

GENERATION MEAN ANALYSIS IN PEARL MILLET
[*Pennisetum glaucum* (L.) R. Br.]

BY

PATEL HIREN SHAMALBHAI

M.Sc. (Agri.)



DEPARTMENT OF GENETICS AND PLANT BREEDING
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
SARDARKRUSHINAGAR – 385 506 [GUJARAT]

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[Registration No. 04-AGRPH-02122-2019]

PATEL HIREN S. Ph.D. (Agriculture) GENETICS AND PLANT BREEDING
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GENERATION MEAN ANALYSIS IN PEARL MILLET
[*Pennisetum glaucum* (L.) R. Br.]

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IN

GENETICS AND PLANT BREEDING

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Name of Student
PATEL HIREN S.

Major Advisor
Dr. N. B. PATEL

DEPARTMENT OF GENETICS AND PLANT BREEDING
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
SARDARKRUSHINAGAR - 385 506

ABSTRACT

The present investigation entitled “Generation mean analysis in pearl millet [*Pennisetum glaucum* (L.) R. Br.]” was carried out using material consisting of ten genetically diverse parents of pearl millet including five B lines as female (05888 B, 98222 B, 01555 B, 1202 B, 02889 B) and five R lines as male (15001 R, 16317 R, 15990 R, 15550 R and 16066 R) selected on the basis of variation in morphological characters. Total six crosses namely, cross 1 (05888 B × 15001 R), cross 2 (02889 B × 16317 R), cross 3 (01555 B × 15990 R), cross 4 (98222 B × 15550 R), cross 5 (1202 B × 16317 R) and cross 6 (05888 B × 16066 R) obtained by crossing of ten diverse parents during *kharif* 2020 and F₂ generation and backcross generations obtained during *summer* 2021 at Center for Crop Improvement (CCI), Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar, Gujarat. The experimental material consisting of six generations (P₁, P₂, F₁, F₂, BC₁ and BC₂) all the six crosses evaluated during *kharif* 2021 in compact family block design (CFBD) with three replications at Center for Crop Improvement (CCI), Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar, Gujarat.

Observations recorded for fifteen different characters subjected to generation mean analysis to assess the gene effects controlling these traits to estimate the extent of relative heterosis, heterobeltiosis, inbreeding depression, narrow sense heritability and genetic advance. The analysis of variance between generations revealed that the mean squares due to generations were significant for all the characters under study except days to maturity for cross 1 and 2, plant height for cross 5, ear head length for cross 2, ear head girth for cross 1, 5 and 6, test weight for cross 5 and 6 and oil content for all six crosses were recorded with non-significant differences indicated that sufficient diversity present among all the generations under investigation.

For grain yield per plant, cross 1 and cross 3 recorded superior *per se* performance. Cross 3 also performed well for traits viz., number of effective tillers per plant, ear head length (cm), test weight (g), harvest index (%) and days to maturity. Mean of F₁ was significantly higher than their respective parent in all crosses except for cross 2 of grain yield per plant indicated over dominance while

in cross 2 indicated partial dominant. Over dominance was observed in most of the crosses in most of the characters. Mean of F_2 was significantly higher/lower than their respective F_1 mean in all the crosses for all characters revealed the presence of inbreeding depression. Back cross generations mean values were found to be either closer or lower than parents or/and/in between F_1 mean value.

In individual scaling test, A, B, C and D, the additive-dominance model was found adequate for traits like for cross 2 of days to maturity; cross 2, 3 and 5 of number of effective tillers per plant; cross 2 and 3 of ear head length (cm); cross 5 and 6 of ear head girth (mm); cross 3 and 5 of test weight (g); cross 1 and 4 of harvest index (%) and cross 2, 3, 4 and 6 of oil content (%). While either the entire four or any three, two or one individual scaling test (out of A, B C and D) were found significant which indicated the presence of digenic interaction as well as joint scaling test was found significant in majority of traits and crosses, indicated the presence of appreciable amount of epistasis and inadequacy of additive-dominance model to calculate various non-allelic gene effects.

Grain yield per plant and most of its component characters with quality parameters, additive (d) gene effects were found to be significant in almost all crosses except for cross 6 of days to flowering, cross 2 and 6 of plant height, test weight for cross 4, harvest index for cross 1, 3 and 4, tannin content for cross 2, zinc content for cross 4, 5 and 6. Whereas additive (d) gene effects were found non significant for all crosses in number of effective tiller per plant except for cross 2, ear head length, ear head girth, days to maturity and oil content. Dominant (h) gene effects were found to be significant in all crosses of days to flowering; number of effective tiller per plant except for cross 3 and 5; test weight; tannin content; iron content; zinc content; carbohydrate except for cross 5; protein content except for cross 1 and 3; plant height except for cross 6, ear head length except for cross 4; days to maturity except for cross 6; grain yield per plant except for cross 6 harvest index for cross 1 and 6; as well as dominant (h) gene effects found to be significant in only cross 2 and 3 of ear head girth and cross 1 and 5 of oil content.

The sign of dominance (h) and dominance $\times$ dominance (l) parameter being opposite indicated involvement of duplicate type of epistasis in the inheritance of a trait. Duplicate type of gene interaction had been detected for most of the crosses where non allelic interaction was present, it could diminish the effect of dominant genes and selection would be restricted in such cases and should look for crossing different parental lines that would lead to complementary epistasis and would increase the expression of the trait under study. Whereas complementary type of epistasis was found in cross 3 and 5 of days to flowering; cross 1 of plant height and cross 4 of iron content. Chi-square value was found significant for best fit model in various crosses for many traits such as days to flowering (cross 3 and 5), plant height (cross 4), days to maturity (cross 3 and 5), grain yield per plant (cross 2 and 3), carbohydrate (cross 1 and 3), tannin content (crosses 1, 2, 3 and 5), iron content (crosses 1, 2 and 5), zinc content (crosses 2, 3 and 5) and protein content (cross 5) indicated that the digenic model was inadequate to explain inheritance of these traits indicating presence of higher order gene interaction.

For grain yield per plant, best heterotic crosses were cross 1, 4, 5 and cross 6. Cross 1 was also observed best heterosis for days to flowering, ear head length, harvest index and protein content, cross 4 was best for ear head length, harvest index, zinc content, oil content and protein content. While cross 5 for harvest index as well as cross 6 for days to maturity, plant height, carbohydrate, zinc content and oil content. Significant inbreeding depression was recorded only for crosses 1, 2 and 4 of days to flowering and for crosses 2, 3, 5 and 6 of days to maturity, for cross 4 of ear head girth, cross 1 of grain yield per plant, cross 1, 3, 4 and 5 of harvest index, cross 2 and 3 of carbohydrate, cross 2, 3 and 6 of tannin content, cross 1, 3 and 4 of iron content, cross 1, 3, 4 and 6 of zinc and cross 1 and 4 of protein content. Whereas for other traits in remaining crosses showed non-significant inbreeding depression. High to moderate heritability with high to moderate genetic advance was observed for number of effective tillers per plant (cross 3), ear head length (cross 4), ear head girth (cross 1, 3, 4 and 5), test weight (cross 1), grain yield per plant (cross 6), harvest index (cross 1 and 5) suggested presence of sufficient additive component may be rewarding for selection of such traits in future breeding programme of pearl millet improvement.

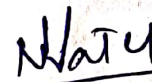
On the basis of *per se* performance, generation mean analysis, narrow sense heritability, genetic advance and inbreeding depression for different crosses showed different gene action of respective traits under study. Additive gene action and additive $\times$ additive type of gene interaction was found superior for days to flowering in all crosses except cross 2; grain yield per plant in cross 5 and 6; carbohydrate in cross 4 and 6; tannin content in cross 1, 3 and 5 and iron content in crosses 1, 3, 4 and 5. So these crosses may be used for exploitation of heterosis for yield and its contributing with quality traits as well as in future breeding programme by utilizing bi parental mating design and recurrent selection method for development of superior pearl millet lines for these characters. Whereas non additive gene action viz., dominant (h) gene action, additive $\times$ dominance (j) gene interaction and dominance $\times$ dominance (l) gene interaction was found superior for days to flowering in cross 4 and 6; plant height in cross 1 and 2; number of effective tiller per plant for cross 1; ear head length in cross 6; ear head girth for cross 2 and 3; days to maturity for cross 3, 5 and 6; test weight for cross 1, 4 and 6; grain yield per plant in cross 1 and 2; harvest index in cross 2 and 3; carbohydrate in cross 2; tannin in cross 2, 4 and 6; iron content in cross 4; zinc content in cross 2, 4 and 6; oil content in cross 1 and 5 as well as protein content in cross 4 and 6. So these crosses or parents may be used for heterosis breeding to utilize high SCA effect for development of superior pearl millet hybrids for grain yield and its contributing characters.

