INHERITANCE STUDIES OF QUANTITATIVE 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 Pearl millet genotypes/lines viz. MGP-322, MGP-328, MGP-335, 13RBS-01 and 13RBS-13. Analysis of variance showed highly significant differences among genotypes for all the characters under study except panicle girth. To study the genetic component of variation and type of gene action controlling the particular trait, Haymans (1954) method was used. The results revealed that non -additive genetic effects were more conspicuous in the inheritance of panicle length, 1000- grain weight and grain yield kg ha^{-1}. Asymmetrical gene distribution was found for all the traits understudy. The graphical analysis showed that panicle length, 1000-grain weight and grain yield kg ha^{-1} were under the control of over dominance which can be easily exploited by heterotic effect.

Key words: Pearl millet, diallel analysis, gene action, non-additive, over dominance and asymmetrical gene distribution.

INTRODUCTION

Pearl millet is an important coarse grain, drought tolerant and warm season cereal crop which is commonly known as Bajra. It is a multiple cereal grown for grain, Stover and green fodder. It has a great potential for making bioethanol (Chakauya and Tongoona, 2008). Pearl millet is the 4th major cereal crop after wheat, rice and maize in terms of area and production in Pakistan. It covers an area of 486 thousand hectares with annual production of 299 thousand tones (Anonymous, 2016).

Non availability of high yielding varieties is the major cause of low production in pearl millet. To cope with the challenges of food security, plant breeders must give due importance for efficient utilization of available genetic resources of pearl millet to maximize the yield potential in terms of high yielding varieties. For this purpose, information pertaining to inheritance of quantitative traits is a pre-requisite for planning and execution of any successful breeding program. Genetic component analysis serves as a useful tool in identifying the genetic architecture of any trait. Several researchers like Dangaria *et al.* (2004), Chotaliya (2005), Ansodariya *et al.* (2006), Bhanderi *et.al.* (2007) and Yadav *et al.* (2012) successfully used diallel analysis to ascertain the genetic mechanism and gene action involved in the expression of different quantitative characters while working on pearl millet crop.

MATERIALS AND METHODS

Five genetically diverse pearl millet lines i.e., Parent 1(MGP-322), Parent 2(MGP328), Parent 3(MGP335), Parent 4(13RBS-01) and Parent 5(13RBS-13) were crossed in diallel fashion at Millets Research Station, Rawalpindi during kharif 2014 to generate diallel set. Five parents along with their 20 F$_1$s were sown in randomized complete block design replicated thrice during kharif 2015. Each genotype consisted of two rows of five meter keeping 75 cm row to row distance and 25 cm plant to plant distance. All the recommended practices were adopted to raise good crop of pearl millet. Data were recorded for panicle length, panicle girth, 1000-grain weight and grain yield kgha[-1] in five randomly guarded plants for each entry. The mean values were used to find out the significance level among genotypes through analysis of variance (Steel and Torrie, 1980) using computer program (Statistix 8.1). The genetic components of variation were calculated according to diallel technique suggested by Hayman (1954) and Jinks (1954) using computerized program Dial 98.

RESULTS AND DISCUSSION

Significant differences were found among the genotypes for all the characters studied except panicle girth, thus indicating the presence of sufficient genetic variability in the experimental material (Table 1).

PANICLE LENGTH

The analysis of F_1 data of panicle length (Table 2) revealed the presence of both additive and non-additive genetic effects in the control of the trait due to the significance of a and b items. Non significance of b_1 and b_2 items indicated the absence of directional dominance and asymmetrical distribution of genes among the parents, respectively. Part of dominance deviation which are not attributing to b_1 and b_2 were observed due to the significance of b_3 item. Non significance of c and d items showed the absence of maternal and reciprocal effects in the inheritance of panicle length. Perusal of Table 4 suggested that dominance genetic variances (H_1 and H_2) played important role in the expression of this character as indicated by the significance of additive genetic component. A positive F value revealed that dominant alleles were more frequent than recessive alleles (Table 4). Value of $(H_1/D)^{1/2}$ greater than unity revealed that excess of dominant alleles is present in the parents. The proportion of genes with positive and negative effects ($H_2/4H_1$) in the parents did not deviate from its expected value of 0.25, denoting symmetry at the loci showing dominance. The value of KD/kr (0.52) suggested that dominant and recessive alleles are equally present in the parents.

Over dominance was observed as the regression line of unit slope intersected the wr- axis below the point of origin (Fig.1). These results are in agreement with Mukherji *et al*. (1981) and Shanmuganathan and Goplan (2006). A perusal of array points along the regression line indicated that parent 1 being closer to the origin carried the most dominant alleles for the trait while parent 2 and 4 possessed the maximum recessive alleles being away from the origin and Parent 1 and 5 contained equal proportion of recessive and dominant alleles.

