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Original Research Paper

Diversity and variability studies in jackfruit (*Artocarpus heterophyllus* Lam.) genotypes of Assam, India

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ABSTRACT

The present study was conducted with 24 jackfruit genotypes selected from six different districts of Assam, India to investigate the extent of variability and diversity among the selected genotypes. Wide variability was observed for desirable traits like fruit weight, number and weight of flakes/kg of fruit weight, TSS, ascorbic acid, total carotenoid, total flavonoid content and total antioxidant activity. The heritability for quantitative and qualitative traits ranged from 84.26% to 99.94%. Fruit weight showed significant positive correlation with leaf width, fruit length, fruit diameter and weight of flakes/kg of fruit. The highest contributor to genetic divergence among quantitative characters was fruit weight (52.50%), followed by number of flakes/kg of fruit (17.32%), among qualitative characters, it was reducing sugar (85.27%), followed by TSS (10.84%). Further, these twenty-four genotypes were grouped into three clusters for quantitative characters and five clusters for qualitative characters.

Keywords: Divergence, heritability, jackfruit, variability

INTRODUCTION

The jackfruit (*Artocarpus heterophyllus* Lam.) belongs to the family Moraceae and is believed to have originated in the rain forests of the Western Ghats of India (Rowe-Dutton, 1985). The flakes of ripe jackfruit are eaten fresh, in fruit salads, while, unripe fruits used as vegetable. Jackfruit pulp is rich in carotene, vitamins and minerals (Samaddar, 1985; Narasimham, 1990). Carotenoids found in jackfruit can prevent several chronic degenerative diseases including cancer (Krinsky et al., 2003). The resveratrol content (3.56 µg/g) found in jackfruit skin is comparatively similar to that found in the skin extracts of grapes (Akshatha et al., 2015). Jackfruit seeds are a good source of starch, dietary fibre (Hettiarachchi et al., 2011) and protein (Swami et al., 2012).

Assam ranks third in the production (212.16 thousand tonnes) of jackfruit in India after Orissa and Kerala (NHB, 2021-22). Jackfruit is an underutilized crop because of its low productivity, poor keeping and processing quality. The jackfruit being highly heterozygous, cross pollinated and seed propagated fruit crop offer wide range of variations which serve as pre-requisite for any improvement programme. As a preliminary step in improvement and commercialization of the crop, the nature of diversity and variability in terms of physico-chemical characters should be investigated by selecting trees with desirable characteristics after thoroughly surveying the growing areas.

Hence, the present study was undertaken to study the extent of variability and genetic diversity among the superior selected jackfruit genotypes of Assam with respect to the morphological and biochemical traits.

METHODS AND MATERIALS

The present investigation was carried out on bearing trees of twenty-four jackfruit genotypes selected after a survey of six agro-climatic zones of Assam during 2017-18. Four healthy jackfruit trees between 10 to 20 years of age were selected in one representative district based on Bioversity International descriptor (Anon., 2000) under each of the six agroclimatic zones of Assam, thereby totalling 24 numbers of genotypes from six different locations of Assam (24° 51.423` to 26° 44.801` N latitude and 92° 44.507` to 94° 12.960` E longitude. The genotypes were coded with initials of the district e.g., CAC for Cachar, GLP for Goalpara, NAG for Nagaon, BIS for Biswanath, KA for Karbi Anglong and JRT for Jorhat followed by the numerical 1 to 4 for tree number.

Timely and periodical observations were recorded on various characters. The four harvested fruits from each selected genotype were collected for two consecutive years and analysed in the laboratory for quantitative and qualitative characteristics. The morphological observations were recorded as per the descriptor developed by Bioversity International (Anon., 2000). TSS, reducing and total sugar of the pulp were estimated according the methods of A.O.A.C. (2004). The titratable acidity content was estimated by the methods of Sadasivam & Manickam (1996). Ascorbic acid was estimated according to Freed (1966). Total carotenoid content on dry basis was determined according to Rodriguez-Amaya (1999). Crude fibre was estimated according to Maynard (1970), total flavonoid (Woisky & Salatino, 1998), total antioxidant activity (TAA) (Molyneux, 2004), and ash content (total mineral) was determined by dry ashing method (Ranganna, 1986).

