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Research Article

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Genetic Parameters of Grain Yield and Its Contributing Characters in Pearl Millet (*Pennisetum glaucum* (L.) R. Br.] Under Varying Environmental Conditions

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ABSTRACT

The present investigation was under taken to the study of genetic analysis in pearl millet in 10x10 diallel set, excluding reciprocals, for grain yield and its 12 component traits, viz., grain yield per plant, days to 50% flowering, days to maturity, productive tillers per plant, plant height, panicle length, panicle girth, biological yield per plant, dry fodder yield per plant, harvest index, test weight, Fe content and Zn content. Genetic components analysis revealed that additive-dominance model fitted for all the characters in all the environments, both additive (D) and dominance (H_1 and H_2) components were significant for all the characters, except additive (D) component in days to 50% flowering and dry fodder yield in E_2 & E_3, days to maturity in E_2, productive tillers in E_3 and plant height, biological yield and grain yield per plant in all the the environments. However, relative magnitude of dominance component(H1 and H2) was higher than additive component for all the characters indicated preponderance of dominant gene action. The ratio of mean degree of dominance as measured by $(H_1/D)^{½}$ was more than unity in all the environments indicating over dominance. The value of $(H_2/4H_1)$ was less than 0.25 indicating asymmetric distribution of positive and negative alleles. The ratio of dominant to recessive alleles was more than unity in all the environments indicating accumulating of dominant genes. Narrow sense heritability estimates were of low to high magnitude for different traits. Heritability estimates (ns) were high 0.303 in E_2 and 0.528 in E_3 for Fe content and 0.116 in E_1 and 0.117 in E_3 for grain yield per plant, but low 0.073 in E_2, 0.080 in E_1 and 0.131 in E_3 for days to maturity. This suggesting that selection based on these traits would lead to rapid genetic improvement. The preponderance of non-additive gene effects of grain yield and its component traits in parents indicated that, heterosis breeding would be practically feasible in pearl millet crop.

Key words: *Pearl millet, gene action, heritability, Pennisetum glaucum*

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INTRODUCTION

Pearl millet *Pennisetum glaucum* (L.) R. Br. is a diploid species having fourteen chromosomes, belongs to the family Poaceae (Gramineae). It is an important cereal crop in arid and semi arid region of the world.It is a most drought tolerant of all cultivated food grain crops, is widely cultivated across the arid and semi-arid tropics of Africa and Asia. In India, Rajasthan is having the largest area and production in the country with low productivity. Pearl millet is largely cultivated under rain fed condition. Fisher[2] was the first to recognize the importance of biometrical techniques to study the genetics of quantitative characters. Later on Fisher[3] partitioned total genetic variance in the three parts; additive (arising from average effect of genes), dominance (arising from allelic interactions) and epistatic part (arising from non-allelic interactions). Yadav *et al.*[11] and Parmar *et al.*[9] were reported non- additive gene action in pearl millet for grain yield and its related characters. The genotype x environment effect in pearl millet varied in nature and magnitude of gene action affecting traits of productivity and efficiency of selection in segregating population. Morphological traits are also important for harnessing the potential yield. Estimates of additive and dominance genetic variance help to choose the most effective breeding procedure to be followed for a crop species. These components of variance do explain the genetic architecture of the population at hand and help to draw up the breeding strategies on the basis of expected performance of progenies. Therefore, the present study was undertaken to elucidate the nature and magnitude of gene action involved in inheritance of grain yield and its components in pearl millet.

MATERIAL AND METHODS

Ten genetically diverse inbreds of pearl millet *viz*., J-2340, MIR-525-2, RIB-192, RIB-494, RIB-3135-18, RIB 57, RIB-335/74, HBL-11, H-77/833-2-202 and G-77/107 were crossed in all possible combinations excluding reciprocals during summer 2015 at ICRISAT, Hyderabad to generate a diallel set. Ten parents' along with their 45 F_1's were evaluated for grain yield and 13 yield components in a Randomized Block Design with three replications at Rajasthan Agricultural Research Institute, Durgarura, Jaipur (Rajasthan), India, during *Kharif*-2015. Each entry was sown in two rows of 4.0 m length having 50 x 15 cm crop geometry. All the recommended cultural practices were adopted to raise good crop of pearl millet. The observation were recorded on five randomly selected plants from each replication and environment, for the characters namely; days to 50% flowering, days to maturity, productive tillers per plant, plant height, panicle length, panicle girth, biological yield per plant, dry fodder yield per plant, grain yield per plant, harvest index, test weight, Fe content and Zn content while, days to 50% flowering and days to maturity were recorded on plot basis. The mean values were used for the analysis of genetic components of variation according to Hayman[5].

