

Generation Mean Analysis using Six Parameters Genetic Model for Yield and Yield Contributing Traits in Pearl Millet (*Pennisetum glaucum* (L.) R. Br)

O. G. Ghume¹, K. K. Barhate² and V. Y. Pawar^{*3}

^{1,3}Department of Agricultural Botany, College of Agriculture Dhule ²ICAR-All India Coordinated Research Project on Pearl Millet, Bajra Research Scheme, (MPKV), College of Agriculture, Dhule, 424 001 (India)

^{*}Corresponding author's email : vypawar2gene@gmail.com (Received : 15.07.2025 Accepted : 22.10.2025)

Abstract

Generation mean analysis study in pearl millet was undertaken to estimate the gene effect controlling in the inheritance of yield and its components using six basic generations viz., P₁, P₂, F₁, F₂, B₁ and B₂ of four different crosses namely DHLBI 21B x DHLBI 28B; DHLBI 36B x DHLBI 28B; DHLBI 21B x ICMB 10899 and DHLBI 36B x ICMB 10899 were studied. For most of the studied traits, additive, dominance, additive x additive, additive x dominance and dominance x dominance were significant. Additive effect significantly contributed for number of effective tillers plants⁻¹, while the magnitude of dominance effect was significantly higher for all characters except number of effective tillers plant⁻¹. For grain yield plant⁻¹ and 1000 grain weight both gene effect additive and dominance are significantly higher. Duplicate type of epistasis was observed in almost all the traits except in few crosses where complementary type of epistasis present. The findings suggested that the reciprocal recurrent selection could be followed improvement of pearl millet traits to exploit all types of gene effect.

Key words : Pearl millet, gene effect, additive, dominance, epistasis, generation mean .

The species *Pennisetum glaucum* (L.) R. Br., often known as pearl millet, is a member of the genus *Cenchrus* and the subfamily *Panicoideae* of the family *Poaceae*. The word "millet" is haphazardly used to a variety of small-seeded annual grass species. In particular, it exhibits protogyny, which makes it a crosspollinated crop (allogamous). The principal pollinator wind-related (anemophily). Diploid (2n=2x=14) is the natural state of pearl millet. Pearl millet crop can able to grow under the adverse agro-climatic condition where other cereal crops like maize and sorghum fail to produce economic yields (Patel *et al.*, 2023). In India, pearl millet was first cultivated between 1500 and 1100 BC. Currently, is the most significant millet in terms of quantity, with an estimated 15–35 million tonnes (Mt) produced globally each year. With an annual production of 30.48 million tonnes and a productivity of 1243 kg ha⁻¹ over 2021–2022, it occupies an area of 32 million hectares (Anonymous 2022). In

terms of area and production, Rajasthan accounted for the largest share of Indian states with 3.74 million hectares and 3.75 million tonnes. Uttar Pradesh came in second with 0.90 million hectares and 1.95 million tonnes, Haryana with 0.48 million hectares and 1.12 million tonnes, Gujarat with 0.45 million hectares and 1.06 million tonnes and Madhya Pradesh with 0.34 million hectares and 0.87 million tonnes. Maharashtra with 5.39 lakh ha. and 5.78 lakh M. tonnes of grain productions with productivity of 1074 Kg ha⁻¹ during 2022–2023 (Anonymous 2023).

The main purpose of pearl millet breeding is to increase grain yield and its component characteristics. However, yield is a very complex character which is governed by polygene and affects many genetic and non- genetic factors, therefore, the knowledge about nature of gene action is essential to increase the efficiency of selection. Generation mean analysis Hayman

(1958) provides information on the relative importance of additive, dominance and non-allelic genetic interactions such as Additive x Additive (i), Additive x Dominance (j) and Dominance x Dominance (l) effects to determining genotypic values of the individual. This kind of study is highly helpful for quickly gaining a general understanding of the many genetic systems involved and for adjusting selection indices to quickly separate generations. However, epistasis is important in the inheritance of quantitative traits besides additive and non-additive effects.

