Indian J. Pl. Genet. Resources **10**(1): 91-96, 1997

GENETIC DIVERGENCE IN PARWAL (*TRICHOSANTHES DIOICA* ROXB.)

V.S.R. Krishna Prasad and D.P. Singh[1]

Central Horticultural Experiment Station (IIHR),
Namkum, Ranchi 834 010 (Bihar)

The genetic divergence in 23 genotypes of parwal has been assessed utilizing generalised distance and cannonical analysis. The 23 genotypes fell into six clusters. Two cannonical vectors needed to be considered to account for about 82% of variation. Geographical isolation has not contributed to the genetic divergence. The observed genetic divergence therefore seems to be possibly due to phenotypic differences in genotypes background. The inter-cluster divergence was maximum in cluster III, where as inter-cluster distance was maximum between cluster I and II. Fruit volume followed by pulp weight and seed weight appeared to contribute maximum to genetic divergence. Genetic drift and selection in different environments seem to cause greater genetic diversity rather than genetic isolation.

Key words : Parwal (Pointed Gourd), genetic, divergence, multi-variate analysis, geographical isolation, genetic drift, pivotal condensation

Parwal (pointed gourd) is an important vegetable crop grown in Bihar, Uttar Pradesh, Orissa, Gujarat, Madhya Pradesh and parts of Andhra Pradesh. It is delicious and nutritious vegetable with good medicinal properties. Recently, it has been reported that the property of lowering blood sugar (Chandrasekha *et al*, 1988), total cholesterol and serum triglycerides and increase the level of phospholipids and HDL-cholesterol (Sharma and Pant, 1988) and anti-ulcer effects (Takano *et al.*, 1990) in *Trichosanthes* fruits.

A meaningful classification of germplasm that enables to distinguish genetically close and divergent types, is a pre-requisite for any plant breeding programme. Anticipating potential danger associated with the use of narrow base in a dynamic breeding programme, research efforts are underway in Central Horticultural Experiment Station to develop parwal hybrids with sustainable yield. With the development of advanced biometric techniques such as multivariate analysis based on Mahalanobsis D^2 statistic (1936), quantification of the degree of divergence among biological populations and assessing the relative contribution of different components to the total divergence at inter and intra cluster levels have now become possible.

---

[1] Assistant Director General (Vegetable crops), *ICAR, Krishi Bhavan, New Delhi 110001

MATERIALS AND METHODS

Twenty-three widely grown genotypes of parwal (long, small, round and oval fruited) from **diara** lands of Bihar and Uttar Pradesh were grown in a randomized block design with three replications at Plandu farm of Central Horticultural Experiment Station, Ranchi. Each entry had one row of five metre length, spacing between rows and within the rows being 1m and 45 cm, respectively. Experiment was repeated for a period of three years. Observations were recorded on five randomly selected plant per replication for each entry on vine length, node number, fruit weight, fruit length, fruit breadth, fruit volume, pulp weight, seed weight and number of seeds per fruit. The fruit yield and number of fruits were recorded on plot basis.

Cannonical analysis and Mahalanobsis generalised distance (1936) were used for assessing the genetic divergence between the population. All possible D^2 values among 23 parwal genotypes were computed utilizing the varietal means and variances in respect of 11 characters. The co-variances between character pairs were also computed (Rao, 1952). For generalised distance, un-correlated linear functions, of the original values were obtained by transforming the original correlated unstandardized character means by the method of pivotal condensation (Rao, 1952). For determining group constellations, a relatively simple criterion suggested by Tocher (Rao, 1952) was adopted.

