The Pharma Innovation

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Inter Germplasm diversity based on tree and yield attributes along with bio-chemical parameters of jackfruit [*Artocarpus heterophyllus* LAM.] Selections of northern Tripura using clustering techniques

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Abstract
In the present investigation, the genetic diversity, existing among the seedling germpalsm of jackfruit (*Artocarpus heterophyllus* Lam.) of northern Tripura state was observed with special reference to clustering patterns of the genotypes. The study was conducted during 2019-21. Both Mahalanobis' D^2 analysis (Tocher's method) and Euclidean analysis (Ward's minimum variance method) grouped the 50 jackfruit genotypes into eight clusters. However, the clusters show variations in different methods with respect to number of genotypes and the actual accessions included in each cluster. In Mahalanobis' D^2 analysis the maximum Inter-cluster distance was observed between Cluster VI and Cluster VIII (i.e. 62655.811). Whereas, Ward's method revealed the highest Inter-cluster value between cluster I and Cluster II (i.e. 1732.753). From both of these clustering techniques, it is evident that genotypes JF-1, JF-12, JF-21, JF-30 and JF-35 are either located in the same cluster or in adjacent clusters, while accessions JF-4 and JF-9 were placed in the same cluster together in both the cases.

Keywords: Clustering, genetic diversity, jackfruit, Mahalanobis' D^2 analysis, Tripura, Ward's minimum variance

Introduction
The word *Artocarpus* is derived from two Greek words "Artos" means bread and "carpos" means fruit (Bailey, 1949) [3]. The jackfruit is commonly known as jack, English adaptation of the Portuguese "jaca" (Popenoe, 1974) [14]. In Hindi, it is commonly known as "Kathal". In north-east India, jackfruit is commonly called by different names by different tribes such as "Thaipung" by Twiprasa of Tripura, "Sohphan" by Khasi and "Tebrong" by Garo of Meghalaya, "Lamkhuang" by Mizo of Mizoram, "Belang" by Adi and "Bala" by Galo of Arunachal Pradesh and "Peyong" by Konyak tribe of Nagaland. The jackfruit also popularly known as the "poor man's fruit", is a species of tree in the Fig, Mulberry and Breadfruit family Moraceae and originated in the rainforests of the Western Ghats of India (Chandler, 1958; Purseglove, 1968 and Popenoe, 1974) [5, 15, 14]. This family Moraceae comprises of about 67 genera with about 1,000 species of mostly tropical shrubs, trees, vines and herbs (Bailey, 1949 and Merrill, 1912) [3, 13]. Jackfruit tree is drought resistant. It is easy to grow (Suchitra, 2015). Although it has high nutritive value and a wide range of uses, still yet, it is recognized as a minor and underutilized fruit (Sankaran *et al.*, 2007) [18]. It is also known as supplementary staple foods, due to presence of high levels of carbohydrates, in times of scarcity in some regions particularly in tribal areas (Frey, 1966) [7]. Tripura being under Eastern Himalayan Agro-Climatic Region produces a major share of jackfruit in India. However, Roy (2008) [17] reported that till date no research study, mostly in view of the exploitation of existing genetic diversity, has been conducted on jackfruit of Tripura, especially in northern Tripura, despite it is being produced in bulk with rich genetic divergence. Keeping a close look at the above scenario, this research survey was conducted to estimate the existence of genetic diversity among different tree as well as fruit morphology along with bio-chemical parameters of ripe fruit of 50 (fifty) numbers of seedling germplasm of jackfruit (in details mentioned in Table – 1), to use this gene pool for future breeding as well as improvement programme of this crop.

Materials and Methods
The region of Northern parts of Tripura State was covered for the study including the hilly zone. Fifty different jackfruit genotypes were identified from eight blocks namely, Kadamtala,

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Jubrajnagar, Kalacherra, Laljuri, Panisagar, Damchera, Dasda, Jampui Hills in the state, following the Bio-diversity International Jackfruit Descriptor 2000, during the years 2019-2021. More than 70% of this area is hilly and forest covered. The terrain is mostly undulating & hilly with small water streams (cherras), rivers and fertile valleys intervening. The climate of this region is tropical in nature and is generally warm and humid. The hilly regions enjoy higher temperature in summer and lower temperature in winter in comparison with the plains. The climatic temperature generally ranges in between 10^0C and 35^0C. Soil is acidic in nature (pH 5.4 – 6.1). Thirty two numbers various quantitative traits related to tree morphology and yield attributes were measured as per suitable scale and units. Different bio-chemical parameters like total soluble solids, acidity, reducing sugar and total sugar content of the ripe fruits of selected jackfruit genotypes had been determined and recorded as per proper methods of estimation. To estimate the genetic divergence, the clustering patterns among the evaluated jackfruit genotypes were determined as follows.

