



Research Article

GENETIC DIVERGENCE STUDIES IN VEGETABLE COWPEA [*Vigna unguiculata* ssp. *sesquipedalis* L. Verdc.]

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Abstract- The investigation was conducted to study the nature and magnitude of genetic divergence among fifty genotypes of vegetable cowpea collected from different agro climatic regions of South India. The data were recorded on nine important traits among all the genotypes. All the genotypes were grouped into four clusters with genotypes from different geographic locations being grouped in the same clusters. The cluster I had the highest number of genotypes. The genotype VS41 remained in a solitary cluster as a divergent genotype that cannot be accommodated in any of the clusters. Pod yield per plant contributed the maximum towards divergence.

Keywords- Vegetable cowpea, Genetic Divergence, Clusters

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Introduction

Cowpea, a common leguminous vegetable is a rich and inexpensive source of vegetable protein. It is a key dietary staple for the poor sector of many developing countries. In India, it has been known from the Vedic times. Yard long bean is a distinct form of cowpea grown as a vegetable crop in southern Asia and Far east for its immature pods. Assessing genetic diversity among the genotypes of cultivated crops is very important to select better genotypes for any breeding programme. The more diverse the parents within a reasonable range, the higher would be chances of improving the characters in question. The most effective method to assess the genetic diversity among the genotypes is the Mahalanobis D^2 statistic. The present investigation was aimed to estimate the magnitude of genetic divergence present in the fifty genotypes and to identify diverse genotypes for further breeding programmes.

Materials and Methods

Fifty genotypes of vegetable cowpea from different regions of South India were laid out in randomised block design with two replications at the College of Agriculture, Vellayani, Thiruvananthapuram during 2002-2003. Source of genotypes is given in the [Table-1]. Normal package of practices recommended for the crop was followed to raise the good crop. Seeds were sown in rows spaced 1 x 0.3 m.

Five plants per genotype were randomly selected to record the biometric observations on pods per cluster, pods per plant, pod yield per plant, pod weight, pod length, pod breadth, seeds per pod, length of harvest period and main stem length. Genetic divergence was studied using Mahalanobis D^2 statistic as described by Rao (1952)[1]. The genotypes were clustered by Tochers method.

Results and Discussion

The fifty genotypes showed considerable variation with respect to the various characters studied as revealed by the analysis of variance. The genotypes were grouped into four clusters [Table-2]. The cluster I was the largest and consisted of 32 genotypes, followed by cluster II with 9 genotypes, cluster III with 8 genotypes

and cluster IV with one genotype. The solitary cluster was also reported by Brahmaiah [2] and Lingaraju [3]. The genotype VS41 remained as a divergent genotype that could not be accommodated in any of the cluster and remained in solitary cluster. The average inter and intra cluster distances were estimated based on the total D^2 values and presented in [Table-3]. The intra cluster distance was maximum in the cluster I (40.9). The inter cluster distances varied from 114.2 (between clusters I and III) to 338.19 (between clusters II and IV). Hybridisation between genotypes falling in the clusters II and IV should result in maximum hybrid vigour and eventually desirable segregates or combinations leading to the development of useful varieties [4,5].

Table-1 Particulars of cowpea genotypes used in the study

Source	Number of genotypes	Genotypes
Instructional farm, Vellayani	5	VS1, VS2, VS3, VS5, VS6
RARS, Mannuthi	10	VS4, VS7, VS8, VS9, VS10, VS11, VS12, VS13, VS37, VS43
Kottayam (VFPCCK)	4	VS14, VS15, VS16, VS17
Mithraniketan	1	VS18
Thiruvananthapuram (from farmers)	16	VS19, VS20, VS21, VS22, VS38, VS39, VS40, VS41, VS42, VS44, VS45, VS46, VS47, VS48, VS49, VS50
Kozhicode (from farmers)	4	VS23, VS24, VS31, VS33
Thrissur (from farmers)	1	VS26
Kanyakumari (from farmers)	1	VS25
Pathanamthitta (from farmers)	1	VS27
Malappuram (from farmers)	6	VS28, VS29, VS30, VS32, VS34, VS35
Wayanad (from farmers)	1	VS36

The cluster mean for the various characters were also estimated and presented in the [Table-4]. The highest cluster means for pod yield per plant (406.05) was in

cluster IV. Among the various characters considered pod yield per plant (175.90) contributed maximum towards divergence indicating the scope for improvement in this particular trait [6, 7]. Comparatively lesser variation was observed for the characters pod breadth and main stem length. The length of harvest period did not reveal any significant variation among the clusters.

Table-2 Clustering pattern of the fifty genotypes

Sl. No.	Cluster	Number of genotypes	Name of genotypes
1	I	32	VS1, VS3, VS6, VS8, VS10, VS11, VS12, VS13, VS15, VS17, VS18, VS19, VS23, VS24, VS26, VS27, VS29, VS30, VS31, VS33, VS34, VS35, VS36, VS37, VS40, VS42, VS44, VS45, VS46, VS48, VS49, VS50
2	II	9	VS4, VS5, VS7, VS14, VS16, VS20, VS21, VS22, VS39
3	III	8	VS2, VS9, VS25, VS28, VS32, VS38, VS43, VS47
4	IV	1	VS41

Table-3 Average inter and intra cluster D^2 values of fifty genotypes of vegetable cowpea

	I	II	III	IV
I	40.9581	114.2490	126.4854	239.4265
II		31.8653	219.4390	338.1983
III			32.1627	124.4262
IV				0

Table-4 Cluster means of the nine characters for 4 clusters of vegetable cowpea

Clusters	Pods/cluster	Pods/plant	Pod yield/plant	Pod weight (g)	Pod length (cm)	Pod breadth (cm)	Seeds/pod	Harvest period	Main stem length
I	1.54	17.21	170.83	11.50	35.75	2.39	16.52	24.91	4.59
II	0.86	8.36	70.11	11.11	35.62	2.21	16.27	23.78	3.22
III	1.74	17.90	286.39	15.23	76.29	2.11	16.80	26.50	4.50
IV	2.67	22.14	406.05	18.48	51.08	2.69	19.27	23.00	5.30
Mean	2.82	16.05	175.90	12.15	36.44	2.32	17.73	24.92	4.40
CV	0.41	0.34	6.43	0.11	0.12	0.00	0.37	0.00	0.01

Grouping of genotypes into different clusters did not reflect the geographical origins of the varieties [8, 9]. The diversity among the genotypes suggests the possibility of improvement by hybridisation and selection.

Conclusion

The results of the present investigation propose that there is ample scope of improvement in the crop due to the presence of considerable genetic variability. The selection of genotypes from cluster IV is suggested for improvement in yield per plant. The hybridization between the genotypes of cluster II and IV may be utilized for improvement in the crop.

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Conflict of interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

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