RESULTS AND DISCUSSIONS

Highly significant variation was found among the 23 parval genotypes in all the characters except node number and fruit weight (Table 1). The D^2 values (253) obtained between 23 parval genotypes showed considerable range (1.29 to 59.85). This wide range suggests the existence of appreciable genetic divergence in the genotypes tested. The 23 populations could be grouped into 6 clusters and composition of different clusters are presented in Table 2. Among these, cluster III consists of 9 genotypes followed by cluster II (5) and cluster I (5), where as, cluster IV, V and VI with one genoptype each. The material under study included collections from **diara** lands of Uttar Pradesh and Bihar with distinct phenotypic fruit characters. Clustering pattern of parval genotypes indicates that geographical isolation has not contributed much to the genetic divergence. The observed genetic divergence, therefore, seems to be possibly due to differences in genotypes background. While, Krishna Prasad *et al* (1993) reported that geographical isolation is no way related to the genetic divergence in the landraces of slicing cucumber. In such situation where the role of geographic isolation is negligble, genetic drift and selection in different environments could lead to greater diversity.

Table 1. Analysis of variance for RBD for 11 characters studied in 23 genotypes of Parwal

Characters	@ Replications (8)	Treatments (22)	Error (1.76)	SEM (±)	CV (%)	CD (1t 5%)	DD (at 1%)
Yield/plot	0.72	5.05**	1.51	0.41	58.21	1.13	1.49
No. of fruits/plot	918.42	5221.03**	2393.73	16.30	69.46	45.07	59.23
No. of seeds/fruit	16.72	27.78**	14.73	1.27	21.88	3.53	4.64
Seed weight	24.86	87.38**	20.66	1.51	22.72	4.18	5.50
Pulp weight	24.86	87.38**	20.66	1.51	22.72	4.18	5.50
Fruit volume	84.98	233.4^{6**}	84.92	3.07	23.17	8.48	11.15
Fruit length	1.04	5.54**	1.19	0.56	16.94	1.00	1.32
Fruit weight	154.06	74.73	88.50	3.13	33.37	-	-
Node number	4350.30	1609.00	1581.43	13.25	63.85	-	-
Vine length	1389.89	4010.13**	992.55	10.50	316.66	29.02	38.14

@ Degrees of freedom in parenthesis **Significant at 1%

Table 2. Composition of different clusters

Cluster number	No. of genotypes in cluster	Name of the genotypes
I	5	CHES-2, CHES-21, CHES-22, CHES-26, and CHES-34
II	6	CHES-5, CHES-8, CHES-11, CHES-19, CHES-21, CHES-28
III	9	CHES-4, CHES-6, CHES-7, CHES-12, CHES-14, CHES-17, CHES- 18, CHES-19, and CHES-29
IV	1	CHES-20
V	1	CHES-14
VI	1	CHES-1

The intra and inter cluster distance of six clusters was presented in Table 3. Three clusters namely, cluster IV, V and VI had only one genotype each. Of the remaining three, intra cluster divergence was maximum in cluster III (D = 2.78) and the minimum for cluster I (D = 1.66). The divergence between cluster II and IV was the least, the "D" value being 1.10. Cluster I was highly divergent from cluster VI followed in order by cluster II and III. The maximum inter cluster distance was reported between cluster I and VI (7.69) followed by cluster II and VI (7.29).

Table 3. Intra and inter cluster D^2 values values in parval

Cluster	I	II	III	IV	V	VI
I	2.76 (1.66)	5.05 (2.24)	8.75 (2.95)	12.10 (3.47)	21.71 (4.65)	59.24 (7.69)
II		5.21 (2.28)	5.05 (2.24)	1.22 (1.10)	17.94 (4.23)	53.15 (7.29)
III			7.73 (2.78)	6.80 (2.60)	14.00 (3.75)	48.96 (6.99)
IV				0	6.77 (2.60)	38.55 (6.20)
V					0	37.92 (6.15)
VI						0

Based on 11 characters, cannonical analysis confirmed the clustering pattern obtained by D^2 statistic. Total contribution of all vectors is 129.58 and per cent contribution of first and second vector was 42.19 and 39.84, respectively. The contribution of each character towards divergence is presented in Table 4. The character fruit volume (22.13%) contributed maximum towards genetic divergence followed by pulp weight (18.58%) and seed weight (14.23%). However, the least contribution was made by vine length (1.19%) followed by fruit length (2.37%). The potent variables like fruit volume, pulp weight and seed weight can be used as parameters in selecting genetically diverse parents for hybridization.

