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SHORT COMMUNICATION

Genetic Divergence Studies in Winged Bean (*Psophocarpus tetragonolobus* (L.) DC.)

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Twenty-one genotypes of winged bean [*Psophocarpus tetragonolobus* (L.) DC.] were studied to understand the extent of genetic diversity based on 12 quantitative traits. Mahalanobis D^2 analysis revealed the presence of high amount of genetic diversity among 21 genotypes, which formed five clusters. Cluster-I had the maximum (7) and cluster-III had the minimum (1) number of genotypes. Intra cluster distance analysis revealed that the Cluster-II had highest intra-cluster distance followed by cluster-I. The inter-cluster divergence (D) was the maximum between the clusters-II and V and the minimum between clusters-I and III. The results indicated that days to first flowering contributed maximum to the total divergence followed by pod weight and days to edible maturity. The Cluster-IV had highest mean value for yield per plant and 100 seed weight and the cluster cluster-V has the highest mean value for number of primary branches per plant. The diverse parents identified could be used for genetic improvement in winged bean.

Key Words: Character association, Cluster analysis, Genetic divergence, Genotypes, Winged bean

A large number of leguminous species, which have not yet been fully exploited are of great potential as a nutritive food. Hence, there is a need to exploit such legume vegetables for better health and nutrition. Among the under-exploited legume vegetables, winged bean (*Psophocarpus tetragonolobus* (L.) DC) is the most important. Since nearly every portion of the plant is edible or can be profitably utilized, several superlatives like 'soya's rival', 'God-sent vegetable' and 'vegetable of twentieth century' have often been used for winged bean. Presently, it is cultivated only for its tender green pods and seeds.

Although it is a highly nutritive summer vegetable, until now no proper research thrust has been given for the genetic improvement of this vegetable, therefore, there is an urgent need to design breeding programme to identify and develop suitable genotypes for specific purposes. The knowledge on genetic diversity or similarity could help to get long term selection gain in plants (Chowdhury *et al.,* 2003). Genetic divergence is crucial for the crop improvement programme. Mahalanobis's D^2 statistics is an ideal tool for estimating genetic divergence in crop plants and to choose the parents without making crosses before the initiation of hybridization programme (Bhatt, 1970). Despite the importance of this vegetable crop, only limited breeding work has been done for its genetic improvement in the past, in order to enhance the productivity levels. Therefore, the present investigation was undertaken to study the nature and magnitude of genetic divergence in winged bean genotypes collected from different geographical regions.

The experimental materials comprised of 21 genotypes of winged bean, which were collected from different parts of the country (Table 1). The experiment was laid out in a randomized block design (RBD) with three replications during April, 2013–March, 2014 at Department of Olericulture, College of Agriculture, Vellayani, Thiruvananthapuram. The experimental site was located at $8^{o}\ 5^{'}$ N latitude and $77^{o}\ 1^{'}$ E longitude

Table 1. Source and place of collection of winged bean genotypes used in the study

Source	Number of genotypes	Genotypes
College of Agriculture, Vellayani	7	PT 1, PT2, PT 3, PT 4, PT 5, PT 20, PT 21
Idukki, Kerala	1	PT 6
Palakkad, Kerala	1	PT 7
College of Horticulture, Vellanikkara	12	PT 8 (Revathy), PT 9, PT 10, PT 11, PT 12, PT 13, PT 14, PT 15, PT 16, PT 17, PT 18, PT 19

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at an altitude of 29 m above mean sea level. Soil type of the experimental site was red sandy clay loam with a pH of 5.2 and warm humid tropical climate. Seeds of each genotype were sown in rows at spacing of 125 cm between rows and 50 cm between plants. Recommended agronomic practices were followed to raise a good crop. Observations were taken on five randomly selected plants for 12 quantitative characters *viz.,* vine length (cm), number of primary branches per plant, days to first flowering, days to first harvest, days to edible maturity, pod length (cm), pod girth (cm), pod weight (g), number of pods per plant, yield per plant (g), number of seeds per pod and 100 seed weight (g). Analysis of variance (ANOVA) was carried out as suggested by Panse and Sukhatme (1964). Genetic divergence was estimated using D^2 statistics of Mahalanobis (1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952). The per cent contribution of characters towards genetic divergence was calculated according to Singh and Chaudhary (1985).

ANOVA for yield and its contributing traits revealed that the genotypes differed significantly for these traits (Table 2). This indicates that there is ample scope for selection of promising lines from the present gene pool aimed at enhancing genetic yield potential of winged bean. The D^2 value varied widely and principal component scores also revealed a good degree of genetic diversity among the genotypes.

Variation was accessed using principal component analysis by taking in to account every variable at once. First four principal components accounted for a total of 86.14 % variability among the accessions using quantitative traits (Table 3). A total of 48.22 per cent of variance of the total variation was observed in the first principal component, PC 2 depicted per cent of variance as 20.17, PC 3 accounted for 11.62 per cent of the total variation and PC 4 contributed 6.11 percent to the total variation. PC 1 showed predominantly the variation in days to first flowering, days to first harvest, primary branches per plant and 100-seed weight. PC 2 was mostly correlated with seeds per pod, yield per plant, vine length and days to first flowering. PC 3 was associated with vine length and days to edible maturity, where as vine length, pod girth and yield per plant made positive contribution to PC 4. Similar findings were also reported by Maria sultan *et al.* (2012) in cluster bean.