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CERTIFICATE – I

Date: 11/01/2023

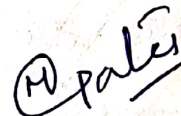
This is to certify that the thesis entitled, “**GENERATION MEAN ANALYSIS IN PEARL MILLET [*Pennisetum glaucum* (L.) R. Br.]**” submitted for the degree of **DOCTOR OF PHILOSOPHY (Agriculture)** in the subject of **GENETICS AND PLANT BREEDING** is a record of bonafide research work carried out by **PATEL HIREN SHAMALBHAI** under my guidance and supervision and that no part of this thesis has been submitted for any other degree, diploma, associateship, fellowship or other similar titles. The assistance and help received during the course of investigation have been fully acknowledged.



(N. B. PATEL)
Major Advisor



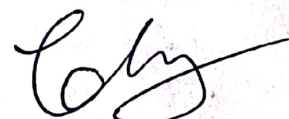
(S. D. SOLANKI)
Minor Advisor



(M. S. PATEL)
Advisor



(K. K. TIWARI)
Advisor



(G. K. CHAUDHARY)
Advisor

**SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR-385 506**

CERTIFICATE – II

Date: 11/01/2023

This is to certify that **PATEL HIREN SHAMALBHAI**,
Department of Genetics and Plant Breeding, Chimanbhai Patel College of
Agriculture, Sardarkrushinagar Dantiwada Agricultural University,
Sardarkrushinagar has made all corrections/modifications in the thesis entitled,
“**GENERATION MEAN ANALYSIS IN PEARL MILLET**
[*Pennisetum glaucum* (L.) R. Br.]” as suggested by the External Examiner and
the Advisory Committee in the oral examination held on **21st NOVEMBER, 2022.**



(S. D. SOLANKI)

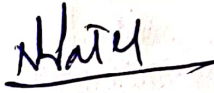
Professor and Head

Department of Genetics and Plant Breeding

C. P. College of Agriculture

S. D. Agricultural University

Sardarkrushinagar-385 506

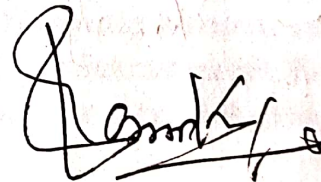

(N. B. PATEL)

**Major Advisor and Associate Professor
Department of Genetics and Plant Breeding**

C. P. College of Agriculture

S. D. Agricultural University

Sardarkrushinagar-385 506



(S. D. SOLANKI)

Principal

C. P. College of Agriculture

S. D. Agricultural University

Sardarkrushinagar-385 506

APPROVED (Seal and Date)



(C. M. MURALIDHARAN)

Director of Research and

Dean, Post-Graduate Studies

S. D. Agricultural University

Sardarkrushinagar-385 506



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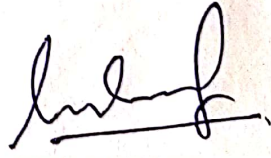
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Place : Sardarkrushinagar
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(PATEL HIREN S.)

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LIST OF ABBREVIATIONS AND SYMBOLS

%	: Per cent
/	: Per
µg	: Microgram
2n	: Somatic chromosome number
C.D.	: Critical Difference
CCI	: Center for Crop Improvement
cm	: Centimeters
d.f.	: Degrees of freedom
<i>et al.</i>	: and others
<i>etc.</i>	: Etcetera
Fig.	: Figure
g	: Grams
GAM	: Genetic Advance as per cent of Mean
GCA	: General Combining Ability
GCV	: Genotypic Coefficient of Variation
$h^2_{(ns)}$	: Heritability in narrow sense
ha	: Hectare
<i>i.e.</i>	: That is
kg	: Kilogram
m	: Meter
mg	: Milligram
ml	: Milliliter
mm	: Millimeter
N	: Normal
nm	: Nanometer
Ns	: Non-significant
°C	: Degree Celsius
P	: Probability
PCV	: Phenotypic Coefficient of Variation
ppm	: Parts per million
rpm	: Revolution per minute
S.K.NAGAR	: Sardarkrushinagar
SCA	: Specific combining ability
SDAU	: Sardarkrushinagar Dantiwada Agricultural University
sq.	: Square
<i>viz.</i>	: Namely
σ	: Sigma

I. INTRODUCTION

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is the staple food of majority of the poor and small land holders, as well as feed and fodder for livestock in rainfed regions of the country. It is world's sixth and India's fourth important cereal food crop after rice, wheat and maize. Pearl millet is a cereal crop that thrives more in the arid and semi-arid tropical regions of Asia and Africa. It is an annual tillering, cross pollinated, diploid ($2n = 2 \times = 14$) crop belong to family *poaceae*, sub-family *panicoideae*, tribe *paniceae* and genus *pennisetum* is believed to be originated to North-Western Africa.

India is the largest pearl millet growing country contributing 42 per cent of production in the world. It was grown on 7.54 million ha with an average production of 10.36 million tonnes with productivity of 1374 kg/ha (Anonymous, 2020^a). The major pearl millet growing states are Rajasthan, Maharashtra, Gujarat, Uttar Pradesh and Haryana which account for more than 90 per cent of pearl millet acreage in the country and commonly grown in rainy (*kharif*) season (June/July-September/October). It is also cultivated during summer season (February-May) in parts of Gujarat, Rajasthan and Uttar Pradesh and during the post-rainy (*rabi*) season (November-February) at a small scale in Maharashtra and Gujarat. In Gujarat, it occupies an area of 4.49 lakh hectares and production of 10.9 lakh tonnes with productivity of 2425 kg/ha (Anonymous, 2020^b). Banaskantha, Anand, Kheda, Kachchh, Mehsana, Bhavnagar and Gandhinagar are major district growing Pearl millet in Gujarat.

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] excels all other cereals due to its unique features C_4 plant with high photosynthetic efficiency, high dry matter production capacity and is grown under the most adverse agro climatic conditions where other crops like sorghum and maize fail to produce economic yields. It requires less input, matures in short duration and is considered as nutritious food, feed and fodder. It is an important coarse grain cereal and forage crop of the arid and semi-arid tropics of the Indian subcontinent and several African regions. Its grains are highly nutritious with high levels of metabolizable energy and protein, have high densities of iron and zinc. Grains are mainly used for human

consumption in the form of diverse food, mostly as leavened and unleavened flat breads and porridges. Dry stover of pearl millet is a major component of livestock ration during the dry period of year (Rai *et al.*, 2008).

Pearl millet is rightly termed as “nutricereal” as it is a good source of energy, carbohydrate, protein, fat, ash, dietary fiber, iron and zinc. It is a rich source of energy (361 Kcal/100 g) comparable to sorghum (349 Kcal/100 g), wheat (346 Kcal/100 g), rice (345 Kcal/100 g) and maize (325 Kcal/100 g). The carbohydrate content of pearl millet is 67.5 g/100 g; with 56 to 65 per cent starch comprising 20 to 22 per cent amylase and 2.6 to 2.8 per cent free sugars mainly sucrose. It is high in fiber (1.2 g/100 g) and α amylase activity. The protein content of pearl millet is (11.6/100 g), comparable to wheat, but higher than rice. It is rich in methionine, but poor in sulphur containing amino acids (Nambiar *et al.*, 2011). With low prolamine fraction, pearl millet is gluten free grain and is the only grain that retains its alkaline properties after being cooked which is ideal for people with gluten allergy. Pearl millet is rich in fat content (5 mg/100 g) with better fat digestibility and rich in unsaturated fatty acids (75 %) with higher content of nutritionally important n-3 fatty acids. It is a rich source of vitamins and minerals with overall mineral content of 2.3 mg/100 g constituting potassium, phosphorous, magnesium, iron, zinc, copper and manganese. It is rich in vitamin 'B' (thiamine, riboflavin and niacin). Along with yield improvement, focus on the nutritional improvement was also given on pearl millet. Development of micronutrient rich pearl millet hybrids and varieties with enhanced levels of Fe and Zn is taken up as priority leading to mainstreaming of bio-fortification in pearl millet and now it is a routine affair. To bring millets into the mainstream and exploiting the nutritional rich properties and promoting their cultivation, Govt. of India has declared Year 2018 as the “Year of Millets” and the year 2023 is declared as “International Year of Millets” by FAO Committee on Agriculture (COAG) Forum [Pearl millet News (2021), ICAR-AICRP on Pearl millet].