Mahalanobis D^2 Statistics
Mahalanobis' D^2 analysis was done to determine the genetic divergence among the genotypes in terms of 'generalised group distance' (Mahalanobis, 1936) [10]. It is a unit less and scale-invariant and takes into account the correlations of the data set. The D^2 values were arranged in increasing order of magnitude. Grouping of strains into various clusters was done by using Tocher's method (Rao, 1952) [16].

Calculation of D^2 values
The generalized distance function (D^2) between two genotypes is simply the sum of square of differences in Y's i.e.,

$$D^2 \ 1.2 = \sum_{i=1}^{p} (Y_{1,i} - Y_{2,i})^2$$

Where, $Y_{1,i}$ is uncorrelated mean value of 1st genotype for character 'i'

$Y_{2,i}$ is uncorrelated mean value of 2nd genotype for character 'i'

D^2 1.2 is D^2 between 1st and 2nd genotypes

Grouping of genotypes into various clusters
The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952) [16].

Average intra-cluster distance

Intra-cluster distances were calculated with the formula= $\Sigma D^2 i/n$

where, $\Sigma D^2 i$ was the sum of distances between all possible combinations (n) of the populations included in a cluster.

Average inter-cluster distance

Average inter-cluster distance = $\frac{D^2}{(n1 \ X \ n2)}$

Where, D^2 = Difference in the mean values between two populations when all the characters are considered simultaneously.

n1 & n2 = number of genotypes of two clusters.

Hierarchical Cluster Analysis (HCA)
Agglomerative hierarchical clustering technique was followed as given by Anderberg (1973) [1].

The formula used to measure squared Euclidean distance was

$$\text{Squared Euclidean distance} \ [\ d_{ij}] = \sum_{K=1}^{P} (X_{ik} - X_{jk})^2$$

Where,
P = Number of genotypes i.e. 50
X_{ik} = Value of ith genotype for k PCA scores
X_{jk} = Value of jth genotype for k PCA scores

Execution of the clustering by Ward's minimum variance method
Distance matrix was converted into dendrogram by using Ward's minimum variance method, where the distance between two clusters is the sum of squares between two clusters summed over all variables. The distance measure between two clusters that denoted as DK and DL measure is defined as –

$$D_{K,L} = \frac{d(\bar{x}_K, \bar{x}_L)^2}{\left(\frac{1}{N_K} + \frac{1}{N_L}\right)}$$

where $\bar{x}_K$ and $\bar{x}_L$ are the mean vectors within clusters CK and CL respectively.

Results and Discussion
Cluster formation through Mahalanobis' D^2 values (Clustering by Tocher's Method)
Grouping of genotypes into various clusters
Various methods have been selected in the analysis of genetic deviation in a number of crop species. Mahalanobis' D^2 multivariate analysis (Mahalanobis, 1936) [10] is one of the important tools for obtaining quantitative valuation of genetic divergence between biological populations. The value of D^2 statistics has been showed in selecting the parental stocks for cross breeding (Malhotra and Singh, 1971 & Dasgupta and Das, 1984) [12, 6]. However, the D^2 statistics assemble a set of potential parents on the basis of genetic divergence with the presumption that the best parent may be those showing the maximum genetic diversity (Bhatt, 1970) [4]. In order to have heterotic response and valuable segregants, George (1976) [8] highlighted the importance of diversity among the parents population. Besides helping in selection of divergent parents in hybridization, D^2 statistics also helps in the measurement of diversification and contribution of relative proportion of each component characters towards the total genetic divergence in breeding for crop improvement (George, 1976) [8].

All the 50 jackfruit genotypes were grouped into 8 clusters (Table - 2) on the basis of morphological, yield attributing and physicochemical characteristics according to Mahalanobis' D^2 values. Intra-cluster distances showed divergence among the genotypes within a cluster, while, inter-cluster distances exhibited relative divergence between the clusters.

Based on group constellation all the 50 jackfruit accessions were grouped into 8 clusters. The cluster I comprised 10 accessions namely, JF-1, JF-11, JF-21, JF-41, JF-31, JF-16, JF-46, JF-26, JF-36 and JF-6 while, cluster II had the

maximum numbers of i.e. 28 genotypes and those are – JF-2, JF-37, JF-17, JF-47, JF-7, JF-32, JF-12, JF-42, JF-22, JF-27, JF-40, JF-45, JF-44, JF-15, JF-34, JF-5, JF-14, JF-24, JF-23, JF-19, JF-38, JF-18, JF-29, JF-35, JF-39, JF-25, JF-3 and JF-30, whereas cluster III had 2 germplasm namely, JF-4 and JF-9. Subsequently cluster IV contented with 5 accessions namely, JF-8, JF-13, JF-28, JF-43 and JF-33, while cluster V comprised of 2 genotypes i.e. JF-10 and JF-20. Cluster VI, VII and VIII having 1 genotype each namely, JF-48, JF-49 and JF-50, respectively. The clustering patterns of genotypes also showed that the genotypes collected from the same location did not necessarily belong to the same cluster, which indicates that genetic drift, natural selection, cross pollination and seedling origin of the plant might be responsible for this diversity rather than geographical distance (Wangchu *et al.*, 2013) [21].

