Madras Agric. J., 82(12): 659-663 December 1995
https://doi.org/10.29321/MAJ.10.A01292

GENETIC DIFFERENTIATION BETWEEN THREE SPECIES OF *Vigna*

K.RENGANAYAKI and S.R. SREE RANGASAMY
Centre for plant Molecular Biology
Tamil Nadu Agricultural University
Coimbatore 641 003.

ABSTRACT

The present investigation was to study the genetic divergence among the three species of *Vigna* viz., *V.radiata*, *V.mungo* and *V.unguiculata* based on biometrical, crossability and biochemical means. Biometrical study revealed that the genotype of the three species resolved into distinct clusters and remained exclusive of the other species. Canonical analysis grouping supported the pattern arrived by D^2 statistics indicating that 100 seed weight, pod length and seed yield are the potent characters causing divergence among the three species. Crossability studies revealed that the cross between *V.radiata* and *V.mungo* was successful and its reciprocal was a failure indicating one way compatability. The protein pattern showed striking similarity between the three species yet there were some bands which were unique in each of the species that may be well utilized as genetic markers for detection of interspecific cross. The hybrids between *V.radiata* and *V.mungo* showed low pollen and seed fertility. Though the hybrid showed sterility and breakdown in F_2, there is ample scope to transfer useful characters of *V.mungo* to *V.radiata*.

KEYWORDS : *Vigna* species, Biometrical, Crossbility Studies, Biochemical Relationship.

Interspecific hybridisation can provide a way by promoting geneflow for desired level of gene combinations. For this purpose, it is essential to know the inter-relationship between the species. The present study was, therefore undertaken to know the genetic relationship and differentiation existing among the three species of *Vigna* Savi..

MATERIALS AND METHODS

The materials of the study consisted of 22 types of *moong*, 20 types of *urd* and 6 types of cowpea belonging to different geographical regions. These were raised during summer 1984 in a randomised block design with three replications. The data obtained from five randomly selected plants were subjected to Mahalanobis 's D^2 analysis to study the genetic divergence between the three species. Tocher's (Rao, 1952) technique to form the composition of different group constellations and canonical analysis. In crossability studies, the following crosses were made using *V.radiata* as female and *V.mungo* as male parents (Co 3 x TMV 1, Co CG 123 x TMV and AC 300 X TMV 1): *V.radiata* as female and *V.unguiculata* as male parents.(Co 3 x Co VU 623, PLS 319 x Co VU 623, Co 3 x Co VU 97 and PLS 19 x Co VU 97) and *V.mungo* as female and *V.unguiculata* as male parents (TMV 1 x Co VU 23, T 9 x Co VU 623. TMV 1 x Co VU 97 and T 9 Co VU 97). In addition, reciprocal crosses of the above said crosses were made. CRS 55, M.1 and MDU 2984 *(V.radiata)*; T 9, Trichy local and Lam BG 295 *(V.mungo)* and Co VU 623, Co VU 97 and KM 1 (V.unguiculata) were used. Globulin (G1) proteins were extracted (Yuma and Bliss, 1978) with sodium dodecyl sulphate - poly acrylamide gel electrophoresis, fixing, staining and destaining procedures suggested by Anderson (1980).

RESULTS AND DISCUSSION

Analysis of varience (Table 1) revealed that the 48 types differed among themselves significantly for all the characters. All the three species *viz., V.radiata. V.mungo* and *V.unguiculata* types were grouped into 16 different clusters.

The interesting phenomenon observed in the clustering pattern was that all the *V.radiata* genotypes grouped among themselves into seven clusters and none of the cluster had *V.mungo* or *V.unguiculata* genotypes. Similarly, all the *V.mungo* genotypes and *V.unguiculata* genotypes resolved into five and four clusters respectively and they had only their own entries. These group constellation are indicative that the three species evaluated in this study are distinct and were differentiated. The assemblage of *V.radiata* and *V.mungo* entirely in different clusters without any exception strongly supports the opinion of Sen and Ghosh (1960) that there is crossability barrier between these two species. Lukoki-Luyeye (1975)