The breeding methods of pearl millet are largely those that are suitable for breeding cross pollinated crops. Its genetic improvement has been carried out through conventional breeding procedures. For developing high yielding composites, synthetics and hybrids, introduction, selection and hybridization are important methods of breeding. In relation to yield, quality traits have also important role for increasing value addition because pearl millet grain is richer

source of iron (18-87 ppm) and zinc (22-88 ppm) (Devart *et al.* 2011). Billions of people around the world suffer from “hidden hunger” or micronutrient malnutrition. Lack of iron impairs mental development and learning capacity in adults, it reduces the ability for physical labour. In the developing countries where sorghum and millets are important food crops, a large number of population suffer from chronic malnutrition. Thus, improvement in nutrient quality of pearl millet grains along with the increased yield may be helpful to alleviate malnutrition. Hence, relation of these traits with yield is to be studied for the selection of appropriate parent for hybridization.

For any crop improvement programme, the ultimate aim of plant breeder is to increase the productivity. For a particular crop, it is important to have information on the nature and magnitude of variability present in the population due to genetic and non-genetic causes. In this context, knowledge regarding genetic variability, heritability and genetic advance is quite useful for formation of a systematic breeding strategy for improvement of yield in desired direction. Yield being a complex and polygenic character which depends on a number of components, is highly influenced by the environment. Therefore, study of the association of such quantitative characters affecting the grain yield is of immense practical value to the plant breeder which helps in evolving effective selection indices. However, this does not provide information of direct and indirect effects of component characters towards dependent variable *i.e.* grain yield.

It is essential to know the mode of inheritance of different yield and quality contributing characters. Awareness of gene action helps in deciding parents for hybridization programmes and in choice of suitable breeding procedure for improvement of various quantitative characters (Singh and Narayan, 2013). Gene action of each quantitative as well as qualitative trait can be evaluated by generation mean analysis. Improvement of quantitative traits through selection depends upon the nature and magnitude of gene effects involved in inheritance of that particular trait. Several models have been developed for generation mean analysis which described by Hayman (1958) and Gamble (1962) for the estimation of genetic components of variation. In this experiment six parameter models is used to estimate all the six gene effects in the presence of epistatic interaction as indicated by scaling or joint scaling test. The formulae proposed by Hayman (1958), it includes six different parameters, m (mean value), d (additive gene

interaction), h (dominance gene interaction), i (additive x additive gene interaction), j (additive x dominance gene interaction) and l (dominance x dominance gene interaction) of P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 generations.

Nature and magnitude of heterosis is one of the important aspects for selection of the right parents for crosses and also help in identification of superior cross combinations that may produce desirable transgressive segregants in advanced generations. The estimates of heterosis and inbreeding depression together provide information about the type of gene action involved in the expression of various quantitative traits. Inbreeding means mating together of individuals which are related to each other by ancestry. It is measured as coefficient of inbreeding, which is the 'probability that two genes at any locus in individual are identical by decent'. Inbreeding depression refers to decrease in fitness and vigour due to inbreeding. Its results due to fixation of unfavourable recessive genes in F_2 generation. Heritability estimates alongwith genetic advance are normally more helpful in predicting the genetic gain under selection than heritability estimates alone.

This analysis provides a systematic approach for identification of superior parents and crosses which is the basic material on which the success of breeding programme depends. Superiority of parents depends on their ability to combine well and on the potentiality to throw transgressive sergeants for trait of interest. Further this will help to select crosses for getting superior progeny which can be useful in further breeding program.

Keeping all these facts in view, the present investigation entitled, **“Generation mean analysis in pearl millet [*Pennisetum glaucum* (L.) R. Br.]”** was undertaken with the following objectives.

Objectives of the study:

- (1) To study the adequacy of additive - dominance for inheritance of grain yield and its component traits.
- (2) To study the nature and magnitude of gene effects for grain yield and its component traits.
- (3) To estimate the extent of heterosis and inbreeding depression for grain yield and its component traits.
- (4) To estimate the extent of heritability and expected genetic advance for grain yield and its component traits.

III. MATERIAL AND METHODS

The proposed investigation on “**Generation mean analysis in pearl millet [*Pennisetum glaucum* (L.) R. Br.]**” was initiated to elicit information on magnitude of gene action, heterosis, inbreeding depression, heritability and genetic advance for seed yield and its component characters. The F₁ hybrids were made at Center for Crop Improvement (CCI), Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar, Gujarat during *kharif* 2020 and subsequently F₁ hybrids along with their both the respective parents were sown in Summer 2021 to produce seed for F₂, BC₁ and BC₂ generations. All six populations were evaluated at Center Center for Crop Improvement (CCI), Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar, Gujarat during *kharif* 2021. The material and methods used were followed are as under.

3.1 Geographical and edaphic details of Sardarkrushinagar

Sardarkrushinagar is situated at semi-arid region of North Gujarat, characterized by hot summer and cold winter. Geographically, it is situated at 24° 12' N latitude and 72° 12' E longitudes with an altitude of 154.52 meters above the mean sea level. The soil of the experimental field was sandy to sandy loam with pH of 7.5. The weather during the growing season was normal and favorable for crop growth. The weakly average meteorological data for the cropping season was presented in Appendix-I.

3.2 Experimental materials

The experimental material consists of six generations viz., P₁, P₂, F₁, F₂, BC₁ and BC₂ derived from six crosses of Pearl millet. The list of female and male parents used in crossing programme is given in Table 3.1.

3.3 Crossing programme

The experimental material consists of parents (male and female) and parents with their hybrids were crossed at Center for Crop Improvement (CCI), Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar, Gujarat during *kharif*-2020 and *summer*-2021, respectively. During crossing programme, panicle emerging out of the flag leaf in respect of both seed and pollen parents, were covered with butter paper bags and stapled tightly to avoid

contamination of foreign pollens. With the full emergence of stigmas but before shedding its own pollen, the female panicles were pollinated by pollens collected from the respective male parents. Immediately after pollination, the seed parent panicles were covered by paper bags and labelled properly. Simultaneously the parents were selfed to obtain genetically pure seed. F₂ seed was obtained by selfing F₁'s either by covering two panicles of the synchronous tillers of the same hybrid plant to obtain sufficient seeds of F₂. A backcross population (BC₁ and BC₂) was obtained by crossing of F₁ with their respective parents P₁ and P₂. At maturity crossed/selfed panicles were harvested separately and dried. List of crosses/material used for present experiment mentioned in Table 3.2.

Table 3.1: Pedigree and their source of females and males of pearl millet used in experiment

Sr. No.	Genotypes	Pedigree	Source
1	05888 B	(SRC II C3 S1-1-1-2 × HHVBC)-5-1-1-2	All genotypes procured from Centre for Crop Improvement (CCI), Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar, Gujarat
2	15001 R	MC 94 C2-S1-3-1-3-3-2-2-B	
3	98222 B	-	
4	01555 B	(BSECBPT/91-40 × SPF3/S91-529)-12-1-1-3	
5	16317 R	((EERC-HS-23)-12-3-1-B × {(MC 94 S1-34-1- × HHVBC)-16-2-1 × (IP 19626-4-2-3)}-B-28-3-1-2-2} × {JBV 3 S1-197-2-4-1}-B-3-P1-3-3-B-B)-13-1-1	
6	15990 R	(ICMS 7704-S1-127-5-1 × RCB-2 Tall)-B-19-3-2-1-5-B-1	
7	15550 R	(ICMR312S1-8-1-1-1-1-B-B-B-1-B × (20216-20249))-22-1-2-3-2-B-B	
8	1202 B	[(ICMB 04888 × ICMB 00444)-9-1-1-4 × [(ICMB 04888 × ICMB 02333)-Bulk]-13-2-1	
9	16066 R	(JBV 3 S1-197-1-1-1 × IPC 655(B))-B-14-3	
10	02889 B	{HHVDBC HS-10-1-2-1-1-4 × [ICMB 99555 × {78-7088/3/SER3 AD/B282/(3/4)EB × PBLN/S95-359}-19-5-B-B]-13-2-B-B-B}-23-4-4-5-1	

3.4 Experimental design

The six generations viz., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of the six crosses were raised in compact family block design (CFBD) with three replications during late *kharif* 2020. Each replication was divided in to six compact blocks, each consists of single cross and blocks were consisted of six plots of six basic generation of each cross.