Analysis of variance was done following the standard method given by Panse & Sukhatme (1985), coefficient of variation by Comstock & Robinson (1952), genetic gain by Johnson et al. (1955), correlation by Al-Jibouri et al. (1958) and Miller et al. (1958) and multivariate analysis (D^2 statistics) by Mahalanobis (1936). Cluster analysis was done using Tocher's method as described by Rao (1952) and contribution of individual characters towards divergence was estimated as described by Singh (1981).

RESULTS AND DISCUSSION

Wide variability was observed in many desirable characteristics such as fruit weight (1.19-10.89 kg), number of flakes per kg of fruit (3.38-38.18), the weight of flake per kg of fruit (0.15-0.54 kg), 100-seed weight (375-900 g), TSS (16.32-29.70 °Brix), TSS acid ratio (50.29-229.57), total sugar

Table 1 : Variability in quantitative and qualitative characters of selected jackfruit genotypes

Character	General Mean	Range	Variation		Coefficient of variation (%)	
			Genotypic	Phenotypic	GCV	PCV
Leaf length (cm)	15.19	10.34-17.94	3.61	3.74	12.51	12.74
Leaf width (cm)	8.58	5.20-10.36	1.38	1.49	13.70	14.24
Fruit weight (kg)	4.61	1.19-10.89	5.68	5.73	51.71	51.92
Fruit length (cm)	28.67	20.33-46.67	47.90	50.05	24.14	24.68
Fruit diameter (cm)	57	40.67-74.00	66.31	68.77	14.29	14.55
Number of flakes/kg of fruit	15.33	3.38-38.18	61.65	62.49	51.22	51.57
Weight of flake/kg of fruit (kg)	0.37	0.15-0.54	0.01	0.01	29.23	29.85
Flake seed ratio	4.46	2.33-5.83	1.10	1.12	23.56	23.68
Flake length (cm)	5.6	3.97-7.37	2.37	2.41	27.50	27.72
Flake width (cm)	4.07	2.50-5.60	0.49	0.52	17.18	17.77
Seed length (cm)	2.87	2.42-3.38	0.05	0.05	7.87	7.95
Seed width (cm)	1.97	1.53-2.51	0.05	0.05	10.95	10.99
100-seed weight (g)	619.83	375-900	18313.96	18930.27	21.83	22.20
TSS (°Brix)	21.83	16.32-29.70	14.18	14.19	17.25	17.26
Acidity (%)	0.24	0.13-0.38	0.01	0.01	41.46	41.94
TSS/Acid ratio	111.87	50.29-229.57	3390.44	3569.16	52.05	53.40
Reducing sugar (%)	6.88	4.65-9.71	1.99	1.99	20.48	20.48
Total sugar (%)	19.58	14.34-26.87	10.46	12.41	16.51	17.99
Ascorbic acid (mg/100g)	8.88	4.92-14.29	8.17	8.67	32.19	33.15
Carotenoid (µg/g)	3.59	1.17-8.04	3.58	3.59	52.68	52.76
Crude fibre (%)	2.35	1.40-3.17	0.15	0.17	16.26	17.29
TFC (mgQE/100 ml)	86.39	44.03-127.45	658.15	660.67	29.70	29.75
TAA (%)	55.09	32.46-80.12	215.61	217.07	26.65	26.74
Seed total mineral (%)	3.83	2.89-5.18	0.35	0.37	15.49	15.80
Seed crude protein (%)	16.59	13.65-21.18	4.22	4.25	12.39	12.43
Seed starch (%)	20.29	9.65-35.30	60.98	61.94	38.49	38.79

(14.34-26.87%), ascorbic acid (4.92-14.29 mg/100 g of juice), carotenoid (1.17-8.04 µg/g of a flake), total flavonoid content (44.03-127.45 mgQE/100 ml of juice), total antioxidant activity (32.46-80.12%) and seed starch (9.65-35.30%) (Table 1). Mitra & Maity (2000) and Singh & Srivastava (2000) also observed wide variation in fruit weight, fruit quality and seed characters.