Table 1. Anova for 16 characters in green gram, black gram and cowpea

Source	D.F.	PLA	LAF	PLH	PBS	PTL	PDL	DLM	DMP	SLW	LAI	POL	NPP	NSP	HSM	PRD	SYD
						Green gram											
Treatment	21	37.67**	217342.00**	369.71**	1.80**	17.30**	22.11**	4.55**	37.81**	0.00$^{n.s.}$	24177.20**	4.25**	424.35**	3.09**	4.44**	24.06**	33.19**
Error	42	2.13	25683.80	8.66	0.42	1.00	1.60	0.76	6.33	0.00	2854.07	0.18	9.60	0.82	0.81	9.05	1.30
						Black gram											
Treatment	19	25.97**	271803.00**	163.10**	3.09**	14.79**	13.32**	11.53**	13.98**	0.00$^{n.s.}$	29823.80**	0.76**	63.93**	1.29**	1.26**	9.89**	6.86**
Error	38	2.86	443516.80	12.89	0.64	0.95	0.72	3.68	4.26	0.00	5253.09	0.06	5.26	0.35	0.11	0.80	0.97
						Cowpea											
Treatment	5	570.66**	1629690.00**	3271.63**	4.58**	17.69**	396.44**	37.76**	160.34**	0.00$^{n.s.}$	181078.00**	120.79**	208.85**	33.52**	86.19**	23.06**	26.26**
Error	10	5.48	77223.20	62.04	0.65	0.38	14.28	2.30	18.37	0.00	8580.30	4.80	5.25	0.78	0.21	1.63	1.63

** Significant at 1 per cent level n.s. Non significant

Table 2. Intra and inter-cluster distance in *V. radiata*, *V. mungo* and *V. unguiculata*

			V. radiata				
	III	IV	V	VI	IX	XI	XII
III	6.66	8.04	8.14	9.33	16.05	10.79	13.21
IV		5.00	6.91	12.39	16.24	8.69	14.84
V			4.32	10.30	17.70	10.54	12.63
VI				6.46	19.53	15.49	9.23
IX					5.87	16.17	21.10
XI						9.73	17.94
XII							11.33
			Average = 14.12				
			V. mungo				
		I	II	VII	VIII	X	
X		4.79	7.30	6.89	7.37	10.02	
II			5.42	10.86	10.24	10.04	
VII				7.80	8.27	11.04	
VIII					5.79	12.99	
X						11.25	
			Average = 8.67				
			V. unguiculata				
			XIII	XIV	XV	XVI	
XIII			-	21.80	24.76	44.48	
XIV				13.35	20.28	43.10	
XV					-	28.19	
XVI						19.24	
			Average = 26.90				

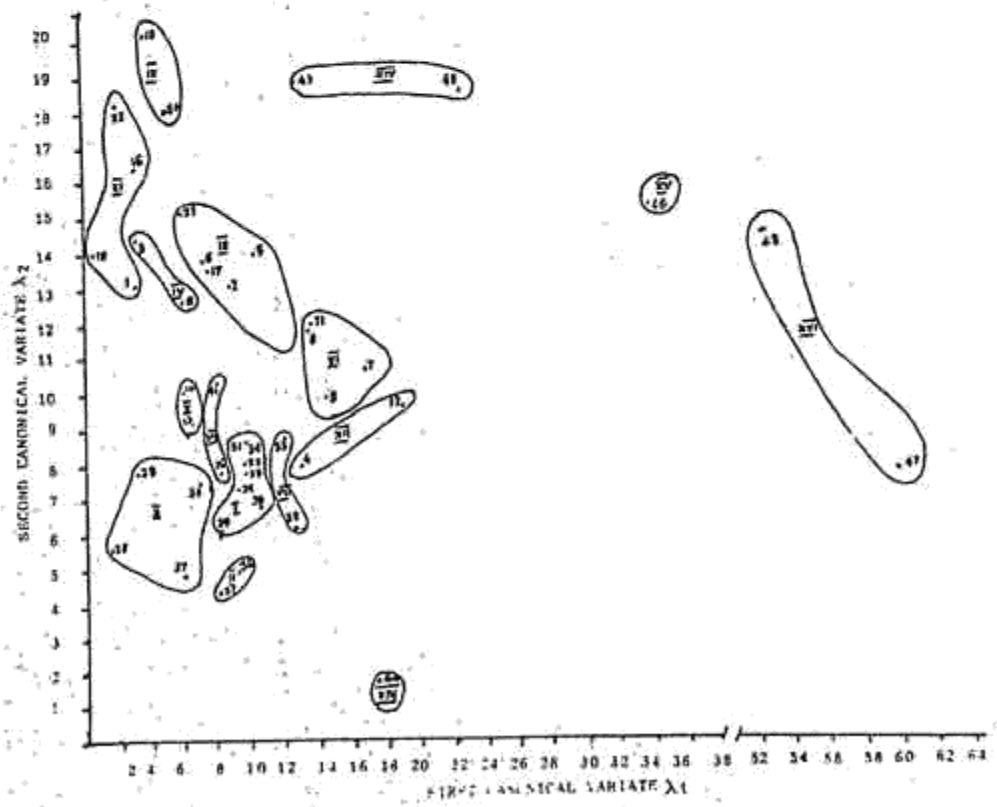

Fig. 1. $\lambda_1 - \lambda_2$ Chart

1-48 indicate the genotypes

I-XVI indicate the clusters based on D^2 analysis and corresponding to table 2 & 3