Table 3.2: List of crosses/material used for present experiment

Sr. No.	Cross designation	P_1	P_2	F_1	F_2	BC_1	BC_2
1	05888 B $\times$ 15001 R	05888 B	15001 R	$P_1 \times P_2$	$F_1 \otimes$	$F_1 \times P_1$	$F_1 \times P_2$
2	02889 B $\times$ 16317 R	02889 B	16317 R	$P_1 \times P_2$	$F_1 \otimes$	$F_1 \times P_1$	$F_1 \times P_2$
3	01555 B $\times$ 15990 R	01555 B	15990 R	$P_1 \times P_2$	$F_1 \otimes$	$F_1 \times P_1$	$F_1 \times P_2$
4	98222 B $\times$ 15550 R	98222 B	15550 R	$P_1 \times P_2$	$F_1 \otimes$	$F_1 \times P_1$	$F_1 \times P_2$
5	1202 B $\times$ 16317 R	1202 B	16317 R	$P_1 \times P_2$	$F_1 \otimes$	$F_1 \times P_1$	$F_1 \times P_2$
6	05888 B $\times$ 16066 R	05888 B	16066 R	$P_1 \times P_2$	$F_1 \otimes$	$F_1 \times P_1$	$F_1 \times P_2$

$\otimes$ indicate selfing.

The crosses were assigned to each block and six generations of a cross were relegated to individual plot within the block. Each block was comprised of eleven rows consisting single row each of P_1 , P_2 and F_1 ; four rows of F_2 and two rows each of BC_1 and BC_2 generations. Each hybrid and parents represented single rows of four meter length spaced at 45 cm between rows and 10 cm between plants. Fertilizers were applied at the rate of 100 kg N_2 /ha, 50 kg P_2O_5 /ha and 50 kg K_2O /ha. Application of N_2 was split into two equal installments *i.e.*, basal and top dressing. All recommended agronomic practices in vogue along with necessary plant protection measures were timely adopted for successful raising and harvesting of the good crop.

3.5 Characters studied

The observation were recorded on randomly selected ten plants in respect of non-segregating generation (P_1 , P_2 and F_1); twenty plants from backcrosses (BC_1 and BC_2) and forty plants from F_2 generation at different growth stages of the crop leaving the border plants on both ends of the row in each replication. Plants were selected at random from each plot. The method used for data collection of individual character is described below.

3.5.1 Days to flowering

Number of days from date of sowing to date of emergence of ear heads in randomly selected plants was recorded in each generation and replication on plant basis.

3.5.2 Plant height (cm)

The plant height was measured in randomly selected plants from base of plant to tip of ear head of main shoot of selected plants at the time of maturity in each generation and replication.

3.5.3 Number of effective tiller per plant

Ear heads bearing tillers per plant of randomly selected plants in each generation and replication were counted and recorded.

3.5.4 Earhead length (cm)

Length of earhead was measured from base to tip of ear head of main tiller of randomly selected plants at maturity stage in each generation and replication.

3.5.5 Earhead girth (mm)

Maximum girth of earhead in middle part of main tiller of randomly selected plants in each generation and replication were recorded.

3.5.6 Days to maturity

Number of days from date of sowing to date of physiological maturity in randomly selected plants was recorded in each generation and replication on plant basis.

3.5.7 Test weight (g)

Weight of 1000 grains of each randomly selected plant was recorded in each generation and replication.

3.5.8 Grain yield per plant (g)

Grain yield of selected plants was weighed and calculated on each randomly selected plant in each generation and replication.

3.5.9 Harvest Index (%)

The grain yield (economical yield) and biological yield (grain yield + dry fodder yield) were recorded and harvest index was worked out by following formula.

$$\text{Harvest Index (\%)} = \frac{\text{Grain yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

3.5.10 Carbohydrate (g/100 g)

The carbohydrate content from harvested seeds was estimated by the method of Hedge *et al.* (1962) for randomly selected plant in each generation of each cross in each replication.

Reagents used:

(1) Anthrone reagent: Dissolved 2g of anthrone in 1 litre of concentrated ice cold H_2SO_4 . Used freshly prepared reagent for the assay.

(2) Glucose stock solution: 200 μg glucose per ml of distilled water

Sample Preparation:

Hundred mg powdered material of pearl millet seeds weighed and hydrolyzed by keeping it in boiling water bath for 3 hours with 5 ml 2.5 N HCl and cooled at room temperature. After cooling, its neutralized using sodium carbonate until effervescence ceases and filtered followed by making final volume to 100 ml. centrifuged at 6000 rpm for 10 min. Supernatant was collected and 10 ml volume was made up using distilled water.

Carbohydrate content estimation:

0.1 ml extracted sample taken in 10 ml glass tube and 1 volume made up using distil water. Further 4 ml anthrone reagent added and mixed well. Mixture was heated at boiling temperature for 8 min in water bath and rapidly cooled then. The developed green to dark color's spectrometry observation recorded at 630 nm. Carbohydrate content in sample was calculated using following equation:

$$\text{Carbohydrate content (g/100 g)} = \frac{\text{Graph factor}}{\text{Aliquote sample}} \times \frac{\text{Total volume of extract}}{\text{Weight of sample}} \times 100$$

3.5.11 Tannin (mg/100 g)

The tannin content was estimated as described by Thimmaiah (2016) with some modification from seeds for selected plants in each generation of each cross in each replication.

Reagents used:

(1) Folin-Denis reagent: 750 ml of water, 100 g of sodium tungstate ($\text{Na}_2\text{WO}_4 \cdot 2\text{H}_2\text{O}$), 20 g of phosphomolybdic acid and 50 ml of 85% phosphoric acid (H_3PO_4) was dissolved. The mixture was refluxed for 2 hr., cooled to 25°C and diluted to 1000 ml with water.

(2) Saturated sodium carbonate solution: 100 ml of water, 35 g of anhydrous sodium carbonate was added, dissolved at 70-80 °C and cooled overnight.

(3) 100 mg of tannic acid was dissolved in 1 liter of water. Fresh solution was prepared for each determination (1 ml = 0.1 mg of tannic acid).

Sample preparation:

Two hundred mg powdered material of pearl millet seeds added in 7.5 ml distil water heated gently for 30 min. Then centrifuged at 6000 rpm for 10 min. Supernatant collected and 10 ml volume made up using distil water.

Tannin content estimation:

One ml extracted sample taken in 10 ml glass tube. 0.5 ml Folin-Denis reagent added and shaken well then 0.5 ml 35 % sodium carbonate added and shaken well. Final 10 ml volume made up using distil water. After 30 min reading was taken using visible light spectrophotometer at 700 nm. Tannin content in sample was calculated using following equation:

$$\text{Tannin content (mg/100g)} = \frac{\text{Graph factor}}{\text{Aliquote sample}} \times \frac{\text{Total volume of extract}}{\text{Weight of sample}} \times 100$$

3.5.12 Iron content (mg/kg)

Iron content of the seeds from randomly selected plants in each generation of each cross in each replication was determined by atomic absorption spectrophotometrically as per suggested by Elwell and Gidley (1967). A sample of 1 gram of fine powdered pearl millet grains was taken and 10 ml of nitric acid was added to it and mixture was kept for a night. Than 10 ml of diacid mixture of nitric acid and perchloric acid (3:1) added. Then the mixture was digested by heating it on hot plate, till it looks apparent (approximately 1 to 1.5 hour). After that the apparent mixture was filtered with the help of filter paper and volume made up to 100 ml by adding distilled water into it. Then the developed 100 ml volume mixture was subjected to spectrophotometer and the readings were noted for iron content.

