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Genetic diversity and its relationship with heterosis in okra

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Abstract : Investigation was carried out to assess the genetic diversity and relationship of heterosis with genetic distance between parental lines for days to flowering, node at which the first flower appeared, days to picking, marketable yield, total yield, fruits per plant, fruit weight, plant height, fruit length, days to appearance of YVMV disease, YVMV incidence, protein content, total minerals and mucilage content. On the basis of D^2 values, 28 parental lines were grouped into five clusters. The clustering of genotypes into different groups was observed to be independent of their geographical origin. No relationship of parental genetic distance with F_1 heterosis and performance could be established indicating that the genetic diversity estimates between parental lines based on D^2 may not be suitable criteria for the prediction of heterosis for most of the traits studied.

Key words: *Abelmoschus esculentus*, Mahalanobis D^2 statistics, Genetic divergence

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] commonly known as *bhindi,* is an annual vegetable crop grown in tropical and subtropical parts of the world. It is one of the major summer and rainy season crops and is grown in all agroecological zones of the country for its tender green fruits. Large number of crosses are attempted and hybrids are evaluated by plant breeders every year, however, all of them do not perform well and are rejected. Lot of resources can be saved and efficiency of plant breeding programmes may be enhanced if suitable method for the prediction of heterosis and performance of F_1 hybrids is available. Despite extensive studies, the genetic basis of heterosis is still an enigma for plant breeders and geneticists. It is difficult to predict the performance of F_1 hybrids and development of superior hybrids remains a number game. However, it has been a generally accepted view that genetic diversity plays role in the manifestation of heterosis (Gupta *et al.,* 1991). Mahalanobis's D^2 statistics as explained by Rao (1952), is the most powerful tool used to measure the diversity among given populations with respect to aggregate of characters. It clusters the genotypes in such a way that variation within a cluster is minimum and between clusters is maximum. This method helps to compare the genetic diversity and geographic diversity as well as in the choice of appropriate parents for hybridization. It is important to determine the relationship of mean performance of F_1 hybrids, mid parent heterosis, better parent heterosis with genetic diversity of parental lines. Hence in the present investigation attempt was made to determine the relationship between genetic diversity and heterosis in okra.

Materials and Methods

The experimental plant material consisted of 28 diverse lines of okra crossed in various combinations to generate 52 hybrids. Fifty two hybrids and 28 parental lines including a standard check Punjab 8 were evaluated in a randomized complete block design with three replications during rainy season of 2009. Each treatment was planted in a single row, with row to row distance of 45 cm and plant to plant distance of 30 cm. Observations were recorded for 14 quantitative characters *viz.*, days to first flowering, node at which the first flower appeared, days to first picking, marketable yield per plant (g), total yield per plant (g), number of fruits per plant, average fruit weight (g), plant height (cm), average fruit length (cm), days to first appearance of yellow vein mosaic virus (YVMV), YVMV incidence (%), protein content (%), total minerals (%), and mucilage content (%). All the recommended package of practices were followed to raise a healthy crop.

The data for parental lines were subjected to D^2 analysis as per the standard method of Mahalanobis (1936). Grouping of the genotypes was accomplished using Tocher,s method as described by Rao (1952). Pearson's

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correlation coefficients (r) were computed as described by Panse and Sukhatme (1985) to establish relationship between genetic diversity of parental lines and mean performance F_1 hybrids, mid parent heterosis and better parent heterosis for all the characters studied.

Results and Discussion

Genetic diversity

The data recorded on the parental lines for 14 above mentioned quantitative characters were used to classify the okra lines based on Mahalanobis D^2 statistics. On the basis of D^2 values, 28 parental lines were classified into five groups (Table1). Cluster II was the largest one with 20 genotypes, whereas, rest of the four clusters contained two genotypes each. The clustering of genotypes into different groups did not follow any specific pattern. For example, group I had genotypes originating from Ludhiana centre, whereas, entries originating from New Delhi and Uttrakhand were clustered together in group III. Similarly, group II consisted of entries originated from diverse eco-geographical regions of the country. Therefore grouping of genotypes into different constellations were observed to be independent of their geographical origin. Similar results have been reported by Bhatt (1970), Singh *et al.,* (1977), Chheda and Fatokun (1982), Ariyo (1987), Dash (1997), Chacko *et al.,* (1998), Ghai *et al.,* (2005), Kumari and Choudhary (2006) and Garg (2011). Hence, it appears that geographical diversity may not be used as an index of genetic diversity. This suggests that forces other than geographical separation are also responsible for divergence. Genetic drift and selection in different environments may cause greater diversity than geographical distance. Biotypes originating in particular habitat have different utility only for certain traits for which selection has been practiced. Therefore the varieties originating at the same place may have different genetic architecture or vice versa (Singh and Singh 1979).

