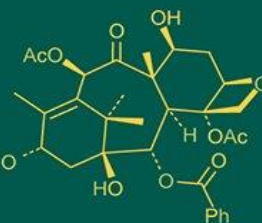
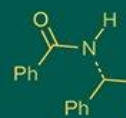
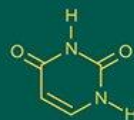
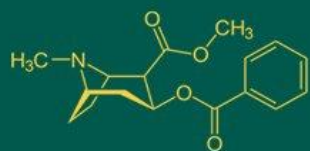


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Multivariate analysis of genetic divergence among winged bean (*Psophocarpus tetragonolobus* L.) genotypes for effective hybridization programme

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Abstract

The present investigation was undertaken to assess genetic divergence among twenty-eight genotypes of Winged bean (*Psophocarpus tetragonolobus* L.) at main experiment station, Department of Vegetable Science, College of Horticulture and Forestry, ANDUAT, Ayodhya, Uttar Pradesh, India, during cropping year 2024–25. Mahalanobis's D^2 statistic and Tocher's method were employed for quantification and clustering of genetic divergence across nineteen characters. All twenty-eight genotypes were grouped into four distinct clusters. cluster III was the largest comprising 11 genotypes, followed by cluster I^[10], cluster II^[6] and cluster IV representing a single genotype. The maximum inter-cluster distance was observed between cluster II and cluster IV (14.203). Based on inter-cluster distances and superior mean performance for yield and yield-attributing traits genotypes belonging to clusters II and IV are identified as promising parents for hybridization programs. Among traits studied internode length (7.70%), pod width (6.87%) and leaflet width (6.15%) contributed most significantly to total genetic divergence.

Keywords: Cluster analysis, Genetic diversity, Mahalanobis D^2 , *Psophocarpus tetragonolobus*, Tocher's method, Winged bean

Introduction

Winged bean (*Psophocarpus tetragonolobus* L.) is a highly versatile yet underutilized food legume native to the humid equatorial tropics of Southeast Asia (Hymowitz *et al.*, 1977)^[3]. It ranks among the most nutritionally complete leguminous crops and forms a valuable component of traditional agricultural systems across tropical regions. It is a self-pollinating diploid species having a somatic chromosome number of $2n=2x=18$ (Harder and Smartt, 1992; Vatanparast *et al.*, 2016)^[2, 12]. The crop is well-adapted to warm and humid tropical climatic conditions and sustains productivity in low-input farming systems across countries including India, Papua New Guinea, Myanmar and the Philippines (Singh *et al.*, 2022)^[10]. Interestingly, all plant parts seeds, pods, leaves, flowers and tuberous roots are edible and nutritionally rich, which forced the National Academy of Sciences (1981)^[7] to describe it as "a supermarket on a stalk". Its notable protein content, atmospheric nitrogen-fixing capacity and broad adaptability position it as a highly promising alternative crop for food and nutritional security in tropical developing nations (Tanzi *et al.*, 2019)^[11]. Genetic improvement of Winged bean begins with judicious selection of parental lines and the establishment of segregating populations from which superior genotypes are identified. A central challenge for breeders is how to choose appropriate parents for hybridization. Crosses between genetically divergent parents are known to generate greater heterosis than those between closely related genotypes. Genetic divergence analysis is therefore a vital tool for evaluating germplasm collections and guiding effective parent selection in crop improvement programmes. The present investigation was undertaken to estimate genetic divergence (D^2) among Winged bean genotypes for identification of suitable parental lines for hybridization.

Materials and Methods

A total of twenty-eight genotypes were evaluated during the agricultural season 2024- 25 at main experiment station, Department of Vegetable Science, College of Horticulture and Forestry, ANDUAT, Ayodhya, Uttar Pradesh, India. The experiment was laid out in a randomized complete block design comprising three replications with a plant spacing maintained at 125 × 60 cm.

All recommended agronomic and crop management practices were followed in a timely manner throughout the growing period. From each replication of every genotype five plants were selected at random, tagged and utilized for data collection. A total of nineteen morphological and yield-related characters were recorded as observations. To assess the extent of genetic divergence among the genotypes, Mahalanobis's generalized distance (D^2) statistic was employed and the genotypes were subsequently categorized into distinct clusters using Tocher's method.

Results and Discussions

Analysis to estimate D^2 value was done on the basis of relative magnitude of D^2 values, all the twenty eight genotypes were grouped into 4 clusters (Table 1). Among the clusters, cluster III was the biggest cluster with 11 genotypes. Cluster I was the second largest cluster with ten genotypes followed by cluster II with six genotypes. The cluster IV were consisting of only one genotype. Similar patterns were also observed by Prasanth *et al.* (2016) [8] and Kashyap (2021) [5].

The inter and intra cluster distances among the genotypes have been shown in table 2. Among all inter-cluster distances recorded the maximum was noted between cluster II and cluster IV (14.203), which was subsequently followed by the distance between cluster III and cluster IV (12.413) and then between cluster I and cluster IV (11.194). Regarding intra-cluster distances the minimum value excluding the solitary cluster was recorded in cluster II (2.640). Cluster IV exhibited an intra-cluster distance approaching nearly zero. Two intermediate clusters falling between the minimum and maximum values were also identified, representing distinct divergence groups. On the other hand, the maximum intra-cluster distance was recorded in cluster I (3.159), with cluster III (2.895) following closely behind it. Roy (2021) [9] and Gadi *et al.* (2025) [1] also reported similar patterns of variable inter and intra-cluster D^2 distances.