3.5.13 Zinc content (mg/kg)

Zinc content of the seeds from randomly selected plants in each generation of each cross in each replication was determined by atomic absorption spectrophotometrically as per suggested by Elwell and Gidley (1967). A sample of 1 gram of fine powdered pearl millet grains was taken and 10 ml of nitric acid was added to it and mixture was kept for a night. Than 10 ml of diacid mixture of nitric acid and perchloric acid (3:1) added. Then the mixture was digested by heating it on hot plate, till it looks apparent (approximately 1 to 1.5 hour). After that the apparent mixture was filtered with the help of filter paper and volume made up to 100 ml by

adding distilled water into it. Then the developed 100 ml volume mixture was subjected to spectrophotometer and the readings were noted for zinc content.

3.5.14 Oil content (%)

Oil content of the sample was determined by Soxhlet as per AOAC (1971). FOSS Soxtec™ 8000 automatic extraction system used for oil estimation. 10 gram of dried fine powder of pearl millet seeds placed in the thimble. Thimble than loaded in soxhlet extractor unit. The initial weight of empty coups (blank) was recorded. Then extraction coups were loaded in extraction unit and poured with 90 ml petroleum ether (60-80 °C). Programme consisting three steps viz. boiling, extraction and recovery started. The final weight of coup taken and fat/oil percentage was calculated using below formula:

$$\text{Oil content (\%)} = \frac{\text{Weight of empty coups (Blank)} - \text{Final weight of coups}}{\text{Weight of sample}} \times 100$$

3.5.15 Protein content (%)

The protein content was estimated in percentage by using NIR spectroscopy technique. NIR spectroscopy instrument manufactured by Dicky John Company USA and measured the protein content of different samples.

3.6 Statistical analysis

The replication wise mean values of different generations for each individual character were subjected to statistical analysis according to compact family block design (Panse and Sukhatme, 1985). The computer facility available at the Department of Agricultural Statistics, Chimanbhai Patel College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar was utilized for statistical analysis. The following procedures for statistical analysis were followed.

3.6.1 Analysis of variance for experimental design

3.6.2 Estimation of gene effects using generation mean analysis

3.6.3 Estimation of heterosis and Inbreeding depression

3.6.4 Estimation of heritability

3.6.5 Estimation of expected genetic advance under selection

3.6.1 Analysis of variance for experimental design

The analysis of variance (Table 3.2) was performed to test the significance of difference among the genotypes for all the characters following fixed effect model as suggested by Panse and Sukhatme (1985).

$$Y_{ijk} = \mu + r_i + F_j + \delta_{ij} + P_{k(i)} + \epsilon_{ijk}$$

Where,

Y_{ijk} = Phenotypic value of the k^{th} progeny of j^{th} family in the i^{th} replication.

r_i = Effect of the i^{th} replication,

F_j = Effect of the j^{th} family

δ_{ij} = Uncontrolled variation associated with j^{th} family in i^{th} replication

$p_{k(i)}$ = Effect of k^{th} progeny of i^{th} replication

ϵ_{ijk} = Uncontrolled variation due to k^{th} generation of j^{th} family in the i^{th} replication.

The analysis was carried out in two stages by taking crosses as families and different generations as progenies as there is no meaning to go for pooled analysis which includes progenies of all the families at a time.

Table 3.3: Analysis of variance for family comparisons

Sources	d.f.	M.S.	E.M.S.
Replications	(r-1)	Mr	$\sigma_e^2 + f \sigma_r^2$
Families	(f-1)	Mf	$\sigma_e^2 + r \sigma_f^2$
Error	(r-1)(f-1)	Me	σ_e^2
Total:	(rf-1)	-	-

Table 3.4: Analysis of variance for generations within family

Sources	d.f.	M.S.	E.M.S.
Replications	(r-1)	Mr	$\sigma_e^2 + g \sigma_r^2$
Generations	(g-1)	Mg	$\sigma_e^2 + r \sigma_g^2$
Error	(r-1)(g-1)	Me	σ_e^2
Total:	(rg-1)	-	-

Where,

r = Number of replication

f = Number of families

g = N of progenies within each family

σ_p^2 = Progeny variance within family

σ_r^2 = Replication variance

σ_e^2 = Error variance

σ_f^2 = Family variance

Before making comparison, a test of homogeneity of error variance for progenies was carried out for each character by applying Bartlett's test of homogeneity as described by Panse and Sukhatme (1985).

From the above table, the following statistics were compute

- (1) Standard error of mean (S.E.m. $\pm$) = $\sqrt{M_6/r}$
- (2) Critical difference (C.D.) = S.E.m. $\times \sqrt{2} \times t(0.05)$ at error of degree of freedom
- (3) Coefficient of variance (C.V.) % = $\frac{\sqrt{M_6}}{\bar{X}} \times 100$

Where,

M_6 = Error mean squares for progenies,

$\bar{X}$ = Mean over progenies within family

3.6.2 Estimation of gene effects using generation mean analysis

The standard statistical procedures were used to calculate means and variances of each generation for each character (Singh and Chaudhary, 2004).

$$\text{Mean } (\bar{X}) = \frac{\sum x_i}{N}$$

Variance for each generation was calculated separately to get variance of that generation. For example, variance of P_1 in replication was calculated as,

$$\text{Variance of } P_1 = \frac{1}{N-1} \left[\sum x_i^2 - \frac{(\sum x_i)^2}{N} \right]$$

$$\text{Variance of mean } (V_{\bar{P}_1}) = \frac{(V_{P_1})}{N}$$

$$\text{Standard error } (S.E._{\bar{P}_1}) = \sqrt{V_{\bar{P}_1}}$$

Where,

N = Total number of observations

The crosses which showed significant differences among various generations for each of the character under study were subjected to generation mean analysis for the estimation of gene effects using six parameter model as suggested by Hayman (1958) and Jinks and Jones (1958).

3.6.2.1 Scaling test

The scaling tests as described by Hayman and Mather (1955) were used to check the adequacy of the additive-dominance model for different characters in

each cross. The adequacy of scale must satisfy two conditions viz. additivity of gene effects and independence of heritable component from non-heritable ones.

The test of first condition provides information regarding the absence or presence of gene interaction. If one of four scaling tests found significant indicates presence of epistatic and inadequacy of additive-dominance model. The A, B, C and D tests were made using the equations for their values and variances.

$$A = 2 \overline{BC_1} - \overline{P_1} - \overline{F_1}$$

$$B = 2 \overline{BC_2} - \overline{P_2} - \overline{F_1}$$

$$C = 4 \overline{F_2} - 2 \overline{F_1} - \overline{P_1} - \overline{P_2}$$

$$D = 2 \overline{F_2} - \overline{BC_1} - \overline{BC_2}$$

Where,

$\overline{P_1}, \overline{P_2}, \overline{F_1}, \overline{F_2}, \overline{BC_1}$ and $\overline{BC_2}$ are the mean value of P_1, P_2, F_1, F_2, BC_1 , and BC_2 generations, respectively.

The variances and standard errors of scaling test were calculated as under.

$$V_A = 4V_{\overline{BC_1}} + V_{\overline{F_1}} + V_{\overline{P_1}} \quad \text{S.E.}_{(A)} = \sqrt{V_A}$$

$$V_B = 4V_{\overline{BC_2}} + V_{\overline{F_1}} + V_{\overline{P_2}} \quad \text{S.E.}_{(B)} = \sqrt{V_B}$$

$$V_C = 16V_{\overline{F_2}} + 4V_{\overline{F_1}} + V_{\overline{P_1}} + V_{\overline{P_2}} \quad \text{S.E.}_{(C)} = \sqrt{V_C}$$

$$V_D = 4V_{\overline{F_2}} + V_{\overline{BC_1}} + V_{\overline{BC_2}} \quad \text{S.E.}_{(D)} = \sqrt{V_D}$$

Where,

$V_{\overline{P_1}}, V_{\overline{P_2}}, V_{\overline{F_1}}, V_{\overline{F_2}}, V_{\overline{BC_1}}$ and $V_{\overline{BC_2}}$ are the variance of mean of the P_1, P_2, F_1, F_2, BC_1 and BC_2 generations, respectively.

