GENETIC ARCHITECTURE OF VARIOUS MORPHOLOGICAL CHARACTERS IN PEARL MILLET

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ABSTRACT

The study was conducted to find out the inheritance pattern and genetic parameters for different attributes in a diallel cross involving five genotypes / lines of Pearl millet. Analysis of variance showed highly significant differences among genotypes for all the characters under study. Haymans (1954) method was used to determine the genetic component of variation and type of gene action controlling the particular trait. The results revealed that non additive genetic effects were more pronounced in the inheritance of plant height, number of tillers per plant and number of nodes per plant. While days to 50% flowering showed additive type of gene action. Asymmetrical gene distribution was present for plant height, number of tillers per plant and number of nodes per plant whereas parents contained the same number of genes for days to 50% flowering character. Lack of directional dominance was observed in all the traits except plant height. The graphic analysis showed that plant height, tillers per plant and nodes per plant were under the control of over dominance which can be easily exploited by heterotic effect. Additive type of inheritance was noticed for days to flowering character.

Key words: Pearl millet, diallel analysis, gene action, additive, over dominance and partial dominance.

INTRODUCTION

Pearl millet is an important cereal crop grown under harsh environment characterized by erratic rainfall and nutrient poor soils (Lakshmana, 2008). Pearl millet is a source of nutritionally superior staple food grain for millions of poor people of under developed countries of the world. It also provides feed and fodder for poultry and livestock respectively as its green fodder is more palatable and devoid of HCN (Hydrogen Cyanide) content as that of sorghum (Lakshmana, 2008).

Pearl millet covers an area of 474.6 thousand hectare in Pakistan amongst which Punjab contributed 423.2 thousand hectare with a production of 273.6 thousand tonnes to the overall production of 301.00thousand tonnes of national production during the year 2013-14(Anonymous, 2014). Among various causes of low production, non availability of high yielding cultivars, poor management and birds attack are important factors. This situation stresses for efficient management of available resources to maximize the yield potential in terms of high yielding varieties. In the past less effort were made to exploit the genetic potential to develop high yielding pearl millet varieties. A systematic and successful breeding work needs an understanding of genetic architecture of quantitative character to be bred. Several researchers like Pethani and Kapoor (1995), Sheoran *et al* (2000), Rasal and Patil (2003), Singh *et al* (2004), Dangaria *et al* (2004), Chotaliya (2005), Ansodariya *et al* (2006), Dhuppe *et al* (2006) and Bhanderi *et al* (2007) used diallel analysis to ascertain the genetic mechanism and gene action involved in expression of different quantitative traits while working on pearl millet crop.

MATERIALS AND METHODS:

The experiment was performed in the research area of Millets Research Station, Rawalpindi. The research material comprised of five pearl millet genotypes selected from pearl millet gene pool having sufficient diversity. Seeds of each genotype were planted in two rows of five meter length of each genotype during kharif 2014. Crosses were made in a diallel fashion including direct and reciprocal crosses at flowering stage.

Seeds of F_1 hybrids along with their parents were planted during second week of July 2015 in a randomized complete design replicated thrice. Each treatment comprised of two rows of five meter length having inter row and inter plant distance at 75 cm and 25 cm respectively. Doze of fertilizer 79 kg N, 57 kg P and 62kg K per hectare was applied. Observation for grain yield and other traits were recorded on five randomly selected plants from each treatment and replication. Data were statistically analyzed following Steel and Torrie (1980). Genetic analysis was

done according to the diallel techniques suggested by Hayman (1954) and Jinks (1954) using computerized program Dial 98. The genetic components of variation i.e., additive effects of genes, dominance effects of genes, symmetry or asymmetry of allele and F value were computed from estimates of variance and covariance. The parameters provide the estimates of relative frequency of dominant to recessive alleles in the genotypes. The information in the gene action and presence of dominant and recessive genes in the parents was also inferred by plotting the covariance (wr) of each array against its variance.

RESULTS AND DISCUSSION

Perusal of Table 1 revealed highly significant differences among the parents and their hybrids (F_1) for all the characters and thus permitted use of Hayman – Jinks model for inheritance studies of these characters.

PLANT HEIGHT

Hayman analysis for plant height is presented in Table 2. Both the additive and dominance effects are responsible for the inheritance of plant height character due to the significance of the items "a" and "b" respectively.