Material and Methods

Parental Material : The parental materials used in the present studies include four genetically diverse and good combining inbred lines of pearl millet (Table 1) i.e. DHLBI 21B, DHLBI 28B, DHLBI 36B and ICMB 10899 respectively, received from Bajra Research Scheme, College of Agriculture, Dhule. The traits included in this experiment were plant height (cm), number of effective tillers per plant earhead length(cm), earhead girth(cm), grain yield per plant(g) and 1000 grain weight(g).

Development of F₁s, F₂s and Backcrosses : The above 4 parents mentioned and 4 crosses viz., DHLBI 21B X DHLBI 28B, DHLBI 36B X DHLBI 28B, DHLBI 21B X ICMB 10899 and DHLBI 36B X ICMB 10899 were received from Bajra Research Scheme, Dhule. They were grown during summer 2023 for obtaining Backcross generation, F₂'s and also made the fresh F₁ and self-seeds of parents. So set to six generation (P₁, P₂, F₁, F₂, B₁, B₂) of 4 crosses. (Table 2).

Field Evaluation : All the six generation four crosses were grown in a randomized block design with three replications contained twenty treatments (4 parents, 4 F₁'s, 4F₂'s, 4B₁'s and 4B₂'s) during *Kharif* 2023 cropping season at Bajra Research Scheme, College of Agriculture,

Dhule. One rows of each non-segregating generation (parents and F₁'s), three rows of backcrosses (B₁'s and B₂'s) and six rows each of F₂'s were entered as one treatment. The row length in each treatment was 4 meters, spaced at 50 cm. The distance between two hills in a row was 15 cm. All the treatment were randomized within the replication using the random number table (Panse and Sukhatme 1995).

Statistical Analysis : As stated by Panse and Sukhatme (1995), an ANOVA was performed on the collected data utilizing a compact family block design. The procedure recommended by Mather (1949) was followed to determine the four scaling tests (A, B, C, and D).

These various scales can be easily calculated using the following straightforward linear combination method:

$$A = 2 \bar{B}_1 - \bar{P}_1 - \bar{F}_1$$

$$B = 2 \bar{B}_2 - \bar{P}_2 - \bar{F}_1$$

$$C = 4 \bar{F}_2 - 2 \bar{F}_1 - \bar{P}_1 - \bar{P}_2$$

$$D = 2 \bar{F}_2 - \bar{B}_1 - \bar{B}_2$$

Where P₁, P₂, F₁, F₂, BCP₁, and BCP₂ are means of different generations, respectively. The variances of the quantities A, B, C, and D were calculated from respective variances of different generations as given below:

$$V(A) = 4V(\bar{B}_1) + V(\bar{P}_1) + V(\bar{F}_1)$$

$$V(B) = 4V(\bar{B}_2) + V(\bar{P}_2) + V(\bar{F}_1)$$

$$V(C) = 16V(\bar{F}_2) + 4V(\bar{F}_1) + V(\bar{P}_1) + V(\bar{P}_2)$$

$$V(D) = 4V(\bar{F}_2) + V(\bar{B}_1) + V(\bar{B}_2)$$

Where, V_A, V_B, V_C, and V_D are the variances of respective scales A, B, C, and D; VP₁, VP₂, VF₁, VF₂, VBCP₁ and VBCP₂ are the variances of P₁, P₂, F₁, F₂, BCP₁, and

BCP₂ generations, respectively. SEs for A, B, C, and D scales were calculated by estimating the square root of the respective variances. The test of deviation from the hypothetical value of zero was tested using the t-test. The calculated t-values were compared with “t” table values at 5 and 1% level of significance at their respective degrees of freedom.