The testing of individual scaling test was carried out by usual t-test. The degree of freedom for 't' test was equal to the sum of degree of freedom for all type of generations involved in a particular scaling test and the degree of freedom of a particular generation was the total number of observations of that generation minus one.

To test the significance of the scales, 't' values were calculated as under.

$$t(A) = A/S.E. (A)$$

$$t(B) = B/S.E. (B)$$

$$t(C) = C/S.E. (C)$$

$$t(D) = D/S.E. (D)$$

The calculated 't' values were compared with the table 't' values at 5% and 1% levels of significance. The significance of any of these scales is taken to indicate the inadequacy of simple additive-dominance model and presence of non-allelic interaction.

- (i) The significance of A and B scale provides evidence of presence of i (additive $\times$ additive) j (additive $\times$ dominance) and l (dominance $\times$ dominance) type of non-allelic gene interactions.
- (ii) The significance of only C scale suggests evidence of l (dominance $\times$ dominance) type of non-allelic gene interactions.
- (iii) The significance of only D scale reveals a test for presence of i (additive $\times$ additive) type of inter allelic interaction.
- (iv) The significance of both C and D scales indicates the presence of i (additive $\times$ additive) and l (dominance $\times$ dominance) type of non-allelic gene interactions.

3.6.2.2 Joint Scaling Test

The Joint Scaling Test (additive-dominance model or non-epistatic model) outlined by Cavalli (1952) was also applied to confirm the adequacy of additive-dominance model to fit the three-parameters model, which consists of estimation of m, (d) and (h) parameters using weighted least square method, followed by a comparison of observed means with expected means. The comparison between observed and expected generation means were made by Chi-square (χ^2) test assuming that the sum of squares minimized in the fitting process distributed as χ^2 . The degree of freedom (d.f.) equals to number of generations minus the number of parameters estimated.

The procedure of weighted least square estimates of the three parameters model may be illustrated as follows:

Expectation of matrix for generation means (Cavalli, 1952).

Generation Coefficients of parameters

$$Y = \begin{pmatrix} P_1 \\ P_2 \\ F_1 \\ F_2 \\ B_1 \\ B_2 \end{pmatrix} \quad X = \begin{pmatrix} m & d & h \\ 1 & 1 & 0 \\ 1 & -1 & 0 \\ 10 & 1 & 1 \\ 1 & 0 & \frac{1}{2} \\ 1 & \frac{1}{2} & \frac{1}{2} \\ 1 & \frac{1}{2} & \frac{1}{2} \end{pmatrix} \quad M = \begin{pmatrix} m \\ (d) \\ (h) \end{pmatrix}$$

The equations can be expressed in a simple form $Y = X.M$

Where,

Y = The vector of observed generation mean

X = The matrix of coefficient of the parameters

M = The vector of parameters m , (d) and (h)

As six generation available in the present study, six equations were calculated for estimating the parameters m , (d) and (h) . These were obtained by equating the observed generation mean to their expectation given in Table 3.5 for three parameters and six parameters.

3.6.2.3 Estimation of components of mean

The weighted least squares procedure as originally given by Cavalli (1952) and described by Mather and Jinks (1971) was followed to estimate the parameters of generation means. As six generations available in the present study, six equations were calculated for estimating the parameters m , (d) and (h) . These were obtained by equating the observed generation means to their exceptions given in Table 3.6.2 for three parameters and six parameters.

Table 3.5: Expectation of generation means for additive-dominance and digenic interaction model

Generation mean	Additive-dominance model			Digenic interaction model					
	M	(d)	(h)	M	(d)	(h)	(i)	(j)	(l)
P₁	1	1	0	1	1	0	1	0	0
P₂	1	-1	0	1	-1	0	1	0	0
F₁	1	0	1	1	0	1	0	0	1
F₂	1	0	0.5	1	0	0.5	0	0	0.25
BC₁	1	0.5	0.5	1	0.5	0.5	0.25	0.25	0.25
BC₂	1	-0.5	0.5	1	-0.5	0.5	0.25	-0.25	0.25

m = mean

(d) = additive effect

(h) = dominance effect

(i) = additive × additive effect

(j) = additive × dominance effect

(l) = dominance × dominance effect

These six equations were weighted with appropriate weights (reciprocal of variance of means) to obtain three normal equations to calculate three parameters. The three simultaneous equations were then solved by way of matrix inversion following general approach proposed by Cavalli (1952). This procedure was adopted for all model-fitting components.

$$M = J^{-1} \times S$$

Where,

M = Column vector of the estimates of parameters

S = Matrix of sector (right hand size)

J = Information matrix

J⁻¹ = Inverse of information matrix (variance covariance matrix)

The expected mean for different generations were then calculated from the inverse matrix. The test of goodness of fit was done by calculating chi-square (χ^2) using following formulae:

$$\chi^2_{(n-p)d.f.} = \sum_{i=1}^n (O_i - E_i)^2 W_i$$

Where,

O_i = observed mean of ith generationE_i = expected mean of ith generationW_i = weight of ith generation

n = number of generation means available

p = number of parameters estimated

The standard error of each parameter (P_i) was calculated as,

$$S.E. (P_i) = \sqrt{C_{ii}}$$

Where,

C_{ii} is the i^{th} diagonal elements of inverse matrix, J^{-1}

When three-parameters or non-epistatic model was inadequate; than unweighted six-parameter model was fitted, which includes digenic interaction effects. The goodness of fit of three parameters model could be tested by Chi-square test as only three parameters have been estimated; whereas goodness of fit of six-parameter model could not be tested by Chi-Square test since all the six generations were used for estimation of various parameters.

3.6.2.4 Estimation of various gene effects

In presence of non-allelic interactions as indicated by scaling test, the various gene effects were estimated using six parameter models as described by Hayman (1958). Additive-dominance model (three parameters) was found inadequate to calculate various non allelic gene effects therefore six parameter model was used.

Gene effects	Method of estimation
Mean (m)	$= \overline{F_2}$
Additive (d)	$= \overline{BC_1} - \overline{BC_2}$
Dominance (h)	$= 2\overline{BC_1} + 2\overline{BC_2} - 4\overline{F_2} + \overline{F_1} - \frac{1}{2}\overline{P_1} - \frac{1}{2}\overline{P_2}$
Additive $\times$ additive (i)	$= 2\overline{BC_1} + 2\overline{BC_2} - 4\overline{F_2}$
Additive $\times$ dominance (j)	$= 2\overline{BC_1} - \overline{P_1} - 2\overline{BC_2} - \overline{P_2}$
Dominance $\times$ dominance (l)	$= \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{BC_1} - 4\overline{BC_2}$

Where,

$\overline{P_1}, \overline{P_2}, \overline{F_1}, \overline{F_2}, \overline{BC_1}$ and $\overline{BC_2}$ are the means of P_1, P_2, F_1, F_2, BC_1 and BC_2

generations, respectively.

The variances and standard errors of each estimate were computed as follow,

$$V_m = V_{\overline{F_2}}$$

$$V(d) = V_{\overline{BC_1}} + V_{\overline{BC_2}}$$

$$V(h) = 4V_{\overline{BC_1}} + 4V_{\overline{BC_2}} + 16V_{\overline{F_2}} + V_{\overline{F_1}} + \frac{1}{4}V_{\overline{P_1}} + \frac{1}{4}V_{\overline{P_2}}$$

$$V(i) = 4V_{\overline{BC_1}} + 4V_{\overline{BC_2}} + 16V_{\overline{F_2}}$$

$$V(j) = 4V_{\overline{BC_1}} + V_{\overline{P_1}} + 4V_{\overline{BC_2}} + V_{\overline{P_2}}$$

$$V(l) = V_{\overline{P_1}} + V_{\overline{P_2}} + 4V_{\overline{F_1}} + 16V_{\overline{F_2}} + 16V_{\overline{BC_1}} + 16V_{\overline{BC_2}}$$

Where,

$V_{\overline{P_1}}$, $V_{\overline{P_2}}$, $V_{\overline{F_1}}$, $V_{\overline{F_2}}$, $V_{\overline{BC_1}}$ and $V_{\overline{BC_2}}$ are the variances of the means of P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 generations, respectively.