The significance of b_1 indicated the presence of directional dominance. The results also showed that parents have asymmetrical gene distribution because of significance of b_2 item. Significance of b_3 item reflecting the presence of specific gene action other than attributed to b_1 and b_2. Non significance of item c and d showed the lack of maternal and reciprocal effects in the inheritance of plant height. Estimates of additive and non additive genetic variance were significant which revealed that both types of genes are contributing towards the expression of plant height trait. The non additive gene effects, however, showed greater influence due to high magnitude of H_1 than D. A positive and significant F value indicated that the proportion of dominant alleles is in excess as compared to recessive alleles. The ratios of $(H_1/ D)^{1/2}$ more than unity predicted the presence of over dominance type of gene action. Deviation of the ratio of $H_2 / 4H_1$ from its expected value of 0.25 reported the asymmetrical gene distribution in the parents. The ratio of h_2/H_2 proposed that six group of genes exhibiting some degree of dominance. The interception of the regression line of Wr-Vrgraph below the origin (Fig. 1) revealing the operation of over dominance type of gene action. These results are in accordance with Shanmuganathan and Gopalan (2006). From the position of the array points along the regression line, it is evident that the genotype 2contained more dominant genes being closer to the origin while genotype 5 had more recessive alleles due to distal position from the origin.

DAYS TO 50 PERCENT FLOWERING.

Different values obtained from Hayman analysis of variance regarding days to 50 % flowering and results are presented in Table 2. Significance of items 'a' and 'b' suggested the role of both additive and non additive gene effects are responsible in controlling days to 50 percent flowering character. Non significance of "b_1" item indicated the absence of directional dominance. The parents contained the same number of dominance genes as b_2 was not significant. The significant value of "b_3" item indicated the presence of specific gene action controlling the trait. The significance of c and d showed the presence of maternal and reciprocal effect in the inheritance of days to 50 percent flowering character. In case c and d items become significant, the mean square of a and b items need to be retested against the mean squares of c and d items, respectively as suggested by Mather and Jinks (1982). After retesting significance level of "a" changed to non significant indicating that maternal effects masked the properties of genes acting additively. Similarly, after retesting of b_1, b_2, b_3 and b against the mean square of d, the significance of all items changed to non significant indicating that effect of dominant gene was masked by the genes with the reciprocal effects.

The perusal of the Table 4 significance of D showed the presence of additive gene action in inheritance of days to 50 % flowering trait. Positive value of F suggested the greater frequency of dominant alleles as compared to recessive one. Ratio of $(H_1/ D)^{1/2}$ showed that flowering character was under the control of partial dominance type of gene action (Fig. 2). As the $H_2 / 4H_1$ did not deviate from its expected value of 0.25 the genes were distributed symmetrical at the loci showing dominance. The value of h_2/ H_2 indicated the involvement of almost two genes exhibiting some degree of dominance. The findings are in accordance with Santhosh (2002).While Shanmuganathan and Gopal (2006) reported over dominance type of gene action for this character. Interception of regression line above the origin of wr axis inferred partial dominance. The distribution of array points showed that genotype 3 contained more dominant genes as compared to other parents due to its placement close to the origin, whereas genotype 2 being farthest from the origin had maximum recessive genes. The remaining genotypes had almost equal number of dominant and recessive genes due to their placement in the middle.

Table 1. Mean square values of various agronomic characters in 5 X 5 diallel cross experiment in Pearl millet.

Source of variation	Degree of freedom	Plant height	Days to 50% flowering	Number of tillers per plant	Number of nodes per plant
Replications	2	0.89	1.45	0.08	0.17
Genotypes	24	967.76**	18.36**	0.39**	1.35**
Error	48	16.78	2.81	0.06	0.28

* and ** Significant at 5 % and 1 % level, respectively.

Table 2 . Hayman's analysis of variance for plant height and days to 50% flowering in 5x5 diallel of Pearl millet.

Item	Plant Height				Days to 50% flowering				
	DF	SS	MS	F- Ratio	SS	MS	F- Ratio	Retested against	
								c	**d**
a	4	8052.38	2013.09	13.17**	269.44	67.36	23.93**	4.30	
b_1	1	1224.12	1224.12	8.01**	0.75	0.75	0.27 n.s		
b_2	4	3227.33	806.83	5.28**	10.72	2.68	0.95 n.s		
b_3	5	3575.30	715.06	4.68**	60.63	12.13	4.31**		1.5
b	10	8026.75	802.68	5.25**	72.10	7.21	2.56*		1.8
c	4	250.07	62.52	0.41 n.s	59.00	14.75	5.24**		
d	6	420.93	70.16	0.46 n.s	40.17	6.69	2.38*		
Total	74								

* and ** Significant at 5 % and 1 % level, respectively.