RESULT AND DISCUSSION

The estimates of genetic parameters, their ratio and narrow sense heritability for grain yield and its components are presented. (Table-1-4).The estimates of components of genetic variance exhibited that both additive (D) and dominance (H_1 and H_2) were highly significant for all the characters, except additive (D) component in days to 50% flowering and dry fodder yield per plant in E_2 and E_3 and days to maturity in E_2 and productive tillers per plant in E_3 and plant height, biological yield and grainyield per plant in all the environments. This clearly indicated that both additive and non- additive components were operative for inheritance of these characters except, days to 50% flowering and dry fodder yield per plant in E_2 and E_3 and days to maturity in E_2 and productive tillers per plant in E_3 and plant height, biological yield and grainyield per plant in all the environments where, only non-additive component was operative. The H_1 component was greater than D for all the characters. These results suggested that although, additive and dominance gene action existed to this character in material used. The estimates of dominance genes effects, corrected for gene distribution (H_2), were significant and therefore, agreed with H_1 estimates obtained.

Further, the ratio of $H_2/4H_1$ was less to 0.25 for all the characters indicating asymmetric distribution of positive and negative alleles. The ratio of $(4DH_1)^{1/2}$+F / $(4DH_1)^{1/2}$ - F indicated the type of alleles which were more frequent. In the present study this ratio was positive and more than unity for all the traits indicated that the parents carried more dominant alleles than recessive one. This was further supported by positive value of "F" in all the cases.Narrow sense heritability estimates obtained in component analysis ranged from low to high for different traits. This was 0.050 in E_2 and0.104 in E_3 for days to 50% flowering, 0..073 in E_2 and 0.131 in E_3 for days to maturity, 0.020 in E_1 and 0.126 in E_2 for productive tillers per plant, 0.162 in E_2 and 0.171 in E_3 for plant height, 0.165 in E_1, for panicle length, 0.41 in E_3 and 0.126 in E_2 for panicle girth, 0.135 in E_3 and 0.149 in E_2 for biological yield per plant, 0.124 in E_3 and 0.175 in E_2 for dry fodder yield per plant, 0.116 in E_2 and 0.117 in E_1 for grain yield per plant, 0.199 in E_3 and 0.202 E_1 for harvest index, 0.159 in E_3 and 0.182 in E_1 for test weight and 0.303 in E_2 and 0.364 E_1 for Fe content, 0.079 in E_1 and 0.287 in E_3 for Zn content. The lower values of heritability clearly indicated that it was much influenced by environment. Graphical analysis was carried out as given by Hayman[5]. Suggesting that selection based on these attributes would lead to rapid improvement. Major part of phenotypic variability was due to addictiveness and possibility of fixing these traits by simple selection. The results was corroborate with the findings of Lakshmana *et al.*[7], Dang *et al.*[1] and Mukherji *et al.*[8] and Vagadiya *et al.*[10].

Table 1: Estimates of components of genetic variance for characters in E_1, E_2 and E_3 environments