After computing scaling tests, if any one of them was found significant then the genetic effects were estimated by fitting the data into six-parameter models of the generation mean

analysis, as suggested by Hayman (1958) to estimate the genetic parameters viz., mean (m), additive gene effects (d), dominance gene effects (h), and three types of nonallelic gene interactions viz., additive × additive (i), additive × dominance (j), and dominance × dominance (l).

$$m = \bar{F}_2 \quad d = \bar{B}_1 - \bar{B}_2$$

$$h = \bar{F}_1 - 4 \bar{F}_2 - \frac{1}{2} \bar{P}_1 - \frac{1}{2} P_2 + 2 \bar{B}_1 + 2 \bar{B}_2$$

$$i = 2 \bar{B}_1 + 2 \bar{B}_2 - 4 \bar{F}_2$$

Table 1. Mean performance Parents, F₁'s, F₂'s, B₁ and B₂ for 6 characters

Name of parents/hybrid	Plant height (cm)	No. of effective tillers plant ⁻¹	Ear head length (cm)	Ear head girth (cm)	Grain yield plant ⁻¹ (g)	1000 grain weight (g)
Parents						
DHLBI-21B (P1)	168.25	2.90	21.87	9.75	17.5	10.93
DHLBI-28B (P2)	144.14	1.70	18.003	9.07	21.8	12.78
DHLBI-36B (P3)	173.62	2.33	21.21	10.36	29.1	12.78
ICMB-10899 (P4)	143.71	1.00	18.58	8.60	15.2	10.45
F₁s						
C I (DHLBI 21B X DHLBI 28B)	163.78	2.60	22.14	10.73	57.60	13.17
C II (DHLBI 36B X DHLBI 28B)	187.33	2.53	21.88	11.95	55.00	12.65
C III (DHLBI 21B X ICMB 10899)	165.80	2.47	22.78	10.58	22.90	13.85
C IV (DHLBI 36B X ICMB 10899)	203.12	2.60	25.63	11.32	29.10	14.83
F₂s						
C I (DHLBI 21B X DHLBI 28B)	170.68	2.30	17.48	9.65	29.67	12.87
C II (DHLBI 36B X DHLBI 28B)	165.90	2.20	19.59	10.93	33.13	11.68
C III (DHLBI 21B X ICMB 10899)	203.46	1.64	21.93	10.42	36.88	12.43
C IV (DHLBI 36B X ICMB 10899)	200.77	1.18	20.92	10.30	31.25	11.20
B₁s						
C I × P1	199.06	1.95	23.08	10.94	56.33	14.38
C II × P1	195.51	1.53	21.83	10.77	56.25	14.45
C III × P1	180.59	0.93	22.07	10.39	51.25	14.53
C IV × P1	188.29	1.20	22.34	10.47	41.00	12.98
B₂s						
C I × P2	210.19	1.17	27.09	11.21	32.50	13.00
C II × P2	193.75	1.10	22.78	10.33	27.88	11.18
C III × P2	237.24	1.57	22.42	11.09	41.25	11.53
C IV × P2	203.60	1.35	21.91	10.95	36.05	9.65
G.M	184.94	1.81	21.78	10.49	36.08	12.57
S.E.±	3.670	0.062	0.457	0.244	3.718	0.653

$$j = 2 \bar{B}_1 - \bar{P}_1 - 2 \bar{B}_2 + \bar{P}_2$$

$$l = \bar{P}_1 + \bar{P}_2 + 2 \bar{F}_1 + 4 \bar{F}_2 - 4 \bar{B}_1 - 4 \bar{B}_2$$

Where P_1 , P_2 , F_1 , F_2 , BCP_1 , and BCP_2 are means of different generations, respectively. Furthermore, the variance component for each estimate was calculated. The significance of the genetic effect is tested using the t-test in a similar manner as in the case of the scaling test. All these statistical analyses were conducted using the DOS-based Excel program, TNAU-STAT-Statistical.