Table 3. Inter-cluster distance between the three species of *Vigna*

	V. radiata with *V.mungo*						
	III	IV	V	VI	IX	XI	XII
I	10.16	10.76	9.31	11.08	16.31	13.15	11.50
II	11.06	11.12	7.18	11.13	20.23	14.80	11.93
VII	11.29	11.73	11.50	13.24	14.53	13.24	14.24
VIII	10.52	13.26	11.94	10.77	18.21	15.62	12.80
X	13.16	11.60	10.12	15.45	18.68	13.62	16.04
	Average = 12.89						
	V.radiata with *V. unguiculata*						
		XIII	XIV	XV	XVI		
III		17.18	14.84	26.68	50.54		
IV		20.90	16.70	30.74	54.58		
V		17.89	18.10	29.63	53.08		
VI		14.68	14.28	22.04	45.08		
IX		25.03	21.17	32.87	55.82		
XI		23.39	19.57	33.11	57.04		
XII		16.70	16.08	22.24	44.14		
	Average = 29.07						
	V. mungo with *V. unguiculata*						
		XIII	XIV	XV	XVI		
I		14.79	17.16	27.17	49.82		
II		14.06	19.19	28.88	51.00		
VII		15.68	17.96	28.98	51.25		
VIII		11.17	16.86	25.37	47.62		
X		19.01	21.19	32.69	55.04		
	Average = 28.24						

also concluded that *V.radiata* and *V.mungo* were distinct species from his study on seed protein.

Among the three species, *V.unguiculata* genotypes were found to have higher inter-cluster distance followed by *V.radiata* and *V.mungo*. The average inter cluster distance between *V.radiata* and *V.mungo* was low (12.90) compared to that between *V.radiata* and *V.unguiculata* (29.08) and *V.mungo* and *V.unguiculata* (28.25) (Table 2, 3).

Canonical analysis further revealed that the genotypes of the two species *viz.*, *v.radiata* and *V.mungo* were clustered among themselves in same plane (Fig.1) while the genotypes of the other species *V.unguiculata* were found clustered in a different plane confirming the results of D^2 analysis. Besides, the clusters of *V.radiata* and *V.mungo* were located very closely (Fig.1) contrary to the clusters of *V.ungiculata* that were far away from other two *V.radiata* and *V.mungo* except for the cluster XIII. This confirms that the two species *viz.*, *V.radiata*, *V.mungo* are related which is further confirmed through crossability studies.

Among the crosses made between *V.radiata*, *V.mungo* and *V.unguiculata* in all possible combinations, only the cross between *V.radiata* and *V.mungo* were successful, when *V.radiata* was used as female parent. The percentage of crossability varied from 1 to 2.46. This supports the opinion of Sen and Ghosh (1960), Singh et al (1975), Verma (177) and Chen *et al* (1975), Verma (1977) and Chen *et al* (1983), Gill *et al* (1983) and Shanmugam *et al* (1983). The failure of cross between *V.radiata* and *V.unguiculata* and between *V.mungo* and *V.unguiculata* indicated that there is no homology between the genomes of *V.radiata* and *V.mungo* to *V.unguiculata*.