Components	**Days to 50% flowering**			**Days to maturity**			**Productive tillers per plant**		
	E_1	E_2	E_3	E_1	E_2	E_3	E_1	E_2	E_3
D ±SE	3.56±2.70	3.09±5.11	2.85 ±4.56	4.36±2.42	3.56 ±4.86	4.67 ±4.16	0.10 ±0.14	0.142±0.10	0.187±0.125
H1±SE	37.33±5.76	52.23±10.89	53.16±9.70	38.06±5.15	57.47±10.37	52.59±8.87	1.64±0.31	1.64±0.22	2.24±0.26
H2±SE	29.84±4.89	50.89±9.25	47.88±8.25	29.86±4.37	54.75±8.81	43.24±7.54	1.48±0.26	1.45±0.19	2.11±0.22
h^2±SE	-0.86±3.27	-0.31±3.19	-0.28±5.52	0.89±2.93	-0.01±5.89	0.84±5.05	1.76±0.17	2.23±0.13	2.06±0.15
F±SE	9.33±6.24	2.72±11.80	5.16±10.52	11.20±5.58	4.06±11.24	10.66±9.65	0.16±0.33	0.22±0.24	0.27±0.28
E±SE	2.61±0.81	3.65±1.54	0.85±1.37	0.45±0.73	0.40±1.46	0.31±1.25	0.01±0.04	0.01±0.03	0.01±0.03
$(H_1/D)1/2$	3.237	4.111	4.314	2.952	4.012	3.335	4.04	3.408	3.468
$H_2/4H_1$	0.20	0.244	0.225	0.196	0.238	0.206	0.227	0.221	0.235
$(4DH_1)1/2+F/$ $(4DH_1)1/2-F$	2.361	1.240	1.530	2.537	1.331	2.031	1.501	1.606	1.529
h^2/H_2	-0.029	-0.006	-0.006	0.030	0	0.020	1.186	1.530	0.977
Heritability in narrow sense	0.078	0.050	0.104	0.080	0.073	0.131	0.02	0.126	0.041

Table 2: Estimates of components of genetic variance for characters in E_1, E_2 and E_3 environments

Components	Plant Height			Panicle Length			Panicle girth		
	E$_1$	E$_2$	E$_3$	E$_1$	E$_2$	E$_3$	E$_1$	E$_2$	E$_3$
D ±SE	152.43±160.77	145.21±158.62	96.23±150.17	19.12±8.54	19.11±8.54	19.12±8.54	0.157 ±0.15	0.142±0.11	0.187±0.125
H1±SE	1900.39±342.23	1896.88±337.65	1670.93±319.66	97.77±18.17	97.75±18.17	97.75±18.18	1.63±0.32	1.64±0.22	2.24±0.26
H2±SE	1782.39±290.86	1775.58±286.96	1576.84±241.67	87.24±15.44	87.22±15.44	87.23±15.45	1.45±0.27	1.45±0.19	2.12±0.22
h^2±SE	3118.33±194.69	3135.60±192.08	2473.91±181.85	15.21±10.34	15.44±10.34	15.24±10.34	1.42±0.18	2.22±0.12	2.07±0.15
F±SE	84.12±370.96	88.63±365.99	21.89±346.5	20.99±19.70	20.97±19.70	20.98±19.70	0.25±0.34	0.22±0.24	0.27±0.29
E±SE	16.48±48.47	16.61±47.82	13.85±45.28	0.16±2.57	0.17±2.57	0.18±2.58	0.01±0.04	0.01±0.03	0.02±0.04
(H$_1$/D)1/2	3.53	3.614	4.167	2.261	2.261	2.261	3.227	3.408	3.468
H$_2$/4H$_1$	0.234	0.234	0.236	0.223	0.223	0.223	0.222	0.221	0.235
(4DH$_1$)1/2+F/ (4DH$_1$)1/2-F	1.170	1.184	1.056	1.641	1.641	1.641	1.657	1.606	1.529
h^2/H$_2$	1.75	1.76	1.569	0.174	0.174	0.174	0.982	1.53	0.977
Heritability in narrow sense	0.168	0.162	0.171	0.165	0.165	0.165	0.105	0.126	0.041

Table 3: Estimates of components of genetic variance for characters in E_1, E_2 and E_3 environments