The analysis of variance revealed highly significant differences among the genotypes for various traits, indicating the existence of variability among the genotypes. The genotypic coefficient of variation (GCV) estimated ranged from 7.87 to 52.68 and phenotypic coefficient of variation (PCV) from 7.95 to 52.76. The estimates of PCV and GCV were high for all the traits, except leaf length and width, fruit diameter, flake width, seed length and width, TSS, total sugar, crude fibre, seed total mineral and seed crude protein (Table 1). Chandrasekhar et al. (2018) also reported high GCV and PCV for fruit length, fruit weight, weight of flakes per kg of fruit and reducing sugar in jackfruit genotypes.

The heritability values for quantitative and qualitative traits ranged from 84.26 to 99.9%. Higher heritability values were recorded for fruit weight, number of flakes per kg of fruit, flake seed ratio, TSS, reducing sugar, total flavonoid content and seed crude protein (Table 2). Chandrasekhar et al. (2018) also reported high heritability for fruit weight, number of flakes per kg of fruit and reducing sugar in jackfruit genotypes.

High heritability coupled with high genetic advance as per cent mean was registered for fruit weight, number of flakes per kg of fruit, TSS acid ratio, carotenoid, acidity, seed starch and ascorbic acid, signifying the effect of additive gene action in governing the expression of these traits. Johnson et al. (1955) suggested that heritability and genetic advance when calculated together would prove more helpful in

Table 2 : Heritability and genetic advance for 26 characters of selected jackfruit genotypes

Character	Broad sense heritability (%)	Expected genetic advance	
		5% intensity of selection	As % of mean
Leaf length (cm)	96.5	3.85	25.35
Leaf width (cm)	92.6	2.33	27.20
Fruit weight (kg)	99.2	4.90	106.23
Fruit length (cm)	95.7	13.97	48.72
Fruit diameter (cm)	96.4	16.50	28.94
Number of flakes/kg of fruit	98.7	16.09	104.96
Weight of flake/kg of fruit (g)	95.9	0.22	59.06
Flake seed ratio	99.0	2.16	48.34
Flake length (cm)	98.4	3.15	56.29
Flake width (cm)	93.5	1.39	34.27
Seed length (cm)	98.1	0.46	16.08
Seed width (cm)	99.1	0.44	22.49
100-seed weight (g)	96.7	274.60	44.30
TSS (°Brix)	99.9	7.77	35.58
Acidity (%)	97.7	0.20	84.55
TSS/acid ratio	95.0	117.08	104.65
Reducing sugar (%)	99.9	2.91	42.25
Total sugar (%)	84.3	6.12	31.28
Ascorbic acid (mg/100 g)	94.3	5.73	64.47
Carotenoid (µg/g)	99.7	3.90	108.53
Crude fibre (%)	88.5	0.74	31.55
TFC (mgQE/100 ml)	99.6	52.82	61.15
TAA (%)	99.3	30.19	54.80
Seed total mineral (%)	96.1	1.20	31.32
Seed crude protein (%)	99.3	4.22	25.46
Seed starch (%)	98.4	15.98	78.78

Table 3 : Genotypic correlation coefficient for quantitative characters

Character	1	2	3	4	5	6	7	8	9	10	11	12	13
1	1												
2	0.6254**	1											
3	-0.1078	-0.1516	1										
4	0.0151	-0.1077	0.9379**	1									
5	-0.2061	-0.1413	0.8475**	0.7665**	1								
6	0.0884	0.0781	0.5502**	0.5241**	0.502*	1							
7	0.1904	0.2199	0.594**	0.5752**	0.6552**	0.6443*	1						
8	0.2771	0.323	-0.2071	-0.2606	-0.0991	-0.496*	0.0073	1					
9	-0.3235	-0.2099	0.2452	0.1695	0.4372*	-0.1883	0.388	0.3687	1				
10	-0.0416	0.1778	-0.4304*	-0.4634*	-0.3951	-0.8116**	-0.3429	0.7143**	0.3273	1			
11	-0.175	-0.2764	0.3975	0.3737	0.4318*	-0.069	0.3881	0.1069	0.6296**	0.1494	1		
12	-0.1679	-0.2179	-0.1254	-0.0841	-0.121	-0.5737**	-0.0648	0.2069	0.3739	0.4809*	0.6562**	1	
13	-0.2541	-0.0724	-0.2015	-0.1559	-0.1816	-0.4543*	0.0019	0.142	0.3466	0.5404**	0.2952	0.5728**	1

1: leaf length (cm), 2: leaf width (cm), 3: fruit weight (kg), 4: fruit length (cm), 5: fruit diameter (cm), 6: number of flakes per kg of fruit, 7: weight of flakes per kg of fruit (g), 8: flake seed ratio, 9: flake length (cm), 10: flake width (cm), 11: seed length (cm), 12: seed width (cm), 13: 100 seed weight (g); *significant at *P*=0.05; **significant at *P*=0.01

predicting the resultant effect of selection on phenotypic expression. Hence, these traits may be effective for selection to improve the quantitative and qualitative attributes of jackfruit.