Table 3. Hayman's analysis of variance for number of tillers per plant and number of nodes per plant in 5x5 diallel of Pearl millet.

Item	Number of tillers per plant						Number of nodes per plant			
	DF	SS	MS	F- Ratio	Retested against		SS	MS	F- Ratio	Retested against
					c	**d**				**d**
a	4	4.56	1.14	20.02**	3.16		6.36	1.59	5.59	
b_1	1	0.03	0.03	0.60 n.s			0.16	0.16	0.57	
b_2	4	0.77	0.19	3.39*		0.73	6.69	1.67	5.88	1.02
b_3	5	1.40	0.28	4.92**		1.08	8.64	1.73	6.07	1.06
b	10	2.21	0.22	3.88**		0.84	15.49	1.55	5.44	0.95
c	4	1.45	0.36	6.37**			0.73	0.18	0.64	
d	6	1.54	0.26	4.50*			9.77	1.63	5.72	
Total	74									

* and ** Significant at 5 % and 1 % level, respectively.

NUMBER OF TILLERS PER PLANT

Values calculated from Hayman analysis of diallel for tillers per plant are given in Table 3. Significance of 'a' and 'b' items suggesting the role of additive as well as dominance gene effects in the genetic control of trait. Absence of directional dominance was observed due to the non significant of item b_1. Asymmetrical gene distribution and specific gene effects among the parents were due to significance of items b_2 and b_3 respectively. The significant c and d items showed the presence of maternal and reciprocal effects in the expression of number of tillers per plant. After retesting the significance of 'a' and 'b' item which were previously significant reduced to non significant. Perusal of Table 4 revealed the importance of non additive genetic variance due to the significance of H_1 and H_2.

Over dominance was indicated for this trait on the basis of $(H_1/D)^{1/2}$ ratio. Deviation of $H_2/4H_1$ ratio from its expected value of 0.25 proposed that genes were scattered in the parents asymmetrically. Graphic analysis showed involvement of over dominance type of inheritance for tillers per plant as the regression line of the unit slope cut the wr-axis below the origin (Fig. 3). The relative distribution of genotype on graph, parent 5 was found to have the most dominant genes for the trait being closer to the origin. While the parent 3 contained the most recessive alleles

being farthest from the origin. Mahudeswaran (1979) and Logasundari and Fazlullah Khan (1996) also reported the over for number of tillers per plant.

Table 4. Estimates of genetic components of variation and proportional values for different quantitative characters in 5X5 diallel of pearl millet.

Components	Plant height	Days to 50% flowering	Number of tillers per plant	Number of nodes per plant
D	521.73* ± 177.75	10.08* ± 3.27	0.08±0.047	0.74* ±0.29
F	404.48* ± 208.15	1.45±3.04	-0.04 ± 0.05	0.84* ±0.37
H_1	563.98* ± 210.16	2.90 ± 2.39	0.14* ± 0.07	1.12* ±0.39
H_2	437.26* ± 153.44	3.01 ± 2.016	0.11* ± 0.05	0.85* ±0.29
h^2	231.79 ± 182.13	-0.38 ± 0.93	-0.004 ± 0.03	-0.02±0.13
E	50.96* ± 10.08	0.94* ± 0.19	0.02* ± 0.004	0.09* ±0.02
$(H_1/D)^{1/2}$	1.040	0.537	1.29	1.23
$H_2/4H_1$	0.194	0.259	0.203	0.190
KD/KR	0.6864	0.57	0.42	0.73
h_2/H_2	0.6626	-0.16	-0.04	-0.03
Heritability (N.S)	0.432	0.716	0.605	0.213

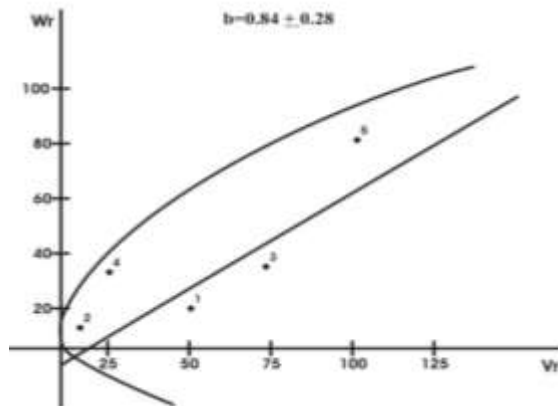***Significant (if the value of parameter divided by its standard error exceeds 1.96)

