

## GENETIC ANALYSIS OF DIFFERENT BIOMETRIC CHARACTERS IN PEARL MILLET

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### ABSTRACT

The present study was undertaken to ascertain the genetic analysis in pearl millet in 5x5 diallel crosses for days to flowering, plant height, number of nodes per plant, panicle length, panicle girth and grain yield. Genetic components analysis suggested that both additive and dominance model fitted for all the characters. Both additive (D) and dominance (H<sub>1</sub> and H<sub>2</sub>) components were significant for all the characters except panicle length where only dominance type of gene action is controlling the inheritance of said parameter. However, relative magnitude of dominance components (H<sub>1</sub> and H<sub>2</sub>) was greater than additive components for all the characters that revealed presence of dominant gene action. Similarly, value of (H<sub>1</sub>/D)<sup>1/2</sup> was more than unity which showed the preponderance of over dominance type of gene action. Asymmetrical distribution of positive and negative genes was evident due the value of (H<sub>2</sub>/4H<sub>1</sub>) that is less than 0.25. The ratio of dominant to recessive alleles was more than unity in days to flowering and plant height parameters indicating the excess of dominant genes. Narrow sense heritability estimates were low to high magnitude for different characters under study. The preponderance of dominant gene action in all characters indicated that heterosis breeding may be the best option for improvement in pearl millet crop.

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

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### INTRODUCTION

Pearl millet is an annual, sexual diploid having fourteen numbers of chromosomes (2n=14) belongs to Poaceae family. It is an important cereal crop of arid and semiarid regions of the world. Pearl millet has good potential to feed human and livestock due to its rich composition of minerals and protein. Breeding and management work may make more competitive with other grains; but efforts are needed to develop high yielding varieties, and a market that will encourage production. Knowledge of inheritance of quantitative characters is a prerequisite for the genetic improvement in any crop. Genetic analysis of different biometric parameters provides an estimation of additive and genetic variance to choose the most efficient breeding procedure to be followed for harnessing the yield potential in any crop. Fisher (1918) was the first to recognize the importance of biometrical techniques to study genetics of quantitative characters. Later on, Fisher (1932) partitioned total genetic variance into three parts; additive, dominance and epistasis. Different researchers like Bhardwaj *et al.* (2015), Khanum *et al.* (2018), Jeeterwal *et al.* (2018), Lakshmana *et al.* (2011), Shanmuganathan and Gopalan (2006) and Yadav *et al.* (2012) used diallel technique to study the gene action controlling different quantitative characters in pearl millet and reported non additive gene action for grain yield and its related traits. Therefore, the present study was carried out to ascertain the nature and magnitude of gene action involved in the inheritance of grain yield and its components in pearl millet under Rawalpindi agro climatic conditions.

### MATERIAL AND METHODS

Five genetically diverse pearl millet lines were crossed in all possible combinations during kharif 2015 at Millets Research Station Rawalpindi. Five parents along with their 20 F<sub>1</sub>s were sown during kharif 2016 in a Randomized Complete Block Design replicated thrice. Each entry was sown in three rows of five meter length by keeping plant to plant and row to row distances of 25cm and 75cm, respectively. The observations were recorded on five randomly selected plants from each entry and replication for the parameters like, days to flowering, plant height , number of nodes plant<sup>-1</sup>, panicle length, panicle girth and grain yield. The data were statistically analyzed following Steel and Torrie (1980). Genetic analysis was done according to the diallel techniques described by Hayman (1954) by using mean values for computation of genetic components of variation.

## RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences among genotypes for all traits (Table-I) which revealed the presence of adequate variability in these characters. The presence of significant differences between means of different traits allowed the data for diallel analysis.

Table I. Mean square values of different characters in 5x5 diallel cross experiment on pearl millet.

