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GENETIC DIVERSITY FOR YIELD AND ITS COMPONENT TRAITS IN PEARLMILLET [*Pennisetum glaucum* (L.) R. Br.]

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ABSTRACT

Pearlmillet is an important cereal crop of the semi arid-tropical region. As a result the crop productivity is challenged in most cultivable regions. In order to enhance the productivity in dry regions, breeders need access to diverse material in their breeding programmes. In the present study, an attempt was made to assess the genetic divergence among the 243 germplasm lines using Mahalanobis D² statistic. Based on the genetic distance (D^2 value), the 243 genotypes were grouped into 16 different clusters indicating diverse nature of material studied. Cluster I was the largest with 129 genotypes followed by cluster III (49 genotypes) and cluster V (24 genotypes) while clusters II and VI, VII, VIII and X to XVI were solitary indicating the grouping of exotic collections in definite groups. Among the various characters, seed yield (27.45%), panicle girth (18.16 %), leaf length (12.20 %) contributed maximum towards the divergence. Cluster IX (9 genotypes) showed the maximum mean value for seed yield. The intra and inter cluster divergence among the genotypes were varying in magnitude. The intra-cluster distance was maximum in cluster IX followed by clusters IV and V. The widest inter cluster distance was noted between cluster V and XVI giving scope for hybridization programme for improvement of Pearl millet genotypes. The distance between clusters II and V was minimal indicating close relationship between those clusters.

KEY WORDS: Pearl millet, D^2 technique, Genetic divergence, Cluster.

INTRODUCTION

Pearlmillet is an important coarse grain cereal crop of dry land agriculture. It is extensively cultivated as a dual purpose crop under large areas in Africa, Asia and Australia while grown as forage crop only in sub-tropics of USA. Globally it ranks 6th cereal crop in importance followed by wheat, rice, maize, barley and sorghum. In India it is fourth most important cereal after crops like rice, wheat and sorghum. Information on genetic diversity analysis helps to identify the genetically diverse genotypes for their use in breeding programmes. Choosing genetically diverse parents will enable the expansion of genetic base and development of superior types and greater success can be achieved through judicious choice of parents for hybridization based on genetic divergence. (Moll and Stuber, 1971) reported that crossing between divergent parents usually produce greater heterosis than those between closely related ones. Of the several methods available Mahalanobis's generalized distance estimated by D^2 statistic (Rao, 1952) is a unique tool for discriminating population considering a set of parameter together rather than inferring from indices based on morphologic al similarities and polygenic relationship.

MATERIALS & METHODS

The material for the present investigation comprised 243 genotypes (Coded as GP-1 to GP-243) of pearl millet. The experiment was carried out in a Randomized Block Design with three replication at Regional Agricultural Research Station, Vijayapur (Karnataka, India), during *Kharif*, 2014. Each plot consisted of two rows each of 5.0 meter length. The spacing between row to row was 50 cm and between plant to plant was 15 cm. Normal and uniform cultural operations were followed during the crop season to raise a good crop. The observations were recorded on individual plant basis on 5 randomly selected plants from each replication for characters *viz*., plant height (cm), no. of tillers/plant, leaf length (cm), leaf width (cm), total panicle length (cm), panicle length(cm) panicle girth (mm), 100 seed weight (g) and seed yield kg per ha. Days to 50% flowering recorded on plot basis. The collected data was subjected to statistical analysis using Mahalanobis's D^2 statistic to assess genetic divergence. The genotypes were grouped on the basis of minimum generalized distance using the Tocher's methods (Rao, 1952).

RESULTS & DISCUSSION

Analysis of variance revealed significant difference among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among them. The parameters of genetic variability revealed high PCV and GCV values for seed yield followed by tillers per plant, panicle length, leaf length and panicle girth respectively, (Table 1) indicating that these traits could be used as selection indices for yield improvement, similar findings were reported by (Mahawar *et al.,* 2004 and Vidyadhar and Devi, 2007). High heritability (> 60 %) was observed in all the characters studied. The high heritability with

high genetic advance was recorded for the character seed yield per ha (98.40%) followed by plant height (96.60%) and tillers per plant (96.30%). The highest genetic advance as *per cent* of mean was observed for seed yield (94.93%) followed by tillers per plant (44.32%), panicle length

(41.00%) and leaf length (40.66%). It indicates that most likely the heritability is due to additive gene effects and selection for these traits may be rewarding. Similar findings have been reported by (Mahawar *et al.,* 2004; Vidyadhar and Devi, 2007) in Pearlmillet.

