non-additive gene action was also found to be significant indicating that the characters are also influenced by dominance and epistatic effect in addition to additive gene action.

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GENETIC DIVERSITY IN PEARL MILLET, *Pennisetum typhoides*

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ABSTRACT

A wide genetic diversity was revealed by the D^2 analysis wherein 41 genotypes of pearl millet *Pennisetum typhoides* (Burm.) S.&H.) fall into as many as fourteen clusters. Based on the average intercluster distances (D), the clusters XIII and XIV were found to be highly divergent from the other clusters. The types P.T.1595 and P.T.834/3 (Cluster XII) were superior for earnumber and grain yield. The types P.T. 928 and P.T. 834/1 (Cluster VIII) were superior for earliness while types P.T. 1611 and P.T. 1620 (Cluster V1) were superior for earlength and straw yield. These types may serve as potential parents for hybridisation programmes.

This investigation was made to study the nature and magnitude of genetic divergence for yield and other important component characters in pearl millet *(Pennisetum typhoides)* (Burm.) S.& H) varieties of diverse origin and to make selection of parents based on the rusults.

MATERIALS AND METHODS

Forty-one genotypes of pearl millet with diverse geographical orgin were chosen from the germplasm bank maintained at the Tamil Nadu, Agricultural University, Coimbatore, for the study. The experiment was laid out in randomised block design with three replications. A spacing 45 X 15 cm. was adopted. Five plants were selected at random in each genotype in each replication. The quantitative diversity of the pearl millet germplasm was estimated by Mahalanobis' D^2 analysis and the results are presented hereunder . For determining the group constellations, a relatively simple criterion was followed.

RESULTS ADN DISCUSSION

Analysis of variances showed significant differences among the types for all characters studies. The plot means of the forty one types for the nine characters were transformed into standardised, uncorrelated mean values and the D^2 values $\frac{n(n-1)}{2}$ were computed for all possible =820 pairs of types. The generalised D^2 values arranged from 1.4703 to 289.9321. By the application of clustering technique, the 41 types were grouped into fourteen clusters. The constituent of different clusters with their source are presented in Table1. Among the 14 clusters, clusters IV,VI and VII were the largest having five types followed by cluster V which had four types. The clustering pattern of different types from varying geographical regions was random.

In the present investigation, as many as nine developmental and economic traits were considered. A wide range of variability among the

Table 1. Composition of D^2 clusters

Cluster	No. of types	Types	Origin
I	2	PT 1614	Andhra Pradesh
		PT 1608	Tamil Nadu
II	3	PT 829/5	Tamil Nadu
		PT 1610	Tamil Nadu
		PT 835/5	Maharashtra
III	3	PT 1854	Tamil Nadu
		PT 1596	Tamil Nadu
		PT 931	Andhra Pradesh
IV	5	PT 826/7	Tamil Nadu
		PT 833/5	Tamil Nadu
		PT 834/2	Maharasshtra
		PT 1654	Tamil Nadu
		PT 1643	Maharashtra
V	4	PT 1607	Tamil Nadu
		PT 1836	Karnataka
		PT 1599	Tamil Nadu
		PT 827/2	Tamil Nadu
VI	5	PT 830/2	Tamil Nadu
		PT 1620	Andhra Pradesh
		PT 1611	Tamil Nadu
		PT 1603	Tamil Nadu
		PT 827/6	Tamil Nadu
VII	5	PT 1597	Tamil Nadu
		PT 1609	Tamil Nadu
		PT 829/8	Tamil Nadu
		PT 950	Punjab
		PT 1896	New Delhi
VIII	2	PT 928	Andhra Prradesh
		PT 834/1	Maharashtra
IX	2	PT 1478	Tamil Nadu
		PT 1477	Tamil Nadu
X	2	PT 932	Andhra Pradesh
		PT 1853	Tamil Nadu
XI	2	PT 835/6	Maharashtra
		PT 833/7	Tamil Nadu
XII	2	PT 1595	Tamil Nadu
		PT 834/3	Maharashtra
XIII	2	PT 1600	Tamil Nadu
		PT 1483	Tamil Nadu
XIV	2	PT 820/6	Andhra Pradesh
		PT 833/2	Tamil Nadu

types was observed in the present study wherein the forty-one types were grouped into as many as 14 clusters based on D^2 values, indicating the existance of a considerable amount of phenotypic diversity in this species. The clustering of types according to geographic origin was observed only in two out of fourteen clusters. The clusters IX and XIII contained types from single geographical soruce, thereby reporting the existence of a parallelism between the geographical distribution and genetic divergence. Further the types

originating from the same place were also found to be distributed in different clusters. Though geographic diversity is an important factor, it thus appears that it is not the only factor determining the genetic divergence. It also indicates that factors other than geographical diversity may also be resposible for such grouping of types.