Results and Discussion

The F_1 of all the crosses recorded significantly higher mean value for all crosses in characters earhead length (cm), earhead girth (cm), grain yield plant⁻¹ (g) and 1000 grain weight (g) than both the parents' indicating dominance except in cross DHLBI 21B x DHLBI 28B of number of effective tillers. In plant height cross DHLBI 36B x DHLBI 28B and DHLBI 21B x ICMB 10899 shows dominance. Mean of F_2 was lower than their respective F_1 mean in all the crosses for characters number of effective tillers, earhead length (cm), earhead girth (cm) and 1000 grain weight (g) revealed the presence of inbreeding depression, except plant height (cm) in cross DHLBI 21B x ICMB 10899 and DHLBI 21B x DHLBI 28B, grain yield per plant (g) in crosses DHLBI 21B x ICMB 10899 and DHLBI 36B x ICMB 10899. The backcross progenies tended to resemble their recurrent female parent in most of the cases. Backcross generations mean values were also found to be either closer or higher than their respective parents or/and/in between F_1 . (Table 1).

Scaling test : All six generations mean values (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) for six distinct traits across all four crossings *viz.*, (DHLBI 21B x DHLBI 28B), (DHLBI 36B x DHLBI 28B), (DHLBI 21B x ICMB 10899) and (DHLBI 36B

x ICMB 10899) first subjected to genetic analysis. Individual scaling tests A, B, C and D of Mather (1949) used to detect the presence of inter allelic gene actions/epistasis.

On the basis of individual scaling test A, B, C and D, the additive-dominance model was found inadequate for description of variation in generation mean for all the six traits of all the four crosses, either the entire four or any three, two or one individual scaling tests (out of A, B, C and D) were found significant which indicated the presence non-allelic gene interaction thus to calculate various non-allelic gene effects, six parameter model used for estimation of genetic components in all crosses.

Gene Action : The generations mean analysis for six basic generations of the all the four cross was used to estimate the components of epistasis and also additive and dominance components. For the trait plant height, additive (d) gene action was significant for all crosses except in cross DHLBI 36B x DHLBI 28B while, dominant(h) was significant for all the crosses except DHLBI 36B x ICMB 10899 and having higher magnitude than additive (d) gene action, indicating predominant of dominance (h) gene action for plant height. For interallelic gene interaction, additive x additive [i] gene action was important for two crosses *viz.*, DHLBI 21B x DHLBI 28B and DHLBI 36B x DHLBI 28B.

The significant additive x dominance [j] gene action present for all crosses except DHLBI 36B x DHLBI 28B. Similarly, significant dominance x dominance (l) gene action was significant in all crosses except DHLBI 36B x ICMB 10899. The significant opposite sign associated with dominance [h] and dominance x dominance [ll] component in all crosses indicated the role of duplicate type of epistasis for this trait Jakhar *et al.*, (2017), Singh *et al.*, (2017), Goah *et al.*, (2020) and Rouamba *et al.*, (2022) observed all three type of gene action with duplicate epistasis.

For trait number of effective tillers per plant, additive (d) gene action was significant for two crosses viz., DHLBI 21B x DHLBI 28B and DHLBI 36B x DHLBI 28B and significant in cross DHLBI 21B x ICMB 10899 while, dominance (h) gene action is significant for two crosses viz., DHLBI 21B x DHLBI 28B and DHLBI 36B x DHLBI 28B and having lower magnitude than additive (d) gene action indicating predominant of additive (d) gene

action for this character. For inter-allelic gene interaction, additive x additive [i] gene action was important for all the crosses except cross DHLBI 36B x ICMB 10899. The significant additive x dominance [j] gene action present for all crosses except DHLBI 21B x DHLBI 28B while, significant dominance x dominance (l) gene action was significant in all crosses. The significant opposite sign associated with dominance [h] and dominance x dominance [l]