TABLE 1: Estimates of variability parameters for different characters of Pearlmillet

Character / Parameters	DFF	PH (cm)	TPP	LL (cm)	LW (cm)	TPL (cm)	PL (cm)	PG (mm)	HSW (g)	SYPH (Kg)
^2g	53.59	791.22	0.77	85.78	0.29	32.84	26.95	15.54	0.05	396260.40
GCV	11.82	16.03	21.92	20.10	16.04	16.44	20.87	17.68	16.45	46.46
^2p	55.95	818.70	0.80	88.91	0.37	36.87	29.63	20.95	0.07	402770.50
PCV	12.08	16.30	22.34	20.46	17.99	17.42	21.88	20.53	19.53	46.84
h^2 (b.s) (%)	95.80	96.60	96.30	96.50	79.50	89.10	91.0	74.20	70.90	98.40
G A 5%	14.76	56.96	1.77	18.74	1.00	11.14	10.20	6.99	0.38	1286.23
GA as % of Mean 5%	23.83	32.45	44.32	40.66	29.45	31.97	41.00	31.37	28.54	94.93
General Mean	61.94	175.52	3.99	46.09	3.38	34.85	24.88	22.30	1.33	1354.99
Exp. Mean next Generation	76.69	232.48	5.76	64.83	4.37	45.98	35.07	29.28	1.70	2641.22

Abbreviations: GCV = Genotypic coefficient of variation; b.s.= Broad sense; h^2 = Heritability; PCV = Phenotypic coefficient of variation; G.A = Genetic advance; ^2g = Genotypic variation; ^2p = Phenotypic variation ; ^2e = Environmental variation

TABLE 2. Distribution of 243 Pearl millet genotypes into different clusters

Cluster	No. of gen.	Genotype
I	129	GP-156, GP-173, GP-174, GP-208, GP-89, GP-210, GP-155, GP-168, GP-175, GP-205, GP-218, GP-119, GP-145, GP-64, GP-140, GP-63, GP-118, GP-91, GP-88, GP-92, GP-154, GP-11, GP-15, GP-12, GP-56, GP-105, GP-133, GP-170, GP-178, GP-98, GP-83, GP-121, GP-57, GP-54, GP-31, GP-61, GP-112, GP-84, GP-23, GP-181, GP-230, GP-163, GP-238, GP-148, GP-44, GP-200, GP-150, GP-206, GP-164, GP-193, GP-34, GP-81, GP-116, GP-82, GP-73, GP-102, GP-33, GP-70, GP-189, GP-16, GP-32, GP-143, GP-172, GP-136, GP-45, GP-10, GP-36, GP-182, GP-160, GP-153, GP-6, GP-48, GP-4, GP-213, GP-42, GP-62, GP-5, GP-51, GP-69, GP-35, GP-128, GP-191, GP-9, GP-141, GP-120, GP-204, GP-233, GP-124, GP-78, GP-202, GP-157, GP-115, GP-159, GP-95, GP-3, GP-94, GP-184, GP-199, GP-166, GP-144, GP-151, GP-106, GP-7, GP-25, GP-38, GP-80, GP-188, GP-161, GP-101, GP-103, GP-99, GP-13, GP-22, GP-223, GP-176, GP-217, GP-60, GP-177, GP-142, GP-185, GP-49, GP-29, GP-225, GP-14, GP-39, GP-68, GP-79, GP-75 and GP-114
II	1	GP-125
III	49	GP-26, GP-53, GP-72, GP-67, GP-100, GP-27, GP-59, GP-52, GP-28, GP-243, GP-30, GP-113, GP-74, GP-17, GP-2, GP-1, GP-231, GP-203, GP-186, GP-183, GP-117, GP-158, GP-129, GP-20, GP-152, GP-107, GP-221, GP-234, GP-109, GP-77, GP-40, GP-242, GP-198, GP-123, GP-209, GP-228, GP-37, GP-147, GP-139, GP-192, GP-85, GP-131, GP-241, GP-87, GP-97, GP-196, GP-96, GP-58 and GP-50
IV	21	GP-135, GP-180, GP-194, GP-187, GP-190, GP-138, GP-222, GP-224, GP-76, GP-167, GP-162, GP-21, GP-132, GP-86, GP-216, GP-110, GP-219, GP-134, GP-235, GP-43 and GP-197
V	24	GP-149, GP-226, GP-122, GP-227, GP-18, GP-41, GP-169, GP-65, GP-130, GP-214, GP-239, GP-240, GP-211, GP-8, GP-126, GP-71, GP-90, GP-55, GP-171, GP-108, GP-207, GP-220, GP-127 and GP-19
VI	1	GP-195
VII	1	GP-66
VIII	1	GP-47
IX	9	GP-146, GP-232, GP-111, GP-201, GP-229, GP-236, GP-137, GP-179 and GP-104
X	1	GP-46
XI	1	GP-165
XII	1	GP-215
XIII	1	GP-218
XIV	1	GP-24
XV	1	GP-98
XVI	1	GP-237