Intra and inter-cluster distance (D^2 value)
The intra and inter-cluster average distance (By Tocher's method) have been given in Table - 3 and Fig. - 1.
Inter-cluster divergence expresses the diversification among clusters (a group of cultivars resembling each other, hence with low intra-cluster divergence). Intra-cluster D^2 values ranged from 0.00 (cluster VI, VII and VII) to 76.375 (cluster II). The intra-cluster distance indicated the diversity among the cultivars grouped in that clusters. Genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters measured. The intra-cluster distance was the maximum in cluster II comprising of 28 genotypes, followed by cluster I (27.165), comprising 10 accessions and cluster IV (24.882), consisted of 5 genotypes, respectively. The clusters VI, VII and VII have only one accession in each cluster; hence intra-cluster distance is zero. The inter-cluster distance was found as the maximum (62655.811) between cluster VIII with cluster VI, with both having only one genotype, followed by the distance (54413.263) between cluster VI with cluster I and subsequent distance (53794.426) between cluster VI (single genotype cluster) with cluster V. The minimum inter-cluster distance (113.774) was observed between cluster III, with 2 genotypes and cluster II, having 28 genotypes, preceded by inter-cluster distance (119.879) observed between cluster IV, possessed 5 accessions and cluster II, having 28 accessions. This finding was similar with the finding of Udin and Mitra (1994) [20]. They obtained higher inter cluster distance than intra cluster distance in multivariate analysis in Seasame.
Cluster I is nearest to cluster II (158.422), preceded by cluster IV (162.837) and farthest from cluster VI (54413.263), followed by cluster VIII (33990.089).
Cluster II is nearest to cluster III (113.774), preceded by cluster IV (119.879) and farthest from cluster VI (53448.441), followed by cluster VIII (36297.054).
Cluster III is nearest to cluster II (113.774), preceded by cluster VI (195.397) and farthest from cluster VI (53430.269), followed by cluster VIII (36333.093).
Cluster IV is nearest to cluster II (119.879), preceded by cluster I (162.837) and farthest from cluster VI (53422.366), followed by cluster VIII (35760.350).
Cluster V is nearest to cluster II (132.056), preceded by cluster IV (168.608) and farthest from cluster VI (53794.426), followed by cluster VIII (37231.868).
Cluster VI is nearest to cluster VII (22730.610), preceded by cluster VIII (37231.868) and farthest from cluster I

(54413.263), followed by cluster V (53794.426).
Cluster VII is nearest to cluster III (22200.652), preceded by cluster II (22453.184) and farthest from cluster VIII (62655.811), followed by cluster VI (23466.553).
Cluster VIII is nearest to cluster I (33990.089), preceded by cluster IV (35760.350) and farthest from cluster VI (62655.811), followed by cluster VII (46150.948).

Hierarchical Cluster Analysis (clustering through Ward's minimum variance method)
The cluster analysis using Euclidean distances provides a useful statistical tool for measuring the genetic diversity among germplasm with respect to characters considered together.

Grouping of genotypes into various clusters
Fifty jackfruit accessions were also grouped into eight clusters through Ward's minimum variance method (Anderberg, 1973) [1] and the distributions of the varieties into different clusters are presented in Table - 4 and Fig. - 2.
Among all the clusters, cluster III contained the maximum number of genotypes i.e. 11 *viz.*, JF-3, JF-5, JF-6, JF-17, JF-31, JF-32, JF-33, JF-42, JF-46, JF-49 and JF-50, while cluster III contained only three accession i.e. JF-4, JF-9 and JF-44. Cluster I, VI and VIII contained 4 accessions each and those are JF-I, JF-12, JF-21 & JF-23; JF-10, JF-15, JF-29 & JF-38 and JF-20, JF-41, JF-43 & JF-47, respectively. Cluster V consisted of 10 accessions i.e. JF-7, JF-8, JF-18, JF-22, JF-25, JF-26, JF-34, JF-36, JF-37 and JF-40, followed by Cluster II with 9 genotypes contained *viz.*, JF-2, JF-13, JF-16, JF-19, JF-24, JF-28, JF-39, JF-45 and JF-48. The remaining cluster i.e. cluster VII had 5 (JF-11, JF-14, JF-27, JF-30 and JF-35) genotypes.