Table 2. Analysis of variance for different quantitative traits in winged bean

Characters	Treatments (df= 20)	CV %
Vine length (cm)	14152.800**	10.14
Primary branches/plant	19.882**	22.46
Days to first flowering	2453.884**	25.20
Days to first harvest	2101.975**	19.32
Days to edible maturity	15.949**	15.86
Pod length (cm)	12.333**	10.72
Pod girth (cm)	1.982**	10.69
Pod weight (g)	28.975**	16.24
Pods/plant	2660.800**	34.39
Yield/plant (g)	906210.000**	35.30
Seeds/pod	13.543**	17.60
100 seed weight (g)	104.930**	18.27

** Significant at P= 0.01

All the 21 genotypes were grouped into five clusters following Tocher's methods (Table 4). Cluster I constitutes of seven genotypes, forming the largest cluster followed by cluster IV and cluster V with five genotypes each. Cluster II consist of three genotypes and clusters III was comprised of single genotype. The pattern of group constellation proved the existence of significant amount of variability. There are forces other than geographical separation such as natural and artificial selection, exchange of breeding material, genetic drift,

Table 3. Principal components for 12 quantitative traits in winged bean

Trait	PC 1	PC 2	PC 3	PC 4
Eigen value	5.786	2.421	1.394	0.734
percentage variance	48.22	20.17	11.62	6.11
Cumulative variance	48.22	68.40	80.02	86.14
Eigenvectors				
Vine length	0.028	0.399	0.364	0.691
Primary branches/plant	0.294	0.301	-0.202	-0.305
Days to first flowering	0.332	0.326	-0.065	-0.030
Days to first harvest	0.315	0.295	-0.233	0.040
Days to edible maturity	-0.244	0.333	0.224	-0.398
Pod length	-0.346	0.279	0.028	-0.035
Pod girth	-0.275	-0.149	-0.495	0.353
Pod weight	-0.395	-0.043	-0.163	-0.143
Pods/plant	-0.350	-0.066	-0.060	-0.030
Yield/plant	-0.279	0.358	-0.220	0.267
Seeds/pod	-0.211	0.455	-0.236	-0.198
100-seed weight	0.214	-0.042	-0.579	0.093

Table 4. Distribution of 21 winged bean genotypes in five different clusters

Cluster	Number of genotypes	Genotypes included
I	7	PT 1, PT 4, PT 8, PT 14, PT 15, PT 20, PT21
II	3	PT 5, PT 10, PT 19
III	1	PT 18
IV	5	PT 7, PT 9, PT 11, PT 12, PT 17
V	5	PT 2, PT 3, PT 6, PT13, PT 16

environmental variation, etc., which are responsible for diversity in winged bean. Therefore, choice of the parents for hybridization should be decided on the basis of genetic diversity rather than geographic diversity. Many earlier studies on D^2 statistics in various crops already showed the lack of parallelism between genetic and geographic diversities. Similar results were also reported by Singh and Singh (2006) in field pea, Dahiya *et al.* (2007) and Pandey (2007) in cowpea, and Mahto and Dua (2009) and Kushwaha *et al.* (2013) in winged bean.

The intra-cluster D^2 value ranged from 0.00 to 46.37, while inter-cluster D^2 value ranged from 44.77 to 269.17 which indicated that the selected genotypes were highly divergent (Table 5). The maximum intra cluster distance was recorded for cluster-II followed by cluster-I and cluster-III, IV and V showed no intra-cluster distance values indicating comparatively homogenous nature of the genotype within the cluster. The high intra-cluster distance in cluster-II indicated the presence of wide genetic diversity among the genotypes in this cluster. The maximum inter-cluster D^2 value was observed between cluster-II and V followed by cluster-I and V, cluster-II and IV and cluster-III and V suggesting that the genotypes belonging to these clusters may be used as parents for hybridization programme to develop desirable type because for a successful breeding programme, selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants (Rai and Dharmatti, 2013). Similar results were reported by Venkatesan *et al.* (2004), Naher *et al*. (2005) in cowpea Arora *et al.* (2005) in cluster bean, and Mahto and Dua (2009) and Kushwaha *et al*. (2013) in winged bean.