$$\begin{array}{llll} \text{S.E. of } m & = & \sqrt{V_m} & \text{S.E. of (i)} & = & \sqrt{V_i} \\ \text{S.E. of (d)} & = & \sqrt{V_d} & \text{S.E. of (j)} & = & \sqrt{V_j} \\ \text{S.E. of (h)} & = & \sqrt{V_h} & \text{S.E. of (l)} & = & \sqrt{V_l} \end{array}$$

The test of significance of each parameter was done by usual 't' test.

$$\begin{array}{llll} t \text{ for } m & = & \frac{m}{\text{S.E. of } m} & t \text{ for (i)} & = & \frac{(i)}{\text{S.E. of (i)}} \\ t \text{ for (d)} & = & \frac{(d)}{\text{S.E. of (d)}} & t \text{ for (j)} & = & \frac{(j)}{\text{S.E. of (j)}} \\ t \text{ for (h)} & = & \frac{(h)}{\text{S.E. of (h)}} & t \text{ for (l)} & = & \frac{(l)}{\text{S.E. of (l)}} \end{array}$$

Significance of gene effects were tested by comparing the calculated values of 't' with table values of 't' at corresponding degree of freedom at 5 per cent (1.960) and 1 per cent (2.576) levels of significance.

The test of significance of each parameter was done by usual t-test. When any one of the parameters of digenic interaction found non-significant, the analysis was done as per best possible estimates by omitting that interaction parameter(s) according to Cavalli's (1952) least square method.

3.6.3 Estimation of heterosis and Inbreeding depression

3.6.3.1 Magnitude of heterosis

Heterosis expressed as per cent increase or decrease of F_1 hybrid over its mid-parent (relative heterosis) (Turner, 1952) and better or superior parent (heterobeltiosis) (Fonseca and Patterson, 1968) were computed as follow:

$$\begin{array}{ll} 1) \text{ Relative heterosis (\%)} & = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100 \\ 2) \text{ Heterobeltiosis (\%)} & = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100 \end{array}$$

Where,

$$\begin{array}{ll} \overline{F_1} & = \text{Mean performance of } F_1 \text{ hybrid} \\ \overline{MP} & = \text{Mean value of parents } [(P_1 + P_2) / 2] \text{ of a hybrid} \\ \overline{BP} & = \text{Mean performance of better parent of respective cross} \end{array}$$

The standard error and calculated 't' values for mid parent heterosis and heterobeltiosis was computed as below,

$$\text{S.E. (M.P.)} = (3 \text{ Me} / 2 \text{ r})^{0.5}$$

$$\text{S.E. (B.P.)} = (2 \text{ Me} / \text{r})^{0.5}$$

Where,

Me = Error mean square

r = Number of replications

The test of significance for heterobeltiosis was done by usual 't' test.

$$t_{(RH)} = \frac{\overline{F_1} - \overline{MP}}{\text{S.E. } \overline{MP}} \quad \text{for relative heterosis}$$

$$t_{(HB)} = \frac{\overline{F_1} - \overline{BP}}{\text{S.E. } \overline{BP}} \quad \text{for heterobeltiosis}$$

The test of significance of the relative heterosis and heterobeltiosis were carried out by comparing the calculated values of 't' with the tabulated values 't' at 5 per cent (1.960) and 1 per cent (2.576) levels of significance.

3.6.3.2 Inbreeding depression

The inbreeding depression (ID) in F_2 generation was calculated as per method described by Warner (1952) using the following formula,

$$\text{Inbreeding depression (\%)} = \frac{\overline{F_1} - \overline{F_2}}{\overline{F_1}} \times 100$$

Where,

$\overline{F_1}$ = Mean of F_1 generation

$\overline{F_2}$ = Mean of F_2 generation

Standard error and 't' value for test of significance for inbreeding depression were estimated as under:

$$\text{S.E. for inbreeding depression} = \sqrt{V_{\overline{F_1}} + V_{\overline{F_2}}}$$

$$t_{\overline{F_1} - \overline{F_2}} = \frac{\overline{F_1} - \overline{F_2}}{\text{S.E.}(\overline{F_1} - \overline{F_2})}$$

Where,

$\overline{F_1}$ = Mean value of the F_1 hybrid

$\overline{F_2}$ = Mean value of the F_2 generation

$V_{\overline{F_1}}$ = Variance of the F_1 generation

$V_{\overline{F_2}}$ = Variance of the F_2 generation

The significance of the inbreeding depression was tested by comparing the calculated 't' value with the table 't' value at 5 per cent (1.960) and 1 per cent (2.576) levels of significance.

3.6.4 Estimation of heritability

Heritability in narrow sense (h^2_{ns})

The narrow sense heritability, as suggested by Warner (1952) was calculated as follows:

$$h^2_{(ns)}(\%) = \frac{[2VF_2 - (VBC_1 + VBC_2)]}{VF_2} \times 100$$

Where,

$h^2_{(ns)}$ = Heritability in narrow sense

VF_2 = Variance of F_2 generation

VBC_1 = Variance of BC_1 generation

VBC_2 = Variance of BC_2 generation

The heritability percentage was categorized by Robinson *et al.* (1949) as given below.

0-30% = Low

30-60% = Moderate

60% and above = High

3.6.5 Estimation of expected genetic advance under selection

The expected genetic advance at 5 per cent level of selection intensity was estimated by using the formula suggested by Johnson *et al.* (1955).

$$\text{Expected genetic advance} = K \cdot h^2_{(ns)} \cdot \hat{\sigma}_P$$

Where,

$h^2_{(ns)}$ = Heritability in narrow sense

$\hat{\sigma}_P$ = Phenotypic standard deviation

K = Selection differential (K = 2.06 at 5 % selection pressure)

Genetic Advance as percent of Mean (GAM)

Expected genetic advance as per cent of mean (expected genetic gain) was estimated by the formula suggested by Johnson *et al.* (1955).

$$\text{Expected genetic advance as \% of mean} = \frac{\text{Genetic advance}}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = Mean of the character under experiment

The genetic advance as per cent mean was categorized as suggested by Johnson *et al.* (1955).

0-10 % = Low

10-20 % = Moderate

> 20 % = High

II. REVIEW OF LITERATURE

The knowledge of the genetic systems controlling the expression of characters will help plant breeders to choose the best breeding and selection procedures. The ultimate goal of any plant breeding programme is to improve genotypes which are better than the existing ones in producing the economic yield. In case of pearl millet, both continuous and discontinuous variations are observed in the economically important characters. Exploiting the genetic variation of these traits through hybridization and selection is primary focus of most of the pearl millet breeders in crop improvement programmes. Proper choice of parents for crop improvement programmes requires the knowledge of gene action and heritability estimates for the planning of effective and efficient breeding programme.

Several studies have been conducted on gene action, heterosis, inbreeding depression, heritability and genetic advance for grain yield and its attributing characters with reference to pearl millet. The available literature and information pertaining to present investigation “**Generation mean analysis in pearl millet [*Pennisetum glaucum* (L.) R. Br.]**” has been briefly reviewed and presented in the following subheadings.

2.1 Gene action

2.2 Heterosis

2.3 Inbreeding depression

2.4 Heritability and Genetic advance

2.1 Gene action

The phenotypic expression of a quantitative trait is affected by three different types of gene actions viz., additive, dominance and epistasis. The additive component and additive $\times$ additive (i) interaction represents the portion of variability that is fixable.

All the crop improvement programmes require a basic understanding of the types of gene action governing the inheritance of quantitative traits of economic importance. Diallel and line $\times$ tester analysis, although effective and widely used but does not provide estimates of non-allelic interactions. Significant epistatic variation clearly indicates the role of epistatic gene action besides additive and

dominance types, which play a major role in the expression of heterotic potential (Jinks, 1955; Hayman, 1958 and Gamble, 1962).

Mather (1949) divided generation means in two components *i.e.*, additive (D), dominant (H). He also provided scaling test for the indication of presence of epistasis familiar as A, B, C, D scaling test.

Cavalli (1952) proposed a joint scaling test for estimating three parameters, *viz.*, m , d and h using weighted least square technique. This also provide test for model for more than three families simultaneously. Epistasis component of genetic variance also partitioned in three components (1) additive $\times$ additive (i), (2) additive $\times$ dominance (j) and (3) dominance $\times$ dominance (l) by several workers (Kempthorne, 1956; Hayman, 1958 and Cockerham, 1961).