PANICLE GIRTH

The analysis of variance regarding panicle girth given in Table 1 indicated that differences among the genotypes were non-significant. Hence, Hayman analysis of variance and genetic components of variation for said character was not calculated.

1000 – GRAIN WEIGHT

The results of analysis of variance of diallel data regarding 1000- grain weight are given in table -2. Significance of item "a" and "b" suggested that both additive and non-additive gene effects are responsible in the inheritance of 1000-grain weight character. Significance of "b_1" indicated the presence of directional dominance. The results also showed that parents have symmetrical gene distribution because of significance of "b_2" item. Significance of b_3 item revealed the presence of specific dominance gene effects. The significance of "c" and "d" showed the presence of maternal and reciprocal effect in the inheritance of 1000- grain weight character which suggested the need of retesting of a and b items against the means squares of c and d items respectively. After retesting, the non-significance of a item indicated that maternal effects had masked the effects of genes acting additively. Similarly, significance of items b_1, b_2, b_3 and b which were previously significant reduced to non-significant indicated the role of reciprocal effects on the development of this trait.

Perusal of Table 4 indicated that both the additive and dominance type of genes action were controlling the inheritance of 1000- grain weight. The dominance gene effects however, seem to be more prominent due to higher magnitude of H_1 than D. The estimates of degree of dominance ratio $(H_1/D)^{1/2}$ greater than unity also suggested the over dominance type of gene action. As ($H_2/4H_1$) deviated from its expected value the genes were distributed asymmetrically at the loci showing dominance. The value of KD/kr suggested that both dominant and recessive alleles are equally present in the parents. The ratio of H_2/h_2 revealed that two groups of genes are exhibiting some degree of dominance. Graphic analysis showed the involvement of over dominance of 1000-grain weight as the regression line of the unit slope cut the Wr – axis below the origin (Fig. 2). The position of array points showed that parent 1 contained the maximum dominant genes due to its closer position to the origin while parent 5 contained most recessive alleles being farthest from the origin. Shanmuganathan and Goplalan (2006) reported non additive genetic control in 1000 grain weight whereas Santhosh (2002) reported partial dominance for 1000- grain weight.

GRAIN YIELD (KG Ha^{-1})

According to results of Hayman analysis variance for grain yield presented in Table 3, both additive and dominance gene effects were equally important for the inheritance of this trait due to the significance of item "a" and "b", respectively. 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 values of "b_3" item indicated the presence of specific gene action controlling the trait. The presence of maternal and reciprocal effects were observed due to significance of "c" and "d" items which suggested the need of retesting of a and b item against mean squares of c and d items. After retesting, the significance of a, b and b_3 item which were previously significant reduced to non-significant.

Significant value of non-additive genetic effects and non-significant value of additive component revealed that grain yield was under the influence of dominant gene effects (Table 4). The proportional value of $(H_1/D)^{1/2}$ indicated the control of over dominance gene action. Present results are in agreement with results of Lakshmana *et al.* (2011) and Bhardwaj *et al.* (2015). Deviation of $(H_2/4H_1)$ ratio from its expected value of 0.25 evidenced the asymmetrical distribution of genes as depicted in analysis of variance. The value of KD/kr indicated that both dominant and recessive alleles are equally present in the parents.

The graphical presentation (Fig. 3) depicted the regression line passed below the point of origin indicating over dominance type of gene action. The distribution of array points on the regression line showed the concentration of dominant genes in the parent 5 due to its placement closer to the origin whereas genotype 3 and 2 being farthest from the origin had maximum recessive alleles while parent 1 and 4 have both dominant and recessive alleles.

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

Source of variation	Degree of freedom	Panicle Length	panicle girth	1000-grain weight	grain yield kg/ha
Replications	2	10.36	0.58	1.31	94.45
Genotypes	24	14.72**	0.69 ns	4.28**	375.91**
Error	48	4.9	0.13	0.26	37.087

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

Table 2 .Hayman's analysis of variance for panicle length and 1000-grain weight in 5x5 diallel of Pearl millet.

Item	Panicle length						1000- grain weight				
	DF	SS	MS	F- Ratio	Retested against		SS	MS	F- Ratio	Retested against	
					c	d				c	d
a	4	127.57	31.89	6.57**	4.5		23.46	5.86	23.16	1.19	
b_1	1	7.25	7.52	1.55ns			11.17	11.17	44.14**		2.45
b_2	4	12.78	3.19	0.66ns			11.42	3.11	12.27**		0.38
b_3	5	154.49	30.90	6.36**		4.35	8.81	1.76	6.96**		0.68
b	10	174.79	17.48	3.60**			32.41	3.24	12.80**		
c	4	15.49	3.86	0.80ns			19.57	4.89	19.33**		
d	6	42.64	7.11	1.46ns			27.32	4.55	17.99**		
Total	74										

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

Table 3. Hayman's analysis of variance for grain yield kgha^{-1} in 5x5 diallel of Pearl millet.