Average intra and inter-cluster Euclidean distance values
The average intra and inter-cluster Euclidean distance were measured on the basis of Ward's minimum variance and are presented in the Table - 5 and Fig. - 3.
Through Ward's method, the 50 jackfruit genotypes were grouped into eight clusters. Among these clusters formed, cluster VIII has the minimum intra-cluster Euclidean distance value of 227.099, preceded by cluster VI (306.350), cluster III (316.956), cluster II (364.390), cluster V (445.784) & cluster VII (630.190) and the maximum value observed in cluster I (780.098). The inter-cluster Euclidean distances varied from 263.900 (between cluster V and cluster II) to 1732.753 (between clusters II and I). All the inter-cluster Euclidean values were lying between these values.
Cluster I is nearest to cluster VII (721.161), preceded by cluster IV (973.102) and farthest from cluster I (1732.753) followed by cluster VIII (1718.183).
Cluster II is nearest to cluster V (263.900), preceded by cluster III (319.734) and farthest from cluster I (1732.753), followed by cluster VII (1016.345).
Cluster III is nearest to cluster V (278.777), preceded by cluster II (319.734) and farthest from cluster I (1425.431), followed by cluster VII (713.901).
Cluster IV is nearest to cluster VI (447.335), preceded by cluster VII (453.871) and farthest from cluster II (975.025), followed by cluster I (973.102).
Cluster V is nearest to cluster II (263.900), preceded by cluster III (278.777) and farthest from cluster I (1581.238), followed by cluster VII (868.059).

Cluster VI is nearest to cluster VII (356.051), preceded by cluster IV (447.335) and farthest from cluster I (1038.897), followed by cluster II (752.443).

Cluster VII is nearest to cluster VI (356.051), preceded by cluster IV (453.871) and farthest from cluster II (1016.345), followed by cluster VIII (1013.657).

Cluster VIII is nearest to cluster V (284.933), preceded by cluster II (337.413) and farthest from cluster I (1718.183), followed by cluster VII (1013.657).

Jagadeesh *et al.* (2007) [9] reported similar pattern of clustering analysis with 95 jackfruit types selected from the hilly and coastal zone of Karnataka (India). The clustering pattern showed that selections from the same area did not necessarily belong to the same cluster. Moreover, selections from different eco-geographic areas were grouped into same cluster and selections from the same geographic area were found to form different clusters. It appears that genetic drift and natural selection under different environmental conditions could cause considerable diversity than geographical distance. Similar pattern of clustering of the selections in order to identify the diverse types by considering few important characters were earlier attempted by Maiti *et al.* (2002) [11] in jackfruit.

Table 1: Location details of various Jackfruit germplasm samples chosen for the present study