Table 5. Average intra (bold face) and inter-cluster distance (D^2) for 21 winged bean genotypes

Clusters	I	II	III	IV	V
I	25.56	54.07	44.77	53.96	169.62
II		46.37	83.32	127.66	269.17
III			0.00	53.53	105.44
IV				0.00	89.16
V					0.00

Table 6. Relative contribution of 12 characters towards genetic divergence in 21 winged bean germplasm

S. No.	Characters	Number of times ranked first	% contribution
1	Vine length (cm)	6	2.86
2	Primary branches / plant	1	0.48
3	Days to first flowering	65	30.95
4	Days to first harvest	20	9.52
5	Days to edible maturity	28	13.33
6	Pod length (cm)	7	3.33
7	Pod girth (cm)	10	4.76
8	Pod weight (g)	31	14.76
9	Pods / plant	2	0.95
10	Yield / plant (g)	2	0.95
11	Seeds / pod	17	8.10
12	100 seed weight (g)	21	10.00
	Total	110	100

The knowledge of the characters contributing to divergence is an important factor and the contribution of an individual character to the total divergence has been worked out in terms of number of times it ranked first (Table 6). This study helps in identifying the diversity in different proportion which ultimately helps in deciding the utilization of genetic material for the improvement of specific character. The maximum contribution to genetic divergence by days to first flowering followed by pod weight, days to edible maturity and 100-seed weight, therefore necessary attention is required to be focused on these characters. There is always difference in opinion in specifying the trait that is contributing high or low towards the genetic diversity. The contribution mainly depends upon the genotypes included in the study and the environment influences over the character. Regarding the least contribution, number of primary branches per plant and pods per plant contributed the least. The minimum contribution by this trait reveals that this trait was least affected in course of evolution.

The comparison of cluster means revealed considerable differences among the clusters of different quantitative characters (Table 7). Cluster-I showed the high mean values for days to edible maturity and number of seeds per pod. Cluster-IV showed highest mean value for pod length, pod girth, pod weight, number of pods per plant, yield per plant and 100-seed weight. The maximum value of cluster mean for vine length, primary branches per plant, days to first flowering and days to first harvest was recorded in cluster-V.

It has been well established that greater the genetic variability in the population higher will be the chances of obtaining desirable gene combination. In the present study, the possibility of choice of highly divergent and desirable types based on D^2 cluster means was also examined. The cluster-IV had the highest cluster mean values for number of pods per plant and yield per plant

Table 7. Cluster mean values for different quantitative characters in winged bean

Cluster Characters	I	II	III	IV	V
Vine length (cm)	668.45	675.90	553.33	767.67	813.33
Primary branches / plant	12.91	8.57	11.33	11.67	15.67
Days to first flowering	117.32	89.00	119.26	175.22	178.83
Days to first harvest	142.59	111.29	146.24	190.35	192.67
Days to edible maturity	15.15	14.57	11.67	11.33	13.67
Pod length (cm)	19.06	19.24	17.58	20.16	14.84
Pod girth (cm)	7.80	7.65	6.76	8.32	5.03
Pod weight (g)	19.61	20.14	14.30	20.76	10.13
Pods / plant	84.73	99.18	47.43	99.42	44.98
Yield / plant (g)	1493.33	1819.52	696.67	2083.33	750.00
Seeds / pod	12.79	11.82	10.75	11.22	8.05
100 seed weight (g)	34.42	29.83	26.96	37.52	27.76

and cluster-V has the highest mean value for number of primary branches per plant. The genotypes in the two clusters may be utilized in crossing programme which may yield in a wide spectrum of variability and for selection for pod yield in the subsequent generations. The lines fall into same cluster having lowest degree of divergence from each other (Fig. 1) and crosses among these lines of the same cluster unable to produce any transgressive segregants. While, the lines belonging to different clusters having maximum divergence. Similarly the cluster-I which had highest cluster mean value for number of seeds per pod and may be selected for crossing with the cluster-IV for obtaining desirable segregants with higher yield.

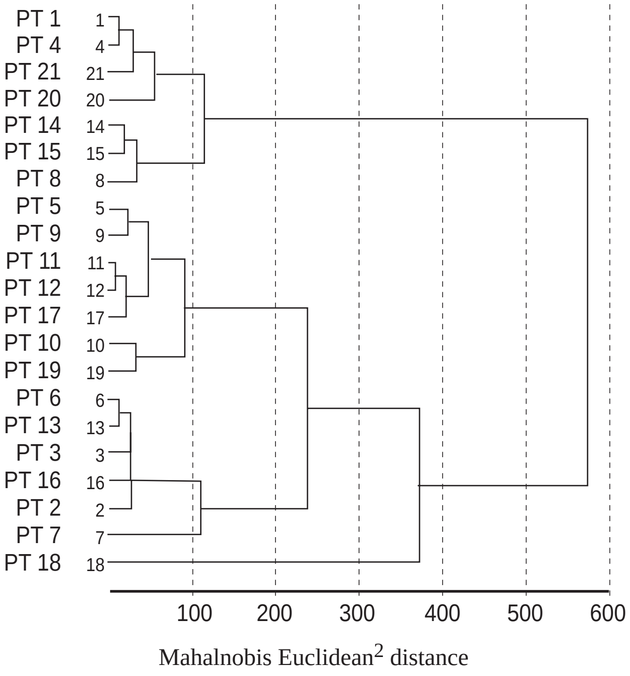

Fig. 1. Euclidean average linkage dendrogram

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