Table 2. Scaling tests for six quantitative characters

Cross	Scaling test				Interallelic gene interaction
	A	B	C	D	
Plant height (cm)					
C I (DHLBI 21B X DHLBI 28B)	66.10**	112.45**	42.76**	-67.89**	All types (i , j , l)
C II (DHLBI 36B X DHLBI 28B)	34.33**	54.92**	-25.70*	-57.47**	All types (i , j , l)
C III (DHLBI 21B X ICMB 10899)	25.26**	163.11**	166.56**	-10.91	All types (i , j , l)
C IV (DHLBI 36B X ICMB 10899)	5.20	60.37**	84.87**	9.65	All types (i , j , l)
Effective tillers plant⁻¹					
C I (DHLBI 21B X DHLBI 28B)	-1.64*	-1.37*	-0.01	1.50**	All types (i , j , l)
C II (DHLBI 36B X DHLBI 28B)	-1.82**	-1.45**	0.36	1.82**	All types (i , j , l)
C III (DHLBI 21B X ICMB 10899)	-3.54**	-0.25	-2.20**	0.79*	All types (i , j , l)
C IV (DHLBI 36B X ICMB 10899)	-2.43**	-0.74	-3.50**	-0.17	All types (i , j , l)
Earhead length (cm)					
C I (DHLBI 21B X DHLBI 28B)	2.18*	14.05**	-14.22**	-15.22**	All types (i , j , l)
C II (DHLBI 36B X DHLBI 28B)	0.56	5.68**	-4.62**	-5.43**	All types (i , j , l)
C III (DHLBI 21B X ICMB 10899)	-0.50	3.41*	1.72	-0.59	All types (i , j , l)
C IV (DHLBI 36B X ICMB 10899)	-2.16	-0.38	-7.34**	-2.40**	A x A (i), D x D (l)
Earhead girth (cm)					
C I (DHLBI 21B X DHLBI 28B)	1.29**	2.62**	-1.77**	-2.84**	All types (i , j , l)
C II (DHLBI 36B X DHLBI 28B)	-0.79	-0.36	0.36	0.76*	A x A (i)
C III (DHLBI 21B X ICMB 10899)	0.36	3.00**	2.05**	-0.65*	All types (i , j , l)
C IV (DHLBI 36B X ICMB 10899)	-0.75	1.99**	-0.39	-0.81*	All types (i , j , l)
Grain yield plant-1 (g)					
C I (DHLBI 21B X DHLBI 28B)	37.66**	-14.39**	-35.73**	-29.50**	All types (i , j , l)
C II (DHLBI 36B X DHLBI 28B)	27.56**	-61.16**	-29.35**	2.13	All types (i , j , l)
C III (DHLBI 21B X ICMB 10899)	62.00**	44.37**	68.87**	-18.75**	All types (i , j , l)
C IV (DHLBI 36B X ICMB 10899)	22.99**	27.87**	21.76**	-14.55**	All types (i , j , l)
1000 grain weight (g)					
C I (DHLBI 21B X DHLBI 28B)	4.76*	0.07	1.53	-1.65	All types (i , j , l)
C II (DHLBI 36B X DHLBI 28B)	3.57**	-3.05*	-4.03*	-2.27**	All types (i , j , l)
C III (DHLBI 21B X ICMB 10899)	4.32*	-1.24	0.69	-1.20	All types (i , j , l)
C IV (DHLBI 36B X ICMB 10899)	-1.68	-6.03**	-8.15**	-0.22	All types (i , j , l)

component in crosses DHLBI 21B x DHLBI 28B, DHLBI 36B x DHLBI 28B and DHLBI 21B x 31 ICMB 10899 indicated the role of duplicate epistasis while, similar sign in cross DHLBI 36B x ICMB 10899 indicate complementary type of epistasis. Kumar *et al.*, (2017), Patel *et al.*, (2021) and Rajpoot *et al.*, (2023) observed similar results as they all observed additive gene action. In the trait earhead length, additive (d) gene action was significant in only one cross DHLBI 21B x DHLBI 28B while, dominance(h) gene action is significant for all the crosses for earhead length and higher in magnitude than additive (d).

Gene action indicates its predominant of dominance (h) gene action. For inter-allelic gene

interaction, additive x additive [i] gene action was important for all the crosses except cross DHLBI 21B x ICMB 10899. The significant additive x dominance [j] gene action present for all crosses except DHLBI 36B x ICMB 10899 and the significant dominance x dominance (l) gene action was significant for two crosses *viz.*, DHLBI 21B x DHLBI 28B and DHLBI 36B x DHLBI 28B. The significant opposite sign associated with dominance [h] and dominance x dominance [l] component in all crosses indicated the role of duplicate type of epistasis for this trait. Godasara *et al.*, (2010) and Goah *et al.*, (2020) observed result with additive x additive (i) epistasis interaction influencing this trait for inheritance.