Sl. No.	Genotypes	Place of collection	Geographical location	
			Latitude (North)	Longitude (East)
1	JF-1	Krishi Vigyan Kendra, Panisagar, Tripura, India	$24^0$15'17.2"	$92^0$9'14.5"
2	JF-2	Prasenjit Das, Roa, Tripura, India	$24^0$15'42.9"	$92^0$10'14.6"
3	JF-3	Anup Nath, Laxmipur, Dasda, Tripura, India	23°57' 40.1"	92°12'7.9"
4	JF-4	Md. Khalil Uddin, Pekucherra, Tripura India	$24^0$15'19.5"	$92^0$10'21.1"
5	JF-5	Himadri Sekhar Das, Bilthoi, Tripura, India	$24^0$16'43.5"	$92^0$8'59.1"
6	JF-6	Lalnunpuia, Purba Hmunpui, Jampui, Tripura, India	$24^0$3'8.2"	$92^0$16'36.8"
7	JF-7	Lalhriatpuia, Vanghmun, Jampui, Tripura, India	$24^0$0'15.9"	$92^0$16' 43.1"
8	JF-8	Narayan Bhowmik, Pratyekroy, Tripura, India	$24^0$24'41.8"	$92^0$11'58.4"
9	JF-9	Bikash Chandra Reang, Satnala, Kanchanpur, Tripura, India	$23^0$59'38.1"	$92^0$12'48.1"
10	JF-10	Aisharai Reang, Laljuri, Tripura, India	$24^0$9'5.0"	$92^0$12'39.8"
11	JF-11	Biswadeep Chakraborty Kameswar, Tripura, India	$24^0$22'54.2"	$92^0$11'18.5"
12	JF-12	Sujit Pal, Baruakandi, Ragna, Tripura, India	$24^0$24'25.1"	$92^0$8'44.8"
13	JF-13	Jamal Hachaini, Rajnagar, Tripura, India	$24^0$19'31.9"	$92^0$7'56.2"
14	JF-14	Barun Rupini, Rahumchhara, Tripura, India	$24^0$14'39.7"	$92^0$15'56.1"
15	JF-15	Subhash Bhowmik, Damcherra, Tripura, India	$24^0$14'38.7"	$92^0$16'40.6"
16	JF-16	Superintendent of Agriculture Office, Kadamtala, Tripura, India	$24^0$27'9.5"	$92^0$13'7.5"
17	JF-17	Utpal Nath, Mantala, Dharmanagar Jail Road, Tripura, India	$24^0$22'9.2"	$92^0$8'46.5"
18	JF-18	Sarat Kumar Halam, Purba Halam Para, Ujan Machmara, Tripura, India	$24^0$8'2.7"	$92^0$13'12.6"
19	JF-19	Bikash Debnath, Purba Tilthoi, Tripura, India	$24^0$18'6.7"	$92^0$8'48.1"
20	JF-20	Buddhimantra Singha Sanicherra, Tripura, India	$24^0$22'44.7"	$92^0$14'6.4"
21	JF-21	Dhirendra Das, Algapur, Dharmanagar, Tripura, India	$24^0$22'49.9"	$92^0$8'31.0"
22	JF-22	Kutub Ali, Bishnupur, Tripura, India	$24^0$26'1.0"	$92^0$11'8.3"
23	JF-23	Taj Uddin, Jubarajnagar, Tripura, India	$24^0$19'20.8"	$92^0$8'28.4"
24	JF-24	Surendra Nath, Noagaon, Purba Tilthoi, Tripura, India	$24^0$18'22.4"	$92^0$8'36.0"
25	JF-25	Lamlingul Halam, Paschim Tilthoi, Tripura, India	$24^0$16'35.5"	$92^0$6'13.3"
26	JF-26	Pritesh Malakar, Maheshpur, Tripura, India	$24^0$27'1.1"	$92^0$1'10.9"
27	JF-27	Abdul Hannan, Jubarajnagar, Tripura, India	$24^0$19'6.9"	$92^0$8'21.8"
28	JF-28	Vanchungngir Halam, Laxminagar, Tripura, India	$24^0$24'26.3"	$92^0$14'19.2"
29	JF-29	Nantu Ghosh, Hurua, Tripura, India	$24^0$22'25.4"	$92^0$12'40.7"
30	JF-30	Arjun Nath, Uttar Padmabil, Tripura, India	$24^0$17'56.6"	$92^0$10'57.5"
31	JF-31	Darsunliyn Halam, Vati Sailen Bari, Bilthoi, Tripura, India	$24^0$15'23.4"	$92^0$7'23.6"
32	JF-32	Goutam Datta, Chandrapur, Dharmanagar, Tripura, India	$24^0$23'49.2"	$92^0$9'27.6"
33	JF-33	Ayub Ali, Purba Halflong, Tripura, India	$24^0$19'26.1"	$92^0$8'7.7"
34	JF-34	Anjana Rani Reang, Ahalyapur, Kanchanpur, Tripura, India	$24^0$3'9.7"	$92^0$12'24.1"
35	JF-35	Khetrajoy Reang, Piplacherra, Damcherra, Tripura, India	$24^0$14'17.5"	$92^0$17'34.1"
36	JF-36	Pintu Nath, Pratyekroy, Tripura, India	$24^0$24'36.8"	$92^0$12'57.6"
37	JF-37	Basudeb Ghosh, Ganganagar, Tripura, India	$24^0$22'24.6"	$92^0$12'39.9"
38	JF-38	Sulaka Nath, laljuri Paper Area, Tripura, India	$24^0$7'7.6"	$92^0$12'12.6"
39	JF-39	Dahanjoy Reang, Hemsukla Para, Ujanc Machmara, Tripura, India	$24^0$6'45.8"	$92^0$13'48.6"
40	JF-40	Rahul Nath, Dakshin Padmabil, Tripura, India	$24^0$17'22.3"	$92^0$11'5.6"
41	JF-41	Ranamoy Das, Helenpur, Dasda, Laxmipur, Tripura, India	$23^0$56'13.3"	$92^0$13'16.3"
42	JF-42	Amir Uddin, Challish Drone, Kadamtala, Tripura, India	$24^0$27'54.8"	$92^0$12'50.5"
43	JF-43	Madhu Debnath, Deocherra, Ramnagar, Tripura, India	$24^0$18'13.7"	$92^0$9'36.8"
44	JF-44	Prasenjit Malakar, Churaibari, Kadamtala Road, Tripura, India	$24^0$26'14.0"	$92^0$14'43.0"
45	JF-45	Toniwa Goswami,East Chandrapur, Dharmanagar, Tripura, India	$24^0$23'35.6"	$92^0$09'57.0"
46	JF-46	Subir Malakar,Padmapur, Dharmanagar, Tripura, India	$24^0$21' 28.0"	$92^0$9' 39.1"
47	JF-47	Dipti Debbarma,Uptakhali,Tripura, India	$24^0$19' 37.1"	$92^0$12' 3.9"
48	JF-48	Tingpaikhup Halam,madhuban word 3,Paschim Tilthoi,Tripura, India	$24^0$16' 28.3"	$92^0$6' 24.5"
49	JF-49	Bappu Chakroborty, Damcherra, Tripura, India	$24^0$14' 18.9"	$92^0$17' 14.7"
50	JF-50	Nishikanta Nath, Mathabpur, Jalebasha, Tripura, India	$24^0$15' 39.7"	$92^0$11' 40.7"