The fruit weight exhibited a highly significant positive correlation with leaf width, fruit length, fruit diameter and weight of flakes per kg of fruit and a significant negative correlation with flake width (Table 3 & 4). The results are corroborated with the findings of Wangchu et al. (2013) in jackfruit. No distinctive correlation was observed among the qualitative characters.

The multivariate analysis of genetic divergence revealed that fruit weight contributed the highest (52.50%) to genetic divergence, followed by the number of flakes per kg of fruit (17.32%) and least by leaf width (0.5%) and flake length (0.5%) among the quantitative characters (Fig. 1).

Among the qualitative characters, the highest contribution to genetic divergence was reducing sugar (85.27%), followed by TSS (10.84%) and least by seed total mineral (0.02%) (Fig. 2).

The 24 genotypes were grouped into 3 clusters (Table 5) based on quantitative characters and

Table 4 : Phenotypic correlation coefficient for quantitative characters

Character	1	2	3	4	5	6	7	8	9	10	11	12	13
1	1												
2	0.5985**	1											
3	-0.1045	-0.151	1										
4	0.0176	-0.1088	0.9308**	1									
5	-0.1976	-0.1471	0.8454**	0.7703**	1								
6	0.0883	0.0835	0.5353**	0.4904**	0.4726**	1							
7	0.183	0.2189	0.5648**	0.5185**	0.602**	0.6485**	1						
8	0.2671*	0.3178**	-0.2054	-0.2541*	-0.0986	-0.4903**	0.0075	1					
9	-0.3124**	-0.2013	0.2427*	0.1696	0.4278**	-0.1883	0.3657**	0.3546**	1				
10	-0.0431	0.1603	-0.4175**	-0.4434**	-0.3798**	-0.7729**	-0.3169**	0.6889**	0.3041**	1			
11	-0.1729	-0.262*	0.3941**	0.3681**	0.4247**	-0.0706	0.3747**	0.1027	0.6097**	0.1362	1		
12	-0.1634	-0.2162	-0.1238	-0.0805	-0.1161	-0.5687**	0.0646	0.2057	0.3625**	0.4624**	0.6442**	1	
13	-0.2497*	-0.0666	-0.1974	-0.1477	-0.178	-0.4433**	0.0038	0.0123	0.3474**	0.5294**	0.293*	0.5519**	1

1: leaf length (cm), 2: leaf width (cm), 3: fruit weight (kg), 4: fruit length (cm), 5: fruit diameter (cm), 6: number of flakes per kg of fruit, 7: weight of flakes per kg of fruit (g), 8: flake seed ratio, 9: flake length (cm), 10: flake width (cm), 11: seed length (cm), 12: seed width (cm), 13: 100 seed weight (g); *significant at *P*=0.05; **significant at *P*=0.01