Components	Biological Yield			Dry Fodder Yield			Grain Yield Per Plant		
	E$_1$	E$_2$	E$_3$	E$_1$	E$_2$	E$_3$	E$_1$	E$_2$	E$_3$
D ±SE	1255.94±1819.97	387.565±629.95	233.53±457.68	1533.75±8.54	457.05±816.64	164.82±477.14	5.19 ±16.75	1.59±5.70	1.45±4.97
H1±SE	18330±3873.97	6429.08±1340.91	4112.80±974.21	17291.05±3729.57	5355.71±1738.31	3609.65±1015.63	176.73±35.67	80.21±12.14	50.76±10.59
H2±SE	16056.15±3292.44	5769.98±1139.62	3675.15±827.97	1505.95±3169.72	4866.96±1477.37	3383.87±863.18	158.38±30.61	73.43±10.31	42.51±9.01
h^2±SE	9940.50±2203.83	4096.98±762.82	2755.77±554.21	5685.90±2121.69	1989.77±988.89	1709±577.77	311.13±20.29	169.18±6.91	54.15±6.03
F±SE	2058.52±4199.21	476.75±2453.48	366.53±1056.01	2555.96±4042.69	390.75±1884.25	136.17±1100.91	11.68±38.66	3.01±13.15	3.77±11.48
E±SE	292.91±548.74	184.17±189.94	57.45±137.00	157.52±2.57	87.86±246.23	45.60±143.86	5.11±5.05	2.10±1.71	1.42±1.50
(H$_1$/D)1/2	3.820	4.073	4.197	3.358	3.423	4.68	5.83	7.097	5.91
H$_2$/4H$_1$	0.219	0.224	0.223	0.217	0.227	0.234	0.224	0.229	0.0
(4DH$_1$)1/2+F/ (4DH$_1$)1/2-F	1.546	1.356	1.460	1.660	1.285	1.197	1.477	1.307	0.0
h^2/H$_2$	0.619	0.710	0.750	0.378	0.409	0.505	1.964	2.304	1.27
Heritability in narrow sense	0.146	0.149	0.135	0.136	0.175	0.124	0.117	0.116	0.0

Table 4: Estimates of components of genetic variance for characters in E_1, E_2 and E_3 environments

Components	Harvest Index			Test Weight			Fe Content			Zn Content		
	E$_1$	E$_2$	E$_3$	E$_1$	E$_2$	E$_3$	E$_1$	E$_2$	E$_3$	E$_1$	E$_2$	E$_3$
D ±SE	12.14±4.01	10.91±8.48	28.01±14.38	0.91±0.43	0.91±0.50	0.62±0.44	27.50±14.46	56.94±19.57	46.93±16.64	24.38±7.18	34.04±18.36	24.77±11.22
H1±SE	49.87±8.55	71.15±18.07	119.90±30.61	3.23±0.91	3.45±1.07	3.09±0.93	167.56.15±30.78	228.15±41.66	177.24±35.43	147.12±15.28	204.86±39.10	165.64±23.9
H2±SE	43.02±7.26	64.70±15.36	95.94±26.01	2.83±0.78	3.02±0.91	2.74±0.79	150.21±26.16	171.55±35.41	153.17±30.11	126.99±12.991	152.86±33.23	133.53±20.31
h^2±SE	15.68±4.86	32.68±10.28	-1.13±17.41	0.26±0.52	0.27±0.61	0.16±0.53	43.59±17.51	0.73±23.70	4.62±20.15	42.57±8.69	58.42±22.24	13.21±13.59
F±SE	12.60±9.27	8.33±19.58	38.45±33.18	0.97±0.99	0.99±1.16	0.69±1.01	1.95±33.37	76.32±45.16	-14.53±38.40	39.02±16.56	65.33±42.38	30.01±25.90
E±SE	1.90±1.21	2.00±2.56	3.19±4.33	0.05±0.13	0.05±0.15	0.06±0.13	0.003±4.36	0.003±5.90	0.004±5.01	0.041±2.16	0.01±5.53	0.01±3.38
(H$_1$/D)1/2	2.027	2.553	2.069	1.887	1.94	2.226	2.468	2.002	1.94	2.45	2.453	2.586
H$_2$/4H$_1$	0.216	0.227	0.20	0.219	0.219	0.222	0.224	0.188	0.216	0.214	0.187	0.202
(4DH$_1$)1/2+F/ (4DH$_1$)1/2-F	1.688	1.351	1.993	1.791	1.776	1.662	1.029	2.007	0.852	1.966	2.285	1.612
h^2/H$_2$	0.365	0.505	-0.012	0.092	0.090	0.058	0.290	0.004	0.030	0.335	0.382	0.099
Heritability in narrow sense	0.202	0.199	0.199	0.182	0.178	0.159	0.364	0.303	0.528	0.079	0.213	0.287

CONCLUSION

The present investigation suggested that in addition to conventional breeding methods to befollowed for the parents identified with both additive and non additive genetic parameters , some non-conventional breeding methods such as diallel selective mating, bi-parental mating and reciprocal recurrent selection may be used to obtain trangressivesegregants in succeeding generations due to preponderance of non-additive gene effects of grain yield and most of its component traits in the parents, heterosis breeding would be practiced in pearl mille. Thus, identified parents and crosses may serve as potential breeding material for developing inbreds, composite/synthetic and hybrid varieties in pearl millet.

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