Table 2: Clustering of jackfruit (*Artocarpus heterophyllus* Lam.) germplasm through Mahalanobis' D^2 values (using by Tocher's Method)

Sl. No.	Cluster number	Number of genotypes in cluster	Genotypes
1	I	10	JF-1, JF-11, JF-21, JF-41, JF-31, JF-16, JF-46, JF-26, JF-36, JF-6
2	II	28	JF-2, JF-37, JF-17, JF-47, JF-7, JF- 32, JF-12, JF-42, JF- 22, JF-27, JF-40, JF-45, JF-44, JF-15, JF-34, JF-5, JF-14, JF-24, JF-23, JF-19, JF-38, JF-18, JF-29, JF-35, JF-39, JF-25, JF-3, JF-30
3	III	2	JF-4, JF-9
4	IV	5	JF-8, JF-13, JF-28, JF-43, JF-33
5	V	2	JF-10, JF-20
6	VI	1	JF-48
7	VII	1	JF-49
8	VIII	1	JF-50

Table 3: Average inter and intra-cluster D^2 values of different jackfruit (*Artocarpus heterophyllus* Lam.) germplasm based on quantitative traits using Tocher's method

Cluster number	Cluster number							
	I	II	III	IV	V	VI	VII	VIII
I	27.165	158.422	203.872	162.837	232.217	54413.263	22827.266	33990.089
II		76.375	113.774	119.879	132.056	53448.441	22453.184	36297.054
III			7.151	195.397	226.395	53430.269	22200.652	36333.093
IV				24.882	168.608	53422.366	22568.182	35760.350
V					18.397	53794.426	22730.610	37231.868
VI						0.000	23466.553	62655.811
VII							0.000	46150.948
VIII								0.000

Table 4: Clustering of jackfruit (*Artocarpus heterophyllus* Lam.) germplasm through Ward's minimum variance method

Sl. No.	Cluster number	Number of genotypes in cluster	Genotypes
1	I	4	JF-1, JF-12, JF-21, JF-23
2	II	9	JF-2, JF-13, JF-16, JF-19, JF-24, JF- 28, JF-39, JF-45, JF- 48
3	III	11	JF-3, JF-5, JF-6, JF-17, JF-31, JF- 32, JF-33, JF-42, JF- 46, JF-49, JF-50
4	IV	3	JF-4, JF-9, JF-44
5	V	10	JF-7, JF-8, JF-18, JF-22, JF-25, JF- 26, JF-34, JF-36, JF- 37, JF-40
6	VI	4	JF-10, JF-15, JF-29, JF-38
7	VII	5	JF-11, JF-14, JF-27, JF-30, JF-35
8	VIII	4	JF-20, JF-41, JF-43, JF-47

Table 5: Average inter and intra-cluster Euclidean distance values of different jackfruit (*Artocarpus heterophyllus* Lam.) germplasm based on quantitative traits using Ward's minimum variance method