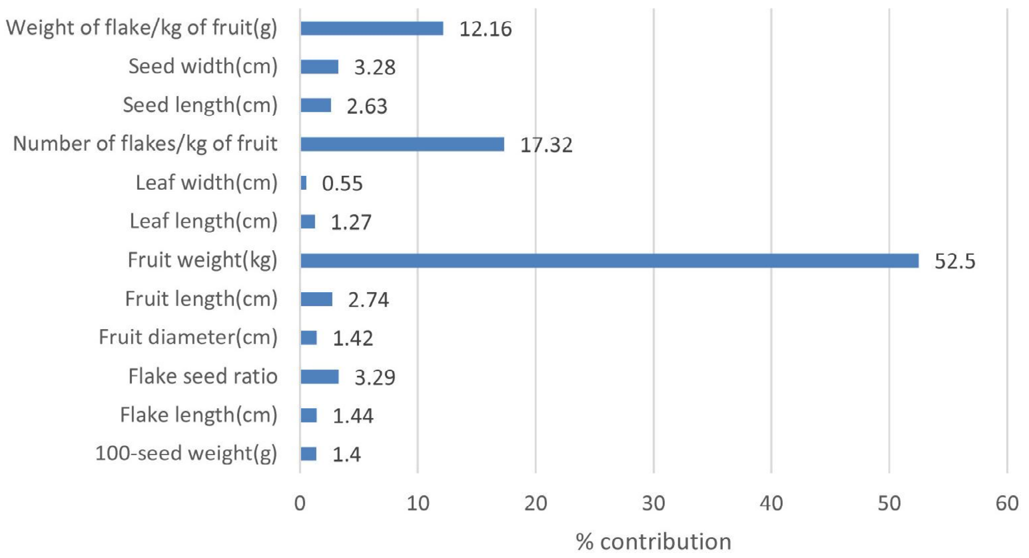

Fig. 1: Contribution of 13 morphological characters to genetic divergence in selected jackfruit genotypes

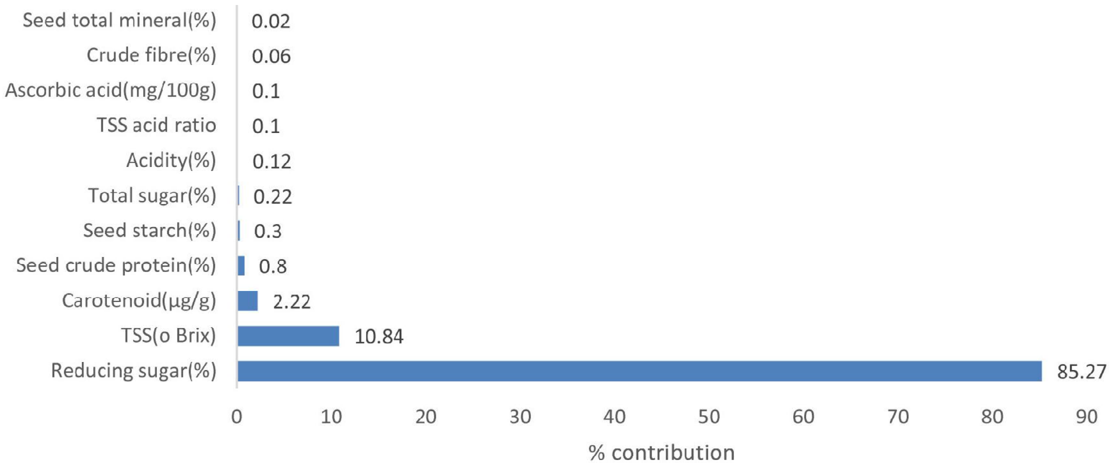

Fig. 2: Contribution of 11 biochemical characters to genetic divergence in selected jackfruit genotypes

Table 5 : Clustering patterns for quantitative characters of selected jackfruit genotypes

Cluster	No. of genotypes	Genotypes
I	19	GLP4, NAG2, KA4, NAG1, JRT1, JRT3, JRT4, JRT2, GLP2, CAC2, KA3, GLP1, NAG4, KA2, CAC1, CAC3, KA1, NAG3, BIS3
II	3	BIS1, BIS4, GLP3
II	2	CAC4, BIS2

Table 6 : Clustering patterns for qualitative characters of selected jackfruit genotypes

Cluster	No. of genotypes	Genotypes
I	6	KA4, JRT4, NAG3, BIS4, GLP3, KA2
II	8	CAC1, GLP1, JRT2, CAC4, BIS2, JRT3, NAG4, CAC3
III	7	CAC2, GLP2, BIS1, GLP4, NAG1, NAG2, JRT1
IV	2	KA1, KA3
V	1	BIS3

5 clusters (Table 6) based on qualitative characters. The clustering pattern of genotypes showed that genotypes featured in a cluster did not necessarily belong to the same geographical area. Therefore, it can be assumed that genetic drift, natural selection, heterozygosity and seedling origin are responsible for this diversity rather than geographical distance.

CONCLUSION

The wide variations observed among the desirable quantitative and qualitative characters among selected 24 genotypes, which can be exploited for improvement of jackfruit through clonal selection. The high heritability and clustering pattern of selected genotypes indicated that the environment has less influence the traits expression and, as such, could be improved by adapting simple selection methods.

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