Based on D^2 values, 243 genotypes were grouped in 16 clusters, indicating the presence of large amount of diversity among the genotypes Table 2. Maximum genotypes (129) were present in cluster I and III (49) followed by cluster V with 24, and cluster IV with 21 genotypes. Clusters II, VI, VII, VIII and X to XIV had one genotype showing these genotypes highly divergent from each other. Present study is corroborative with the

findings of (Savery and Parsad, 1995; Mahawar *et al.,* 2004; Vidyadhar and Devi, 2007). The intra and inter-cluster D^2 values among the 16 clusters are presented in Table 3 and Fig. 1. The intra-cluster distance was maximum (223.6) in cluster IX followed by cluster IV (171.95) and cluster V (169.3). These results are in agreement to the earlier findings by Vidyadhar and Devi (2007) and Govindaraj *et al*. (2011).

TABLE 3. Average intra and inter-cluster distance based on corresponding D² values

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	107.18															
II	168.16	0														
III	225.76	414.06	152.11													
IV	266.80	230.50	338.59	171.95												
V	205.16	116.51	455.83	387.14	169.3											
VI	287.73	508.09	202.49	246.46	585.79	0										
VII	222.17	536.88	197.99	492.47	497.69	219.48	0									
VIII	510.99	915.10	225.02	629.30	928.30	230.73	207.52	0								
IX	429.03	705.32	280.68	419.99	782.73	285.76	143.30	221.83	0							
X	284.71	350.99	255.46	492.53	391.21	566.06	285.76	460.08	608.03	0						
XI	319.28	366.53	197.84	286.76	485.69	280.27	457.62	330.31	380.47	183.53	0					
XII	523.73	522.38	402.38	246.29	736.85	271.44	758.92	570.60	427.21	560.58	185.84	0				
XIII	629.87	359.81	936.10	386.23	495.84	284.90	871.75	1604.18	1166.31	907.04	693.47	527.85	0			
XIV	266.02	417.97	205.75	313.97	446.96	397.21	232.61	354.70	382.44	150.09	113.60	337.05	788.37	0		
XV	294.87	957.65	507.44	514.35	412.35	283.77	828.80	501.11	443.55	812.67	382.77	1002.13	1017.26	617.97	0	
XVI	821.14	957.65	560.04	478.68	1173.98	283.77	828.80	501.11	443.55	914.37	382.77	1017.26	153.75	492.15	1120.20	0

TABLE 4. Mean values of genotypes present in different clusters for different characters

Cluster\Char.	DFF	PH (cm)	TPP	LL (cm)	LW (cm)	TPL(cm)	PL(cm)	PG(mm)	HSW(g)	SYPH(Kg)
I	61.28	171.81	3.69	43.72	3.30	33.87	23.72	22.12	1.35	1184.65
II	63.00	137.10	3.80	36.00	3.65	38.00	27.25	23.55	1.40	1992.00
III	60.52	186.10	4.77	52.30	3.59	37.04	27.08	22.51	1.30	1135.82
IV	64.86	187.36	4.17	46.82	3.49	35.40	24.56	21.46	1.30	2525.42
V	64.79	137.79	3.66	38.30	3.11	33.51	23.90	23.05	1.35	1374.51
VI	68.00	229.45	3.80	61.80	3.35	31.25	21.00	20.65	0.80	1887.20
VII	53.50	199.40	2.80	57.50	3.60	26.25	26.25	23.70	1.40	270.20
VIII	57.00	212.50	4.85	65.00	3.30	43.75	33.50	20.65	1.25	721.00
IX	65.89	239.15	3.98	57.14	3.64	40.23	28.72	22.15	1.27	1565.27
X	50.00	134.45	5.90	37.00	3.40	36.00	38.00	23.40	1.45	813.80
XI	70.50	159.20	6.10	54.00	4.15	39.00	35.50	23.70	1.35	2060.20
XII	67.00	202.00	6.40	53.00	3.45	28.00	22.00	20.65	1.35	3227.00
XIII	70.50	139.15	4.55	33.25	2.40	34.30	23.00	18.75	1.30	3777.80
XIV	54.00	170.70	4.85	47.75	4.65	22.00	35.50	19.25	1.35	1652.20
XV	62.00	177.80	0.55	61.25	4.10	36.00	24.50	23.10	1.20	994.00
Contribution %	11.01	11.73	13.40	12.20	0.45	2.35	3.04	18.16	0.21	27.45