Cluster number	Cluster number							
	I	II	III	IV	V	VI	VII	VIII
I	780.098	1732.753	1425.431	973.102	1581.238	1038.897	721.161	1718.183
II		364.390	319.734	975.025	263.900	752.443	1016.345	337.413
III			316.956	709.303	278.777	497.554	713.901	413.303
IV				879.208	762.823	447.335	453.871	914.525
V					445.784	571.144	868.059	284.933
VI						306.350	356.051	746.773
VII							630.190	1013.657
VIII								227.099
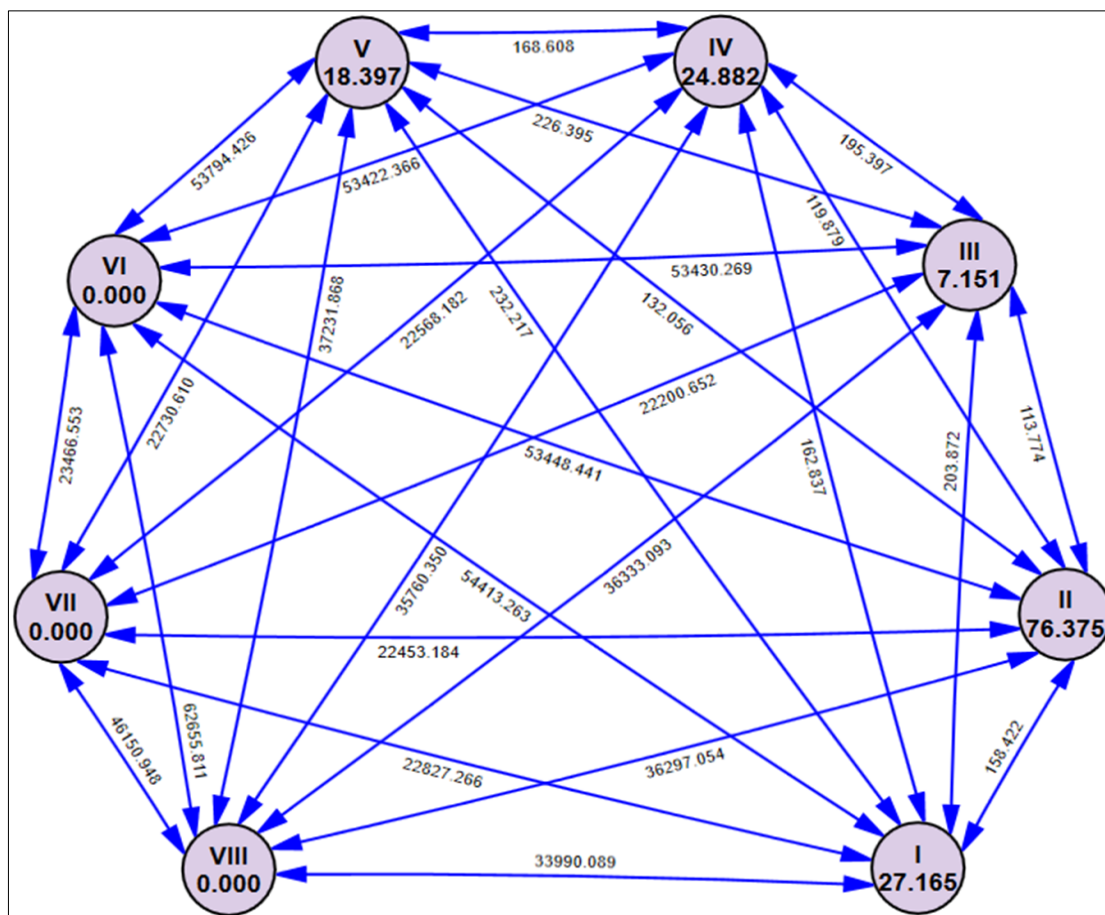
Fig 1: Average inter and intra-cluster distance (D² value) through Tocher's method [not to the scale]
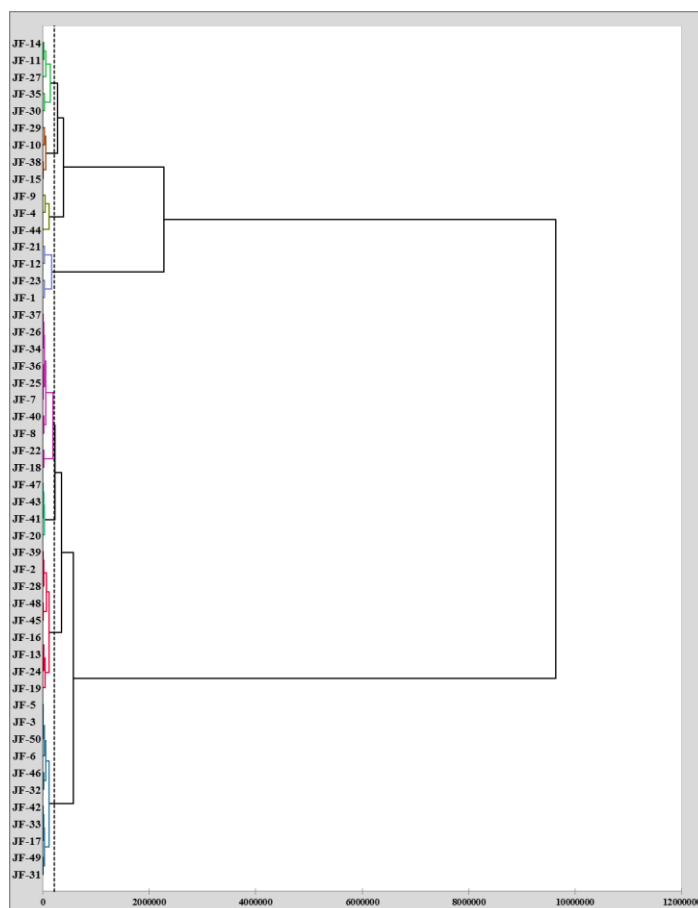
Fig 2: Dendrogram generated through Ward's minimum variance method for jackfruit (*Artocarpus heterophyllus* Lam.) Germplasm
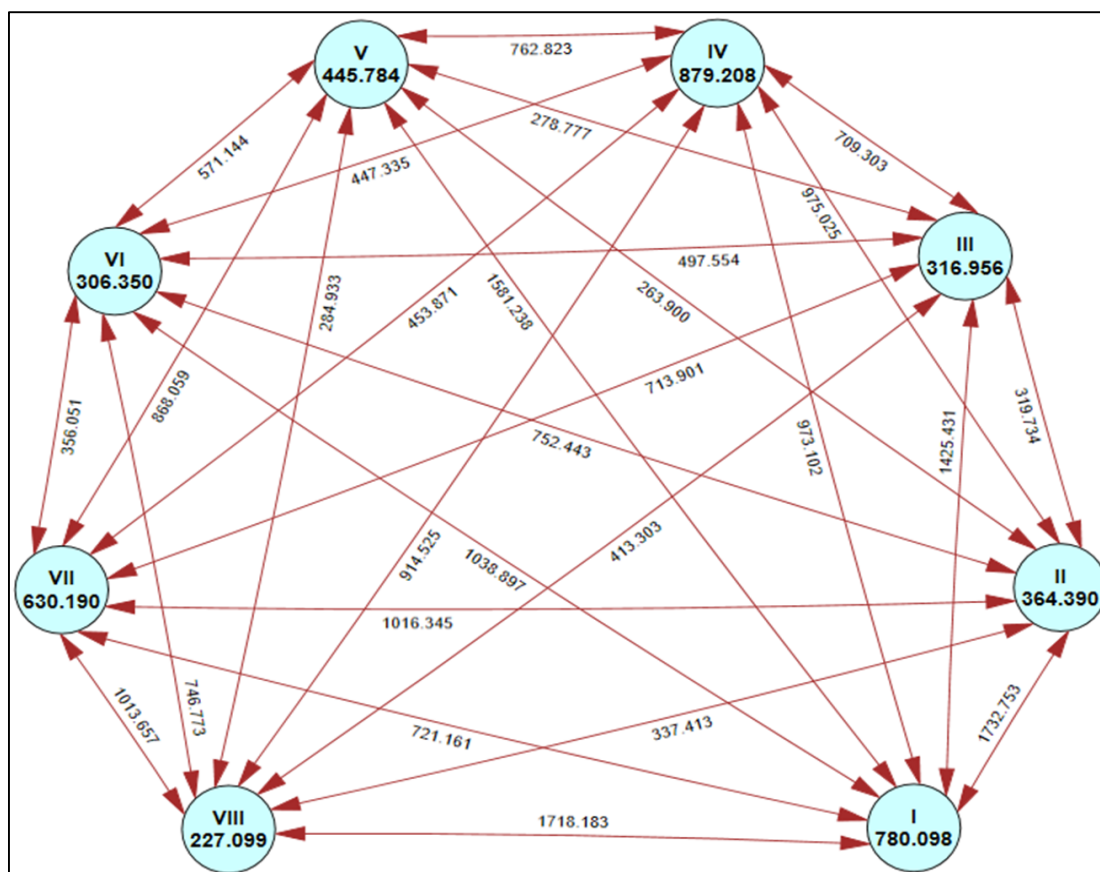
Fig 3: Average inter and intra-cluster Euclidean distance value [not to scale]