Table 3. Estimation of gene actions for six quantitative characters in four crosses

Character	Cross	Components						Type of epistasis
		m	d	h	i	j	l	
Plant height (cm)	C I (DHLBI 21B X DHLBI 28B)	170.68**	-11.12**	143.38**	135.79**	-23.18**	-314.35**	Duplicate
	C II (DHLBI 36B X DHLBI 28B)	165.89**	1.76	147.19**	114.95**	-10.29	-204.19**	Duplicate
	C III (DHLBI 21B X ICMB 10899)	203.46**	-56.65**	33.49*	21.81	-68.92**	-210.92**	Duplicate
	C IV (DHLBI 36B X ICMB 10899)	200.77**	-15.31**	27.84	-19.30	-27.58**	-46.26	Duplicate
Effectiv e tillers plant ⁻¹	C I (DHLBI 21B X DHLBI 28B)	2.29**	0.78**	-2.41*	-3.00**	-0.14	6.02**	Duplicate
	C II (DHLBI 36B X DHLBI 28B)	2.21**	0.46*	-2.79**	-3.63**	0.19*	6.90**	Duplicate
	C III (DHLBI 21B X ICMB 10899)	1.65**	-0.65**	-1.07	-1.59**	-1.64**	5.38**	Duplicate
	C IV (DHLBI 36B X ICMB 10899)	1.18**	-0.15	1.18	0.34	-0.84**	2.83*	Comp.
Ear head length (cm)	C I (DHLBI 21B X DHLBI 28B)	17.48**	-4.01**	32.64**	30.44**	-5.94**	-46.66**	Duplicate
	C II (DHLBI 36B X DHLBI 28B)	19.59**	-0.95	13.13**	10.86**	-2.56*	-17.10**	Duplicate
	C III (DHLBI 21B X ICMB 10899)	21.93**	-0.31	3.74*	1.18	-1.95**	-4.09	Duplicate
	C IV (DHLBI 36B X ICMB 10899)	20.92**	0.42	10.54**	4.80**	-0.89	-2.27	Duplicate
Ear head girth (cm)	C I (DHLBI 21B X DHLBI 28B)	9.65**	-0.27	6.96**	5.69**	-0.66**	-9.61**	Duplicate
	C II (DHLBI 36B X DHLBI 28B)	10.93**	0.44	0.71	-1.52*	-0.21	2.67*	Comp.
	C III (DHLBI 21B X ICMB 10899)	10.42**	-0.69**	2.65**	1.30*	-1.32**	-4.66**	Duplicate
	C IV (DHLBI 36B X ICMB 10899)	10.31**	-0.48*	3.46**	1.63*	-1.39**	-2.86*	Duplicate
Grain yield plant ⁻¹ (g)	C I (DHLBI 21B X DHLBI 28B)	29.67**	23.83**	96.83**	59.00**	26.02**	-82.28**	Duplicate
	C II (DHLBI 36B X DHLBI 28B)	33.13**	48.38**	24.89**	-4.25	44.36**	37.85**	Comp.
	C III (DHLBI 21B X ICMB 10899)	36.87**	10.00**	44.20**	37.50**	8.82**	-143.88**	Duplicate
	C IV (DHLBI 36B X ICMB 10899)	31.25**	4.95**	35.68**	29.09**	-2.44*	-79.96**	Duplicate
1000 grain weight (g)	C I (DHLBI 21B X DHLBI 28B)	12.87**	1.38	4.56*	3.30	2.35*	-8.14*	Duplicate
	C II (DHLBI 36B X DHLBI 28B)	11.68**	3.28**	4.35*	4.55**	3.31**	-5.07	Duplicate
	C III (DHLBI 21B X ICMB 10899)	12.42**	3.00**	5.56*	2.40	2.78**	-5.49	Duplicate
	C IV (DHLBI 36B X ICMB 10899)	11.20**	3.33**	3.71*	0.44	2.18**	7.27**	Comp.