Table 1. Clustering pattern of parental lines used in the present study

Cluster No.	Entries
I	POS-1 and POS-17
II	POS-27, Selection-2, Hissar Unnat, LOG 1, Parbhani Kranti, LOG 2, VRO-21, IC-332458, VRO-22, IC-117231, Pusa-A-4, VRO-10, Punjab Padmini, POS-9, KS-442, Arka Abhay, Vrasha Uphar, IC-112451, IC-305634 and Pusa Makhmali
III	NR-22-1 and PB-266
IV	VRO-6 and Punjab-8
V	Pusa Sawani and IC-90185

Table 2. Inter and intra cluster values for 28 genotypes

Cluster	I	II	III	IV	V
I	75.4	640.97	1064.51	1273.98	1441.08
II		156.81	279.35	347.73	449.29
III			57.1	388.5	131.03
IV				277.6	443.88
V					341.7

Inter and intracluster average D2 values among the parental lines have been presented in Table 2. The maximum value for intercluster distance (1441.08) was observed between cluster I and V, followed by cluster I and IV (1278.98), I and III (1064.51), I and II (640.97), II and V (449.29) and so on.Minimum and maximum intracluster distances were observed within clusters III (57.1) and V (341.7), respectively.

Cluster means for various traits studied in the present investigation have been depicted in Table 3. Cluster IV recorded highest average values for marketable yield, number of fruits per plant and protein content. Similarly cluster V exhibited lowest values for days to first picking and per cent virus incidence. Therefore, it may be rewarding to include VRO-6, Punjab-8, IC-90185 and Pusa Sawani in the breeding programmes for development of early, high yielding cultivars with high protein and low per cent virus incidence.

Association of parental diversity with F_1 performance

Correlation of genetic distance between parental lines with mean performance of F_1 hybrids, heterosis over better parent (BPH) and heterosis over mid parent (MPH) has been presented in Table 4. Correlation coefficient between genetic distance and better parent heterosis was observed to be non significant (r = -0.1082) for marketable yield. Highest better parent heterosis (BPH) of 59.81 % was recorded by Arka Abhay x VRO-6. The genetic distance between Arka Abhay and VRO-6 was observed to be 198.3. Parental lines Arka Abhay and LOG 1 recorded a genetic distance of 201.1 which is close to that of exhibited by Arka Abhay and VRO-6, however, their hybrid exhibited -45.86 % BPH for marketable yield. Similarly, other crosses of parental lines with similar genetic distances like Punjab-8 x KS-442 (204.7) and PB-266 x VRO-22 (204.2) recorded BPH value of -40.11 and 52.14 per cent, respectively. Thus, better parent heterosis for marketable yield of F_1 hybrids could not be predicted based on parental distance estimates obtained from D^2 statistics. The correlation coefficients between genetic distance and other quantitative traits were observed to be non significant except better parent heterosis for days to first picking and YVMV incidence. This indicated that genetic

Table 3. Cluster means for agronomic characters in okra

Characters	Days to 1st flowering	Node at which 1st flower appeared	Days to 1st picking	Marketable yield/ plant (g)	Total yield/ plant (g)	Number of fruits /plant	Average fruit weight (g)	Plant height (cm)	Average fruit length (cm)	Days to 1st appearance of YVMV	YVMV incidence (%)	Protein content (%)	Total mineral (%)	Mucilage content (%)
I	44.33	4.17	51.67	39.02	42.13	6.25	6.26	84.62	7.62	43.83	65.62	1.02	1.05	0.54
II	44.62	4.40	49.05	82.56	91.32	12.29	6.71	96.05	7.28	42.63	36.08	1.05	1.36	0.65
III	45.17	4.27	50.17	69.60	72.75	9.69	6.75	96.44	7.24	45.33	23.24	0.97	1.15	0.52
IV	43.17	4.43	47.84	139.21	155.08	20.35	6.80	93.43	7.38	39.83	25.65	1.26	0.96	0.63
V	43.67	3.93	47.50	76.81	81.41	11.76	6.74	93.11	7.12	44.67	17.98	0.93	1.03	0.65