Item	Grain yield kgha^{-1}					
	DF	SS	MS	F- Ratio	Retested against	
					c	d
a	4	2185.64	546.41	14.74**	0.98	
b_1	1	114.82	114.82	3.10ns		
b_2	4	20.04	20.04	0.54ns		
b_3	5	362.82	362.82	9.79**		0.85
b	10	200.91	200.91	5.42**		0.45
c	4	552.61	552.61	14.91**		
d	6	425.81	425.80	11.49**		
Total	74					

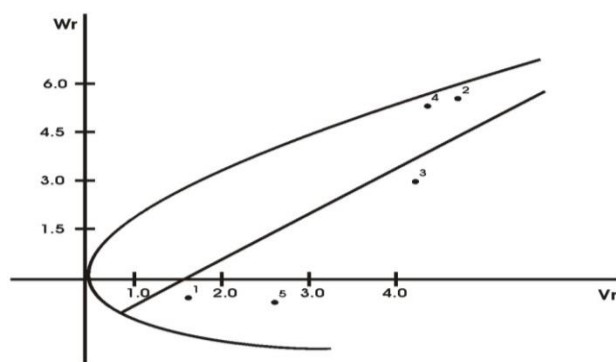*,Significant; at 5% and **, Significant 1 % level.

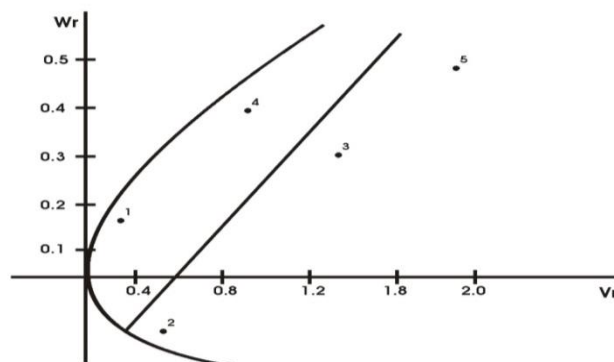Fig. 1 Wr-Vr graph for panicle length in pearl millet

Fig. 2 Wr-Vr graph for 1000-grain weight in pearl millet
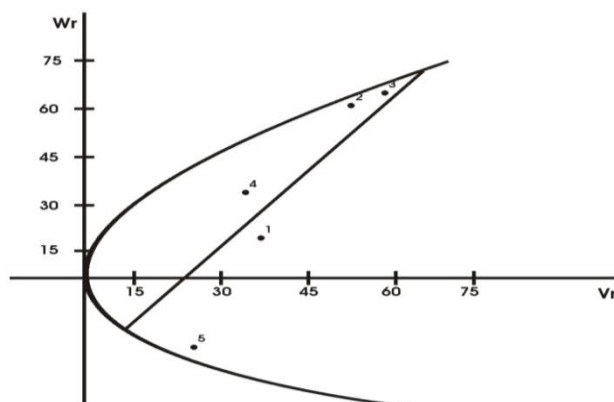

Fig. 3 Wr-Vr graph for grain yield kg/ha in pearl millet

Table 4. Estimation of genetic components of variation and proportional values for different quantitative characters in 5x5 diallel of Pearl millet.

Components	Panicle length	Panicle girth	1000-grain weight	Grain yield
D	4.48±3.34	0.17±0.09	0.049*±0.23	54.24±29.42
F	0.541±3.52	0.09±0.12	0.31±0.35	-17.08±26.09
H_1	8.08±4.88	0.48*±0.16	2.56*±0.522	105.81*±43.54
H_2	8.54±4.41	0.46*±0.14	1.99*±0.39	110.21*±40.09
h_2	0.67±2.83	-0.02±0.04	2.34*±0.73	17.38±29.49
E	1.62*±0.32	0.04*±0.01	0.08*±0.02	12.36*±2.54
$(H_1/D)^{1/2}$	1.34	1.67	2.29	1.397
$H_2/4H_1$	0.264	0.237	.195	0.260
KD/kr	0.522	0.58	0.57	0.44
h_2/H_2	0.09	-0.07	1.46	0.19

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

D: Variance due additive effects   **F:** Frequency of dominant/recessive alleles
H_1: Variance due to dominant   **H_2:** Proportion of positive and negative genes
h_2: Dominance effects   **E:** Expected environmental component of variation
$(H_1/D)^{1/2}$: Degree of dominance   **$H_2/4H$**: Proportion of genes with positive & negative effects
KD/kr: Proportion of dominant & recessive genes   **h_2/H_2:** Number of groups of genes

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(*Accepted for publication February 2018*)