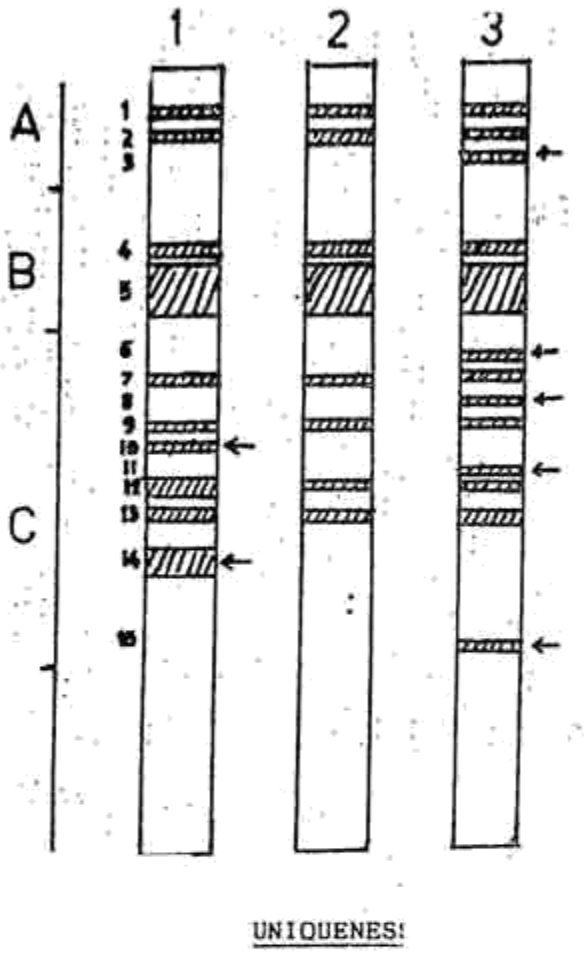

Fig.2. Interspecific Variation in Globulin (G_1) of *vigna* species

Seed protein gloubulin (GI) sub-units of *Vigna* were divided into arbitary group A, B and C based on their mobility in SDS - PAGE (Fig. 2). A sub-units were slow moving and C sub-units were fast moving. B was intermediate in mobility. Group B banding pattern was seen uniformly in all the varieties of the three species clearly. In group A sub units 1 and 2 could be seen in all the three species whereas the band 3 was not seen in *unguiculata*. The C group sub units showed remarkable uniqueness for the banding pattern in the three species. The bands 6, 8 and 11 were unique bands of *V.unguiculata* and were not seen in the varieties of *V.radiata* and *V.mungo*. Bands 12 and 13 were seen both in *V.radiata* and *V.unguiculata*. The presence of the two bands could not be ruled out in *V.mungo* as they were seen faintly. Two darkly stained bands 10 (thin) and 14 (thick) appeared to be the uniqueness of *V.radiata* varieties. The uniqueness of *V.mungo* varieties is the absence of the bands typical of *V.radiata* (10 & 14) and those of *V.unguiculata* (3. 6,8,11 and 15). There were some bands which were unique to each of the species and these results are in accordance with the results obtained in D^2 analysis where the genotypes of the same species grouped themselves with the exclusion of the genotypes from the other species.

This study concludes that among the three species taken for the study, only *V.radiata* and *V.mungo* show genome homology, enabling crossing between these two species. Hybrids obtained from these cross will be utilised further for improving the plant type, quality and yield.

REFERENCES

ANDERSON. B.(1980) Anderson's Brilliant Blue 'R' staining procedure in LKB 2001 Vertical Electrophresis unit. **Laboratory manual,** Sweden.

CHEN, N.C., BAKER, L.R. and HONMA, S. (1983). Interspecific crossability among four species of *Vigna* food legumes. **Euphytica 32:** 925-937.

GILL, A.S. VERMA, M.M., DHALIWAL, H.S. and SANDU, T.S. (1983): Interspecific transfer of resistance of mung bean yellow mosaic from *V.mungo* to *V.radiata* **Curr.Sci.,52:**31-33.

LUKOKI-LUYEYE. (1975) Distinction between *Vigna radiata* and *V.mungo* **Bulletin des Recherches Agronounique de Gembloux 10:**373-373.

RAO, C.R. (1952) **Advanced Statistical Methods in Biometrical Research.** John Wiley and Sons, New York.

SEN, N.K. and GHOSH, A.K. (1960) Interspecific hybridization between *Phaseolus aureus* Roxb (green gram) and *P.mungo* (black gram). **Bull.Botan.Soc.Bengal 14:** 1-4.

SHANMUGAM, A.S., RATHNASWAMY, R. and SREE RANGASAMY, S.R. (1983) Crossability studies between green gram and black gram. **Curr.Sci.,52:** 1018-1020.

SINGH, P., SINGH, I.B., SINGH, V. and SINGH,H.G. (1975) Interspecific hybridization between mung *(Phaseolus aureus)* **Sci. & Cult.,41:** 233-234.

YUMA and BLISS, F.A. (1978). Seed proteins of common bean. **Crop Sci.,18:** 431-437.

VERMA,N.P. (1977). Recombined progenies in interspecific cross between green *Phaseolus aureus* Roxb. Syn.*Vigna radiata* and blackgram *(Pohaseolus mungoL.* Syn.*Vigna mungo)* **Mysore J.agric.Sci., 11:**431-437.

(Received: April 1991 Revised:September 1995)