With reference to the cluster wise mean values presented in Table 3, the mean pod yield/hectare and seed yield/hectare were found to be the highest in cluster IV (167.74 q and 49.5 q, respectively), whereas the lowest mean values for both these traits were recorded in cluster II (30.97 q and 5.88 q, respectively). Among the remaining clusters, cluster I registered the highest mean value for total soluble solids (5.38), while cluster II did not record the highest mean value for any of the traits under study. The highest mean value for number of

flowers/inflorescence (10.20) was exhibited by cluster III. Meanwhile, cluster IV which was represented by a single genotype demonstrated the highest mean values across all the remaining traits which included number of seeds/pod (18.37), seed index (40.70 g), pod length (28.33 cm) and others. The similar pattern of cluster-specific superiority for different individual traits, where different clusters recorded maximum mean values for different characters was observed by Mishra (2019) [6].

In the current study, the percentage contribution of various key traits toward genetic divergence was calculated and has been presented in Table 4. Among all the characters evaluated for their contribution to genetic divergence internode length recorded the highest contribution of 7.70%, followed by pod width (6.87%) and leaflet width (6.15%). Similar findings were also observed by Prasanth *et al.* (2016) [8], who reported that certain morphological traits accounted for a higher share of divergence than others. Similarly documented by Kant *et al.* (2022) [4] and Kashyap (2021) [5].

Table 1: Distribution of 28 genotypes of Winged bean into four clusters.

Clusters	No of genotypes	Genotypes
I	10	NDWB-22-01, NDWB-22-02, NDWB-22-06, NDWB-22-07, NDWB-22-08, NDWB-22-09, NDWB-22-11, NDWB-22-12, NDWB-22-13 and K. Annapurna (C)
II	6	NDWB-22-05, NDWB-22-15, NDWB-22-22, NDWB-22-23, NDWB-22-24 and NDWB-22-26
III	11	NDWB-22-03, NDWB-22-04, NDWB-22-10, NDWB-22-16, NDWB-22-17, NDWB-22-18, NDWB-22-19, NDWB-22-20, NDWB-22-21, NDWB-22-25 and NDWB-22-27
IV	1	NDWB-22-14

Table 2: Inter and intra (diagonal) cluster values of average of D^2 and D values.

Clusters	I	II	III	IV
I	3.159			
II	4.878	2.640		
III	3.765	3.190	2.895	
IV	11.194	14.203	12.413	0.003

Table 3: Cluster means for nineteen characters in 28 diverse accessions of Winged bean.

traits		LL	LW	TLL	IL	NFI	PL	PW	NPC	NPP	GPW	NSP	SI	AA	TSS	DM	GPYP	SYP	GPYH	SYH
I	Mean	7.35	6.92	20.10	12.36	10.04	18.30	3.45	1.66	33.37	23.20	11.88	38.61	20.63	5.38	10.11	0.780	0.150	104.18	20.06
	SE±	1.59	1.11	2.14	0.40	1.39	1.99	0.25	0.12	9.96	2.32	0.80	2.24	2.45	0.40	0.41	0.260	0.040	34.53	5.58
II	Mean	8.22	6.00	19.60	13.07	9.85	15.80	3.09	1.39	11.83	18.56	9.91	33.05	20.98	5.26	10.21	0.220	0.040	30.97	5.88
	SE±	0.97	0.95	1.72	0.49	1.93	2.71	0.14	0.12	1.28	2.19	1.70	2.17	3.17	0.40	0.22	0.040	0.010	7.40	1.74
III	Mean	8.75	7.69	21.11	12.66	10.20	17.80	3.36	1.33	14.61	22.16	12.40	36.32	18.19	4.93	9.95	0.320	0.070	42.44	8.60
	SE±	0.70	0.52	1.67	0.21	1.59	1.98	0.14	0.30	3.04	3.08	1.22	3.52	1.63	0.46	0.50	0.090	0.020	11.56	2.60
IV	Mean	13.48	11.39	36.96	15.89	9.50	28.33	3.55	2.07	50.25	24.99	18.37	40.70	24.58	4.45	10.86	1.250	0.380	167.74	49.54
	S	0.	0.	0.	0.	0.	0.	0	0	0.	0.	0.	0.	0.	0	0.	0.	0.	0.	0.
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Table 4: Relative contribution of nineteen characters towards genetic divergence in 28 Winged bean germplasm

S. No.	Characters	Percent contribution
1.	Leaflet length (cm)	5.86
2.	Leaflet width (cm)	6.15
3.	Trifoliate leaf length (cm)	5.63
4.	Internode length (cm)	7.70
5.	Number of flower/inflorescences	5.15
6.	Pod length (cm)	5.49
7.	Pod width (cm)	6.87
8.	Number of pods/clusters	6.09
9.	Number of pods/plants	4.69
10.	Tender/Green pod weight (g)	5.26
11.	Number of seeds/pods	3.68
12.	Seed index (g)	4.94
13.	Ascorbic acid (mg/100g)	4.70
14.	Total soluble solid (° Brix)	5.03
15.	Dry matter (%)	6.02
16.	Green pod yield/plant (kg)	3.29
17.	Seed yield/plant (kg)	3.97
18.	Green pod yield/hectare (q)	4.72
19.	Seed yield/hectare (q)	4.75

Conclusion

The D² analysis grouped twenty-eight genotypes into four clusters revealing considerable genetic divergence. Crosses between genotypes from clusters II and IV exhibiting maximum inter-cluster distance are recommended for hybridization to obtain superior segregants. Internode length, pod width and leaflet width were the major contributors to genetic divergence.

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