Table 4. Percent contribution of each character towards genetic divergence

	Character	Frequency of appearing Ist rank	% contribution towards genetic divergence
1.	Yield/plot	15	5.93
2.	No. of fruits/plot	11	4.35
3.	No. of seeds/fruit	27	10.67
4.	Seed weight	36	14.23
5.	Pulp weight	47	18.58
6.	Fruit volume	56	23.13
7.	Fruit breadth	12	4.74
8.	Fruit length	6	2.37
9.	Fruit weight	22	8.70
10.	Node number	18	7.11
11.	Vine length	3	1.19

The character means over clusters (Table 5) showed wide range in their values clusterwise. The genotypes of cluster I showed maximum pulp weight and fruit volume; whereas the genotype CHES-14 present in cluster V showed maximum for number of fruits, no. of seeds per fruit, seed weight and fruit breadth. The only genotype i.e. CHES-1 present in cluster VI showed maximum mean values for the characters yield per plot, fruit length, fruit breadth, node number and vine length. The superiority showed by these two genotypes *viz.*, CHES-1 and CHES-14 for majority of the attributes can be successfully be exploited in the future breeding programme.

Table 5. Cluster means for eleven characters in Parval

	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Clster V	Cluster VI	Total Mean
1.	Yield/plot (kg)	1.93	2.15	2.02	2.01	1.84	3.82	2.29
2.	No. of fruits/plot	63.10	72.50	71.45	63.11	87.77	75.30	72.20
3.	No. of seeds/fruit	18.70	17.50	17.12	15.22	19.27	15.80	17.86
4.	Seed weight (g)	5.43	5.10	5.70	6.54	7.19	56.69	5.94
5.	Pulp weight (g)	22.25	20.00	20.62	14.64	11.51	16.89	17.65
6.	Fruit volume (cc)	45.63	38.02	38.42	31.15	39.80	41.22	39.04
7.	Fruit breadth (cm)	2.89	2.88	3.12	3.17	3.22	2.97	3.04
8.	Fruit length (cm)	6.08	5.99	6.56	6.12	7.26	9.44	6.90
9.	Fruit weight (g)	28.37	27.97	28.31	25.01	26.18	32.33	28.02
10.	Node number	74.30	68.04	47.87	61.20	46.00	73.82	61.86
11.	Vine length (m)	6.30	5.90	5.08	5.74	3.72	6.59	5.55

ACKNOWLEDGEMENTS

The authors are grateful to the DIrector, Indian Institute of Horticultural Research, Bangalore for providing necessary facilities and thankful to Sri J.S. Rao, Technical Officer (T-7), Section of Economics and Statistics, IIHR Bangalore for his help in statistical analysis.

REFERENCES

Chandrashekhar, B., B. Mukherjee and S.K. Mukherjee. 1988. Blood sugar lowering effect of *Trichosanthes indica* Roxb. in experimental rat models. *International J. Crude Drug Res.* **26**(2): 102-106.

Krishna Prasad, V.S.R., D.P. Singh and R.P. Singh. 1993. Biological divergence in the land races of Indian cucumber (*Cucumis sativus* L.) *Indian J. Hort.* **50**(1) : 57-63.

Mahalanobsis, P.C. 1936. On generalized distance in statistics. *Proc. Nat. Acad. Sci.* (India) **2**: 49-55.

Rao, C.R. 1952. Advanced statistical Methods in Biometrical Research. John Wiley and Sons, New York.

Sharma, G. and M.C. Pant. 1988. Preliminary observations on serum biochemical parameters of albino rebbits fed on the seeds of *Trichosanthes dioica*. Roxb. *Indian J. medicam Res.* 87 (Abstr.) 398-400.

Takano, F., F. Yoshizanki, K. Suzuki, N. Soyan, T. Ando and S. Hisamichi. 1990. Anti ulcer effects of *Trichosanthes* fruits, *Chemical and pharmaceuticals Bulletin* **38**(5) : 1313-1316.