The variation in clustering pattern of types from the same geographical source have been reported to be due to environmental factors also (Clausen and Haisey, 1958). The authors felt that even a single component of environment such as temperature could cause differences between and within races of crop plants. Another reason attributed for such variation is the differential adaptation of various types belonging to the same eco-geographical origin.

The intra and inter cluster D^2 and D values among the fourteen clusters are presented in Table 2. The intra-cluster generalised distance ranged 1.21 to 6.56. The lowest intracluster distance was recorded by the cluster I and the maximum by cluster XIV. The highest inter- cluster divergence was noted between the clusters XIII and XIV (13.46). The intercluster distance was the least between the clusters II and V (2.51).

Based on the inter-cluster average distance (D), the clusters XIII and XIV were found to be highly divergent from all other clusters. The types involved in these clusters on one hand, and the types of other clusters on the other may serve as potential parents in heterosis breeding. A scrutiny of Tamil Nadu, Andhra Pradesh and Maharashtra types distributed in different clusters. shows varying degrees of inter-cluster divergence. Inter -crossing of the divergent types from the same region because of their better adaptation may be more rewarding than choosing types from other regions for a breeding programme as suggested by Gupta amd Singh (1970)

The cluster means for the various characters are presented in Table 3. The cluster VI had the highest mean values for plant height, ear length and straw yield. The cluster XII had the highest mean values for ear number and grain yield. Similarly highest mean values for the characters namely, days to flowering, tiller number, ear girth, and

Table 2.   Intra and Inter-cluster average D^2 and D (within parenthesis) values

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	1.47	10.60	31.32	11.19	7.32	43.69	14.93	23.70	24.05	27.75	33.87	16.69	38.07	77.90
	(1.21)	(3.26)	(5.60)	(3.35)	(2.71)	(6.61)	(3.86)	(4.87)	(4.90)	(5.27)	(5.82)	(4.09)	(6.17)	(8.54)
II		2.18	10.47	7.52	6.31	23.60	19.88	44.29	21.28	12.66	25.90	24.99	70.47	46.65
		(1.48)	(3.24)	(2.74)	(2.51)	(4.86)	(4.46)	(6.66)	(4.61)	(3.56)	(5.09)	(4.99)	(8.34)	(6.83)
III			3.82	16.87	24.03	13.88	30.40	81.91	36.19	13.14	23.46	49.58	10.83	87.74
			(1.95)	(4.11)	(4.90)	(3.73)	(5.51)	(9.01)	(6.02)	(3.63)	(4.84)	(7.04)	(10.24)	(6.91)
IV				5.09	8.37	24.02	10.78	36.86	14.10	23.17	22.68	22.44	94.17	66.60
				(2.26)	(2.93)	(4.90)	(3.28)	(6.07)	(3.75)	(4.81)	(4.76)	(4.74)	(9.96)	(8.17)
V					3.30	36.15	16.99	26.53	13.57	24.89	33.43	14.73	51.67	61.15
					(1.82)	(6.01)	(4.12)	(5.15)	(3.68)	(4.99)	(5.78)	(3.84)	(7.19)	(7.82)
VI						18.62	32.88	95.29	47.51	31.25	35.80	53.65	107.43	67.54
						(4.32)	(5.73)	(9.76)	(6.89)	(5.59)	(5.98)	(7.32)	(10.36)	(8.22)
VII							9.12	28.63	21.80	45.62	42.16	18.12	38.38	102.97
							(3.02)	(5.35)	(4.67)	(6.75)	(6.49)	(4.26)	(6.20)	(10.15)
VIII								7.57	32.03	85.12	86.90	21.99	25.88	144.82
								(2.75)	(5.66)	(9.23)	(9.32)	(4.69)	(5.09)	(12.03)
IX									8.82	43.23	33.97	23.75	55.85	80.36
									(2.97)	(6.57)	(5.83)	(4.87)	(7.47)	(8.99)
X										11.14	19.21	56.71	111.83	28.26
										(3.34)	(4.38)	(7.53)	(10.57)	(5.32)
XI											11.66	60.79	96.95	44.97
											(3.41)	(7.80)	(9.85)	(6.71)
XII												17.30	39.74	104.08
												(4.16)	(6.30)	(10.20)
XIII													41.30	181.24
													(6.43)	(13.46)
XIV														43.03
														(6.56)