Source of Variation	d.f	Days to 50% flowering	Plant height (cm)	No. of nodes plant <sup>-1</sup>	Panicle length (cm)	Panicle girth (cm)	Grain yield kg ha <sup>-1</sup>
Replications	2	0.37	20.64	0.01	0.11	0.17	17.96
Genotypes	24	13.53**	708.31* *	1.45**	10.75**	1.96**	585.21**
Error	48	2.61	45.67	0.36	0.89	0.08	53.95

The estimates of genetic parameters, their ratios and narrow sense heritability for days to 50 % flowering, plant height, number of nodes per plant, panicle length, panicle girth and grain yield are presented in Table-II. The estimates of components of genetic variance exhibited that both variance due to additive effects (D) and variance due to dominance effects (H<sub>1</sub> and H<sub>2</sub>) were significant for all the characters except number of nodes plant<sup>-1</sup> and panicle length where only dominance was controlling the inheritance of these traits. It is evident from Table-II that H<sub>1</sub> component was greater than D for all the parameters under study which indicates dominant type of gene action. The estimates of dominance genes effects corrected for gene distribution (H<sub>2</sub>), were significant and therefore, agreed with H<sub>1</sub> estimated obtained.

Table 2. Estimation of components of genetic variance for different characters.

Components	Days to flowering	Plant height	No. of nodes per plant	Panicle length	Panicle girth	Grain yield
D ± S.E	5.0689 ± 0.8058 *	266.83 ± 53.57 *	-0.3 ± 0.11	0.51 ± 0.61 n.s	1.10 ± 0.39 *	171.61 ± 17.71 *
H <sub>1</sub> ± S.E	7.61 ± 2.17 *	587.66 ± 144.66 *	0.94 ± 0.29 *	5.68 ± 1.65 *	2.70 ± 1.06 *	287.30 ± 47.84 *
H <sub>2</sub> ± S.E	6.73 ± 1.97 *	454.09 ± 131.21 *	0.71 ± 0.26 *	5.25 ± 1.49 *	1.92 ± 0.96 *	272.76 ± 43.39 *
h <sub>2</sub> ± S.E	0.52 ± 1.33 n. s	92.06 ± 88.59 n.s	-0.24 ± 0.17	-0.07 ± 1.01 n.s	2.02 ± 0.65 *	595.84 ± 29.29 *
F ± S.E	2.95 ± 2.01 n.s	185.50 ± 133.80 n.s	0.16 ± 0.26 n.s	-1.08 ± 1.53 n.s	1.82 ± 0.98 *	-113.80 ± 44.25 *
(H <sub>1</sub> /D) <sup>1/2</sup>	1.23	1.48	-5.92	3.32	1.56	1.299
H <sub>2</sub> /4H <sub>1</sub>	0.22	0.19	0.18	0.23	0.18	0.24
h <sub>2</sub> /H <sub>2</sub>	0.077	0.20	0.34	-0.013	1.05	2.18
Heritability in narrow sense (h <sup>2</sup> )	0.24	0.26	0.92	0.81	0.01	1.43
KD/ KR	1.622	1.61	0.32	0.52	-0.88	0.59

Data presented in Table-II showed that value of (H<sub>1</sub>/D)<sup>1/2</sup> is greater than unity in all the characters except number of nodes plant<sup>-1</sup> which suggested the over dominance is controlling the inheritance of these characters. The ratio of H<sub>2</sub>/4H<sub>1</sub> was less than 0.25 for all the characters showing asymmetrical distribution of positive and negative alleles. The value of KD/ KR (proportion of dominant and recessive genes in the parents) suggested that dominant alleles are more frequent in days to flowering and plant height due to being positive and more than unity. While both dominant and recessive alleles are equally present in the parent due to the ratio less than unity. Low narrow sense heritability estimates were obtained for days to flowering, plant height, panicle length i.e., 0.24, 0.26 and 0.01, respectively, which indicated that it was these were much influenced by environment. Higher narrow sense heritability was obtained for panicle length, number of nodes plant<sup>-1</sup> and grain yield indicating that environment had

played minor role for the expression of these traits. The results are in agreement with the findings of Bhardwaj *et al.* (2015), Khanum *et al.* (2018), Jeeterwal *et al.* (2018), Lakshmana *et al.* (2011), Shanmuganathan and Gopalan (2006) and Yadav *et al.* (2011).

## DISCUSSION

Present studies suggested that for additive and dominance genetic parameters, breeding methods i.e., bi parental mating and reciprocal recurrent selection may also be used in addition to conventional breeding methods to select transgressive segregants in succeeding generation due to preponderance of non additive gene effects for grain yield and yield components. , traits in the parents, heterosis breeding may be practiced in pearl millet. In this way, selected parents and their crosses can serve as potential breeding material for the development of inbred lines, composite/synthetic varieties and hybrids in pearl millet crop.

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(Accepted for publication December 2018)