Note:

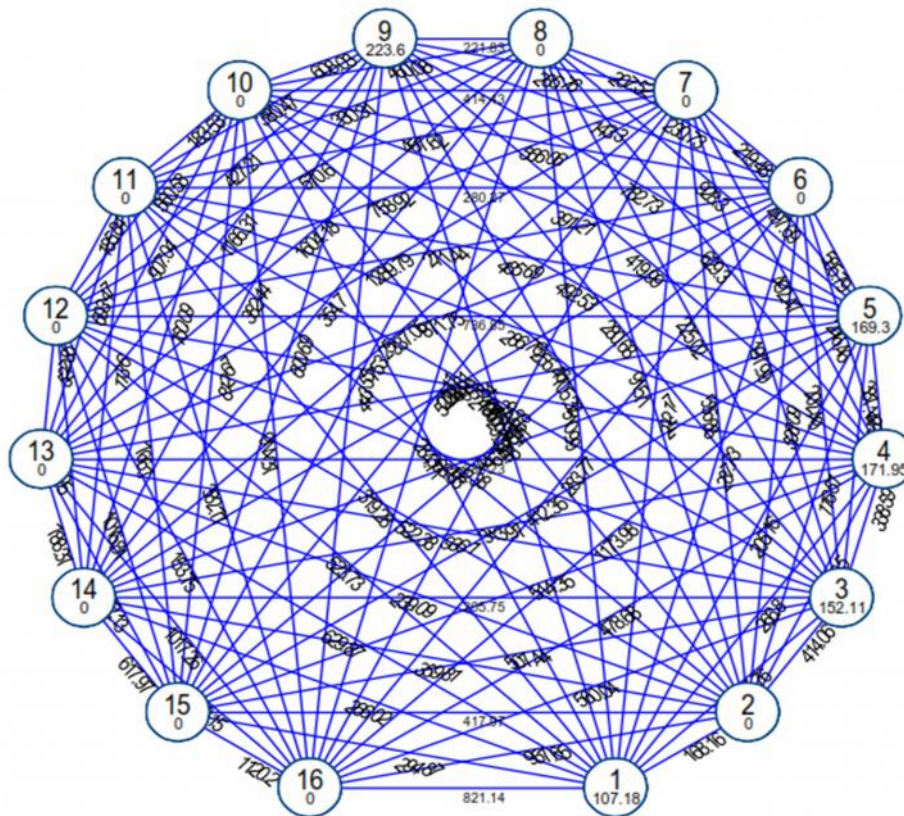|	
PH: Plant Height	**TPP:** Tillers per plant
PL: Panicle length	**PG:** Panicle girth
LL: Leaf length	**LW:** Leaf width
HSW: Hundred seed weight	**DFF:** Days to 50% flowering
TPL: Total panicle length	**SYPH:** Seed yield per hectare

FIGURE 1. Mahalnobis Euclidean Disatnce (Tocher's(Tocher's Method, Not to the Scale)

The maximum (1173.98) inter-cluster distance was observed between cluster V and cluster XVI and minimum (116.51) inter-cluster distance was present between clusters II and cluster V. Cluster II, VI, VII, VII and X to XIV may be selected for more effective crossing programme and should result in wide spectrum of variability to operate selection in segregating population. Presence of diversity among pearl millet genotypes of the present study is in accordance with earlier reports (Yadav, 1994; Hepziba *et al.,* 1995; Mukeshkumar *et. al.,* 2015). The existence of diversity among the genotypes was also assessed by the considerable amount of variation in cluster means for different characters Table 4. Based upon the cluster mean performance the cluster XIII had high mean values for seed yield per ha (3777.80) and days to 50% flowering (70.50), cluster IX for plant height (239.15), cluster VIII and XIV for tillers per plant (4.85), cluster XVI for leaf length (74.75) and panicle girth (25.45), cluster XIV for leaf width (4.65), cluster VIII for total panicle length (43.75). While cluster X had high mean values for panicle length (38.00) and 100 seed weight (1.45). Based upon D^2 values, per cent contribution of different characters towards divergence was obtained. Among the ten characters studied the most important characters contributing to the divergence were seed yield per ha. (27.45%), panicle girth (18.16%), tillers per plant (13.40%) and leaf length (12.20%). These results are in agreement to the earlier findings by (Vidyadhar and Devi, 2007; Mukeshkumar *et.al.,* 2015).

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