Table 4. Association of genetic distance with F_1 performance and heterosis

	BPH	MPH	*Per se* performance
Character			
Marketable yield	-.1082	0.0124	-0.0533
Total yield	-0.1187	0.0364	-0.0928
Fruits per plant	-0.1407	0.0412	-0.0417
Average fruit weight	-0.0525	-0.0256	-0.0181
Average fruit length	-0.1627	-0.1307	0.1497
Days to 1st flowering	-0.2585	-0.3386	-0.1985
Node at which 1st flower appeared	0.1160	0.1163	0.1065
Days to 1st picking	-0.2818*	-0.3912**	-0.1603
Plant height	0.1150	0.1506	0.0652
Days to 1st virus appearance	-0.0219	0.0634	0.2641
YVMV incidence	0.3008*	-0.1583	0.0599
Protein content	-0.0648	-0.0993	0.0122
Total mineral content	0.1426	0.1507	0.0136
Mucilage content	0.1206	0.0964	0.0863
r^2	5%	0.273	
	1%	0.354	

BPH and MPH refer to better parent heterosis and mid parent heterosis, respectively.

diversity estimates between parental lines obtained using D^2 cannot be used for the precise prediction of better parent heterosis for most of the traits studied. Partap *et al.,* (1980) also reported no consistency between the divergence of parents involved in crosses and heterosis shown by the hybrids.

The correlation coefficients between genetic distance and mid parent heterosis (MPH) were observed to be non significant for all the traits studied except days to first picking. Genetic distances between parental lines viz. Punjab-8 and KS-442 and PB-266 and VRO-22 were observed to be 204.7 and 204.2 respectively. However, their F_1 hybrids exhibited mid parent heterosis value of -24.35 and 53.37 per cent, respectively for marketable yield.

Based on the Dy values, F_1 hybrid of diverse parents Punjab-8 and POS-17 (Dy = 1548.6) recorded mean marketable yield of 65.67 g per plant, whereas, almost same average marketable yield per plant (63.13 g) was produced by the cross Punjab Padmini x Varsha Uphar, though the parents possessed Dy value of 99.3. The parents Arka Abhay and LOG 1, P-8 and IC-117231, Punjab-8 and KS-442, Arka Abhay and VRO-6 exhibited similar Dy values of 201.1, 200.8, 204.7 and 198.3, respectively. However, their respective hybrids recorded an average marketable yield of 41.88 g, 127.39 g, 96.6 g and 187.2 g per cent, respectively. In all, no significant association was observed between genetic distance of parental lines and the mean performance of their respective hybrids for all the traits studied.

Thus the results suggested that genetic distance based on the Mahalanobis D^2 statistics have little predictive value for the prediction of mid parent heterosis, better parent heterosis and mean performance of F_1 hybrids for most of the characters studied.

सारांश

जाँच दिनों के लिए माता–पिता की लाइनों के बीच आनुवंशिक फूल दूरी, नौड जिस पर पहले फूल दिखाई दिया। उठा करने के लिए दिन के साथ आनुवंशिक विविधता और संकट के संबंध का आकलन करने के लिए बाहर किया गया था। विपणन उपज, कुल उपज, संयंत्र फल का वजन, प्रति फल ऊँचाई, फल, बाई पी एम वी रोग, वाई वी एम वी घटना प्रोटीन सामग्री, कुल खनिज और कम सामग्री की उपस्थिति के लिए दिन है। D^2 मूल्यों के आधार पर 28 माता–पिता की लाइनों को पांच समूह में बाटा गया है। अलग समूह में जीनो टाइप के क्लस्टरिंग उनके भौगोलिक मूल के स्वतंत्र होने के लिए मनाया गया। यह दर्शाता है कि माता–पिता D^2 पर आधारित लाइनों के बीच आनुवंशिक विविधता का अनुमान उपयुक्त मानदंडों अध्ययन लक्षण के अधिकांश के लिए संकट की भविष्यवाणी के लिए नहीं हो सकता है। F_1 संकर और प्रदर्शन के साथ माता–पिता की आनुवंशिक दूरी का काई संबंध स्थापित किया जा सकता है।

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