Comp. = Complementary

For trait earhead girth, additive(d) gene action was significant for two crosses *viz.*, DHLBI 21B x ICMB 10899 and DHLBI 36B x ICMB 10899 while, Dominance (h) gene action is significant for all the crosses except DHLBI 36B x DHLBI 28B and higher in magnitude than the additive (d) gene action indicates that character is predominantly govern by dominance (h) gene action. For interallelic gene interaction, additive x additive [i] gene action was significant for all the crosses while, significant additive x dominance [j] gene action present for all crosses except DHLBI 36B x DHLBI 28B. Similarly, significant dominance x dominance [l] gene action was significant for all the crosses except cross DHLBI 36B x DHLBI 28B which is significant. The significant opposite sign associated with dominance [h] and dominance x dominance [l] component in all the crosses indicated the role of duplicate type of epistasis except DHLBI 36B x DHLBI 28B which is of same sign indicate complementary type epistasis. Similarly, Bhadalia *et al.*, (2012), Kumar *et al.*, (2013), Patel *et al.*, (2014) and Goah *et al.*, (2020) observed influence of additive as well as non additive gene action for this trait.

In a trait grain yield plant⁻¹, additive (d) gene action and dominance (h) gene action both are significant for all the crosses in grain yield plant⁻¹ indicating both gene action is predominant for grain yield per plant. For inter-allelic gene interaction, additive x additive [i] gene action was significant for all the crosses except DHLBI 36B x DHLBI 28B while, additive x dominance [j] gene action and dominance x dominance [l] gene action were also significant for all the crosses. The significant opposite sign associated with dominance [h] and dominance x dominance [l] component in all the crosses indicated the role of duplicate type of epistasis except DHLBI 36B x DHLBI 28B which is of same sign indicate complementary type epistasis. Suryawanshi *et al.*, (2016),

Jakhar *et al.*, (2017), Kumar *et al.*, (2017), Singh *et al.*, (2017) Goah *et al.*, (2020) and Rouamba *et al.*, (2022) observed similar results for the grain yield plant⁻¹ that presence of all three types of gene action with duplicate epistasis.

In a trait 1000 grain weight, additive (a) gene action and dominance (d) gene action both are significant for all the crosses except cross DHLBI 21B x DHLBI 28B for additive (d) gene action whereas both dominance gene action and additive gene (d) action were important for this character. For inter-allelic gene interaction, additive x additive [i] gene action was significant in only cross DHLBI 36B x DHLBI 28B while, additive x dominance [j] gene action was significant in all the crosses and dominance x dominance [l] gene action was significant in two crosses *viz.*, DHLBI 21B x DHLBI 28B and DHLBI 36B x ICMB 10899. The opposite sign associated with dominance [h] and dominance x dominance [l] component in crosses DHLBI 21B x DHLBI 28B, DHLBI 36B x DHLBI 28B and DHLBI 21B x ICMB 10899 indicated the role of duplicate epistasis while, similar sign in cross DHLBI 36B x ICMB 10899 indicate complementary type of epistasis for this character. Suryawanshi *et al.*, (2016), Jog *et al.*, (2016), Kumar *et al.*, (2017) and Rouamba *et al.*, (2022) observed influence of non-additive gene effect with presence of epistasis with duplicate epistasis.

To conclude, in the present investigation, non-allelic (epistasis) interaction played pertinent role in determination of various characters in pearl millet. In many crosses magnitude of dominance(h) was higher than additive(d) indicating presence of dominance gene action for most of the character studied, so improvement may do through heterosis breeding while, in crosses where additive gene action is predominant then simple selection should be followed. In a cross where non-

additive gene action was predominant, so there we can go for recurrent selection for SCA and reciprocal recurrent selection while, in a cross where additive gene action was significant, we can go for mass selection and recurrent selection for GCA. In many crosses where duplicate epistasis is observed, so we refuse selection whereas, in crosses which show complementary epistasis simple selection must be followed.

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