Conclusion

In the present investigation, both Mahalanobis' D^2 analysis (Tocher's method) and Euclidean analysis (Ward's minimum variance method) grouped the 50 jackfruit genotypes into eight clusters. However, the clusters show variations in different methods with respect to number of genotypes and the actual accessions included in each cluster. In D^2 analysis the largest cluster was cluster II, with 28 genotypes and cluster VI, VII and VIII comprised of only one accession each *viz.*, JF-48, JF-49 and JF-50, respectively. The maximum Inter-cluster distance was observed here between cluster VI and cluster VIII (i.e. 62655.811). Whereas, Intra-cluster D^2 values ranged from 0.00 (cluster VI, VII and VIII) to 76.375 (cluster II). In Ward's method cluster III was the largest having 11 accessions, followed by cluster V, having 10 genotypes. On the other hand, cluster IV was consisted of least numbers (i.e. only three) of genotypes *viz.*, JF-4, JF-9 and JF-44. Among these clusters constructed, cluster VIII had the minimum intra cluster distance of 227.099 among the grouped genotypes, while the highest value was observed in cluster I (879.208). This system revealed the highest Inter-cluster value between cluster I and cluster II (i.e. 1732.753). From both of these clustering system it is evident that genotypes JF-1, JF-12, JF-21, JF-30 and JF-35 are either located in the same cluster or in adjacent clusters, while accessions JF-4 and JF-9 were placed in the same cluster together in both the cases. This might be an indication towards the distinctiveness of these genotypes from the other genotypes under the present study. This result may be pointing towards the fact that with respect to majority of the tree and yield attributes along with bio-chemical parameters these genotypes possessed considerable divergence, which

could be exploited in very effective manner during development of new selection or recombinant cultivars of jackfruit through the incorporation of the favourable traits.

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