Table 3.   Cluster means for the nine characters in pearl millet

Cluster	Plant height (cm)	Days to flowering	Tiller number	Ear number	Ear length (cm)	Ear girth (cm)	Grain weight (mg)	Straw yield (g)	Grain yield (g)
I	196.14	47.24	3.35	2.78	28.67	7.57	793.67	114.22	15.05
II	178.14	47.65	3.22	2.51	26.73	8.25	697.17	123.93	13.48
III	188.91	48.64	2.26	1.84	28.53	8.91	548.65	103.37	10.35
IV	180.89	48.01	2.37	1.70	25.33	8.17	750.57	74.61	7.53
V	167.05	48.24	3.38	2.50	24.39	8.10	754.96	107.69	12.53
VI	205.58	51.17	2.72	1.46	29.06	8.89	781.63	149.63	9.32
VII	190.42	47.95	2.28	1.65	28.42	8.74	746.75	80.57	10.30
VIII	145.54	43.26	3.04	2.55	23.70	8.08	838.04	64.14	10.31
IX	128.96	50.51	1.97	1.35	20.94	8.48	606.97	48.93	7.98
X	190.45	48.47	3.00	2.70	29.03	7.80	528.00	106.10	12.04
XI	178.65	52.38	2.23	1.24	27.34	7.49	498.40	53.18	5.27
XII	183.63	50.87	3.70	2.81	27.65	8.67	795.72	105.37	17.45
XIII	189.63	46.36	2.82	1.74	25.83	7.24	1145.02	112.16	8.89
XIV	166.81	52.07	4.63	2.80	24.94	7.18	487.40	136.50	14.98
Range	128.96 to 205.58	43.26 to 52.38	1.97 to 4.63	1.24 to 2.81	20.94 to 29.06	7.18 to 8.91	487.40 to 1145.02	48.93 to 149.63	5.27 to 17.45
General mean	180.30	48.86	2.83	2.02	26.72	8.27	709.50	100.85	10.71

grain weight, were registered by the clusters XI,XIV, III and XIII respectively. The lowest mean values for plant height, tiller number, ear length and straw yield were recorded by the cluster IX while the cluster XI registered the lowest mean values for tiller number, grain weight and grain yield. The lowest mean values for the traits, days to flowering and ear girth were recorded by the clusteres VIII and XIV respectively.

Hence, inter crossing the types from these clusters may result in a wide range of variability and subsequent selection for these traits would result in genotypes with higher grain yield combined with earlines. Under such conditions, Chaudhary et al. (1975) suggested that selection of

one type from each cluster and testing them by a series of diallel anyalysis may prove to be highly fruitful. Since clusters XIII and XIV were the widest in their genetic divergence, the two types may also be tested for heterosis breeding.

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HERITABILITY AND CORRELATION STUDIES OF VARIOUS COMPONENTS OF DRY MATTER PRODUCTION IN *Sesamum indicum*

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ABSTRACT

Fifty genotypes of *Sesamum indicum* belonging to various geographical background were grown in a field experiment during 1986 and five components,namely, root weight, stem wight, leaf weight, capsule weight and seed yield were recorded. Data subjected to heritability and correlation studies revealed that the highest genotypic coefficient of variability, heritability and genetic advance were observed for the component stem weight indicating additive gene action. Lower heritability and genetic advance as per cent of mean were recorded for root weight and seed yield indicating that variation in these characters was governed more by environment rather than the heritable genetic component. Stem weight had high genotypic correlation to seed yield followed by capsule weight, root weight and leaf weight respectively.

Sesame (*Sesamum indicum* L. is an important oil seed crop of tropics and subtropics. Variability has been exhaustively studied by several workers for various yield attributes. Total dry matter production is very important aspect with high heritability and high genetic advance and its direct effects are maximum to yield than any other plant character as recorded by Reddy and Stephen Dorairaj (1987). Very few workers studied the varia bility for dry matter production. The present investi gation is an attempt to study heritability and correla tion of various components of dry matter production.

MATERIALS AND METHODS

. Fifty genotypes of various plant types of wide geographical origin were grown in 1986 in a

randomised block design with four replications. Observations were recorded on root weight, stem weight, leaf weight, capsule weight and seed yield from 5 samples in each genotypes from every replication. Phenotypic and genotypic variabilities and heritability (broad sense) were estimated Phenotypic and genotypic coefficients of variabilities (PCV and GCV) were estimated as per Burton (1952). Genetic advance (GA) was estimated according to Johnson et al. (1955a) and phenotypic and genotypic correlations were worked out according to Johnson et al. (1955b).

RESULTS AND DISCUSSION

Analysis of variance revealed that all treatments were highly significant. Highest PCV