters	Cluster number												
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
Age of the tree (year)	25.5	21.7	15.7	32.0	41.0	26.0	36.0	21.0	18.5	32.0	31.0	26.0	23.0
Leaf size (cm ²)	73.1	69.4	99.1	93.8	133.9	90.8	101.4	117.4	65.5	120.1	115.3	119.5	93.4
Fruit yield/tree	33.2	30.3	50.0	102.3	60.8	338.0	199.3	37.9	37.3	71.9	52.3	27.3	212.3
Fruit weight (g)	2007.5	4550.5	4135.2	2387.7	4355.5	4107.1	4846.3	5533.6	4659.7	6763.7	9170.0	1560.0	2135.0
Wt of edible part w/o stone(g)	724.0	1903.3	1569.6	976.2	1688.6	1593.5	1808.0	2612.5	1902.0	2600.9	3914.0	550.0	781.0
Rind weight (g)	915.4	1837.9	1590.0	953.2	2033.2	1820.1	1826.6	1866.8	1632.1	2611.3	3359.3	860.0	921.6
Rachis wt. (g)	205.3	264.7	619.4	249.3	294.5	372.4	550.1	314.9	682.5	698.6	1102.5	72.3	120.0
No. of flakes/fruit	67.0	137.4	93.1	56.0	67.2	57.2	128.2	130.2	127.8	157.6	425.0	26.0	64.3
No. of stones/fruit	65.0	134.2	92.0	55.7	66.0	56.7	123.7	126.9	123.7	157.4	397.0	26.0	62.3
Spine no. (3cm ²)	51.8	41.9	33.4	33.5	36.5	38.3	41.9	33.4	31.5	49.2	31.0	56.3	43.0
Stone wt/10 stones(g)	50.3	42.8	49.2	40.0	57.0	59.2	57.5	38.1	45.5	58.7	24.0	30.0	50.0
Stone size(cm ²)	3.4	4.1	4.3	3.6	3.4	4.2	4.3	4.1	3.6	4.9	2.9	2.9	4.1
Rind : flake ratio	1.2	1.0	1.0	1.0	1.2	1.6	1.1	0.7	0.8	1.1	0.9	1.5	1.2
TSS (°B)	20.5	18.3	16.2	21.6	21.5	16.9	19.3	19.8	15.1	17.9	19.9	17.0	25.9
Total sugar (%)	17.5	14.7	13.9	19.7	17.7	14.4	17.1	17.4	12.5	14.7	17.9	15.5	21.9
Titration acidity(%)	0.4	0.2	0.3	0.1	0.2	0.2	0.3	0.2	0.4	0.3	0.2	0.3	0.2
Vitamin C (mg/100 g juice)	5.9	8.4	6.2	8.3	6.8	7.2	6.6	8.4	5.9	7.0	11.1	6.2	7.8
TSS : acid ratio	65.1	96.1	61.5	150.8	82.6	84.4	58.9	99.1	42.7	75.1	104.7	54.9	161.9

zero for clusters I, IV and V as well as XI, XII and XIII, as they comprised of two and one genotypes, respectively. Average values of intra cluster distance was highest in cluster X (172.7) and lowest in cluster IX (71.7). Maximum values of inter cluster distance was observed between cluster III and IV(14319.1) followed by cluster II and IV(11744.3) and cluster I and IV(10335.6). Minimum values of inter cluster divergence was recorded between cluster I and II(153.5) followed by those between clusters XI and X (218.1). The criterion used for selection of genotypes as parents for crop improvement programme using D^2 analysis is the inter cluster distance. Those genotypes included in clusters with maximum inter cluster distance are

of edible part, fruit weight, rind weight, rachis weight, number of flakes, stones number, and vitamin C cluster XI exhibited highest values, while for rind : flake ratio cluster VI was highest. The cluster is also showing diversity from all other clusters. All above evidence indicates that this cluster may be utilized in genotypes selection or crop improvement programmes in jackfruit.

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