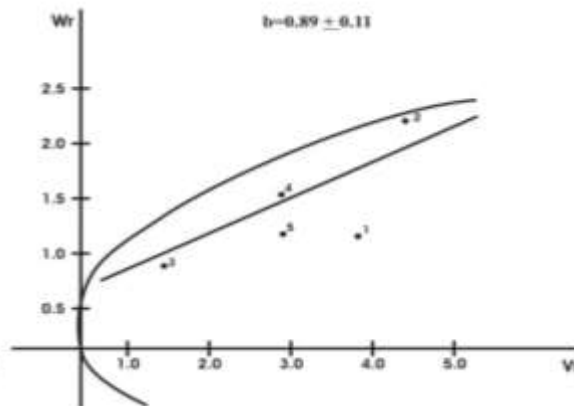Fig.1. Wr-Vr graph for plant height in pearl millet.

Fig.2. Wr-Vr graph for days to 50% flowering in pearl millet.
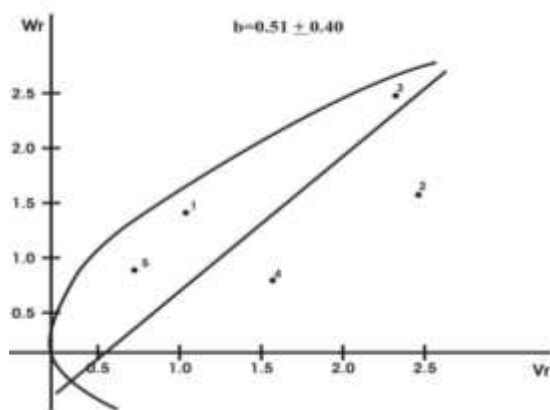
Fig.3. Wr-Vr graph for number of tillers per plant in pearl millet.
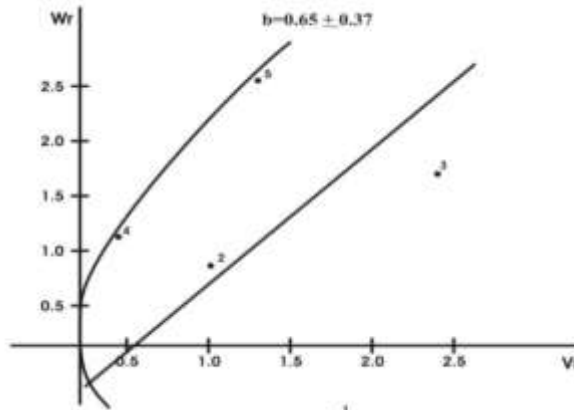
Fig.4. Wr-Vr graph for number of nodes per plant in pearl millet.

NUMBER OF NODES PER PLANT

The analysis of variance of diallel table regarding nodes per plant is given in Table 3. Significance of items "a" and "b" suggested that the both additive and non additive gene effects controlling the inheritance of said plant trait. Non significance of b_1 item indicated the absence of directional dominance. Due to the significance of b_2 and b_3

uneven genes distribution among parents and part of dominance deviation which are not attributable to b_1 and b_2 were observed.

Absence of maternal effect and presence of reciprocal effects were obvious due to non significance of item "c" and significance of item "d" respectively. After retesting the means of items which were previously significant now reduced to non significant i.e b_1, b_2 and b_3. Perusal of Table 4 indicated that both additive and dominance types of gene action were controlling the inheritance of number of nodes per plant. The dominance gene effects however, seems to be more prominent due to higher magnitude of H_1 than D.

The estimates of degree of dominance ratio of $(H_1/D)^{1/2}$ greater than unity also suggested the over dominance type of gene action. As the $H_2/4H_1$ deviated from its expected value of 0.25, the genes were distributed asymmetrical at the loci showing dominance. The value of kd / kr suggested that both dominant and recessive alleles are equally present in the parents. Graphical configuration of variance and covariance for said character reflected that the regression line intercepted the wr-axis below the origin indicating the over dominance. (Fig. 4). The estimates of mean degree of dominance also revealed the existence of over dominance. From the regression line, it is evident that parent 4 had an excess of dominant genes while parent 3 possessed greater number of recessive genes because of distal position from the origin.

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