Jinks and Jones (1958) proposed three parameter model to estimate genetic components using six generations in the absence of epistasis. While Hayman (1958) described six parameter model using six generations which provide the information of additive, dominant and epistasis components of genetic variance.

Information regarding the various types of gene action and their relative importance in the inheritance of economically important trait in pearl millet is summarized here.

Murty *et al.* (1967) used a group of 184 randomly chosen elite inbreds of pearl millet belonging to advanced generations of diverse crosses as male parents in crosses with two male sterile lines and examined for the magnitude and nature of heterosis and their gca effects including the male sterile lines. Non-additive gene action was present in all the three characters, *i. e.*, tiller number, ear length and ear girth, while substantial additive gene action was also present for ear length. The inbred and hybrid analyses showed partial dominance for tiller number and ear girth, and overdominance for ear length, in the crosses with Tift. 23A. In the hybrids with Tift. 18A, partial dominance for tiller number and ear length but slight over dominance for ear girth was observed. Substantial heterosis in the hybrids for ear length in both the backgrounds of Tift. 23A and Tift. 18A was also observed.

Lal and Singh (1968) evaluated six generations *viz.*, P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 from the crosses of two S_7 lines, *viz.*, 200 and 424 of pearl millet. They observed complete dominance for plant height, number of internodes, number of branches, number of spike bearing branches, days to flower, long and broad leaves, thick peduncles, long spikes and bold grains. Partial dominance of better parent was

observed for stem thickness. No dominance or nearly complete additive effect of the genes was observed in the expression of number of tillers, number of spike bearing tillers, peduncle length and spike thickness.

Mahadevappa (1968) studied complete diallel cross of ten pearl millet inbred parents which was used to estimate of gca and sca for grain yield and eight other related characters viz., length and diameter of peduncle, surface area of primary ear, density of grain, yield of primary ear, plant height, tillering capacity and yield of straw. Length and diameter of peduncle, density of grain, plant height and yield of straw was not much under the influence of additive gene action. However, for yield of primary ear, tillering capacity and yield of grain might additive genes may account for the significant gca, as seen in many parents with respect to each of the above characters.

Singh *et al.* (1974) studied line $\times$ tester analysis of combining ability involving five male-sterile lines from different sources and 10 inbred of pearl millet developed at CCSHAU, Hisar, India. Additive $\times$ additive and additive $\times$ dominance types of gene interaction were found to predominate in the material under study for days to flowering, plant height, total tiller, ear per plant, earhead length, 1000 seed weight and grain yield per plant.

Sagar (1990) studied plant height in six crosses of pearl millet using six generations at two stages of crop growth, seedling to panicle initiation and anthesis, in four environments representing various levels of moisture stress during summer (March-June) season. The analysis of F_2 and the back crosses indicated the prevalence of non-allelic interactions. Additive dominance model was inadequate in 27 of the 36 cases. Both additive and dominance effects were important with preponderance of the latter. The presence of epistasis, observed from the analysis of generation means, was concluded and confirmed by the existence of digenic interactions. Duplicate epistasis played a major role in character expression.

Wilson *et al.* (1990) collected over 300 landraces of pearl millet were collected in Burkina Faso and grown at the Coastal Plain Experiment Station in Tifton/GA. At Tifton, these landraces were predominantly tall and late-maturing. The inbred Tilt 85DB was used as a donor of genes for the dwarf and early characteristics, and was crossed to nine randomly selected landraces from Burkina Faso. The parents, F_1 , F_2 , and backcrosses to each parent were grown in the field and evaluated for plant height at anthesis and time in days from planting to anthesis. In general, plant

height of F_1 s was taller than the tallest parent, and in all crosses the maturity of F_1 s was intermediate between the parents. Joint scaling tests revealed that additive genetic effects were highly significant for both traits, but dominance and epistatic-genetic effects contributed to the inheritance of each trait in some crosses. The low gene numbers, high heritability estimates, and preponderance of additive-genetic effects suggested that selection for these traits should be effective.

Joshi and Desale (1996) carried out generation mean analysis to obtain information on gene action for seven quantitative characters in pearl millet (*Pennisetum glaucum* L.) and evaluated the four parents, six F_1 s, six F_2 s and twelve backcross progenies from six crosses. The results indicated a predominance of dominance component for the other characters. Non-allelic interaction effects were predominant for plant height, 1000-grain weight and grain yield per plant.

Singh *et al.* (1999) studied the nature and magnitude of gene effects of quantitative traits in pearl millet (*Pennisetum glaucum* L.) using six generations of three crosses *viz.*, W-504 $\times$ PPMI-318, W-504 $\times$ PPMI-618 and W-504 $\times$ PPMI-619. The three parameter model was satisfactory to detect the genetic difference in crosses, W-504 $\times$ PPMI-318 and W-504 $\times$ PPMI-618 for diameter of the spike and in cross W-504 $\times$ PPMI-618 for number of effective tillers per plant. For all other quantitative traits in all three crosses, the presence of digenic interaction played an important role for governing these traits.

Vinita *et al.* (1999) studied genetic analysis of data of six basic generations of each of the three crosses of pearl millet (*Pennisetum glaucum* L.) involving one grey (D-763) and two white grained parents (W-367-2 and W-123) was used to elucidated the inheritance of grain density, grain weight and protein content. Additive gene effects was significant for protein content in one of the crosses, while additive gene effects as well as non-additive gene effects were indicated for grain weight and protein content in all the three crosses except for protein content in one cross.

Singh *et al.* (2000) studied six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) of three crosses *i.e.* PPMI 318 $\times$ PPMI 618, PPMI 318 $\times$ PPMI 619 and PPMI 618 $\times$ PPMI 619 for estimation of gene action in pearl millet. The least square estimates of the parameters of m , (d) , (h) , (i) , (j) and (l) revealed inadequacy of additive dominance model for diameter of the ear head for cross PPMI 318 $\times$ PPMI

618 inter allelic interactions. They observed duplicate epistatic interaction was observed for all the traits.

Rasal and Patil (2003) studied combining ability of five male sterile lines of pearl millet in crosses with eight diverse genotypes in Line $\times$ Tester fashion. The involvement of additive gene action was observed for leaves/main shoot and grains/sq. cm. area of main ear. The non-additive gene action was observed for flag leaf area, 1000 grain weight, fodder yield and harvest index.

Ansodariya (2004) carried out heterosis study in pearl millet F_1 hybrids derived from 10×10 diallel and reported predominant role of additive gene action for plant height, earhead length, earhead girth, 1000-seed weight; non-additive gene action for dry fodder as well as grain yield per plant, while both were equally important for days to flowering, days to maturity and effective tillers per plant.

Dangaria *et al.* (2004) carried out line $\times$ tester analysis involving nine male sterile lines and nine pollinators of pearl millet. They reported the predominant role of non-additive genetic variance for days to 50 % flowering, days to maturity, plant height, earhead length, earhead girth, 1000-grain weight, dry fodder yield and grain yield per plant and that of additive genetic variance for effective tillers per plant.

Sagar and Yadav (2004) studied five single crosses of pearl millet using six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) for estimation of gene effects under rainfed conditions. The invariably superior performance of F_2 and both backcrosses over F_1 and parents, respectively, suggested the role of non-additive interactions.

Shanmunganatham and Gopalan (2006) studied fifty-five single cross hybrids derived from 11×11 diallel cross without reciprocals. The 11 genotypes involved in the crosses were: IP 20381, PY 5665, GP 15071, PT 5600, PT 5651, IP 20334, PT 5136, IP 19125, IP 20389, GP 16239 and IP 20350. Both additive and dominance components were significant, with the predominance of dominance effects for most of the grain and stover yields and yield characters viz., days to 50% flowering, plant height, tiller number per plant, productive tiller number per plant, leaf number per plant and 1000-grain weight.

Bhandari *et al.* (2007) studied combining ability 8×8 diallel set, excluding reciprocals, for grain yield and its 12 attributes in pearl millet. The predictability ratio of gca and sca revealed preponderance of additive genetic variance for plant height, ear head length, ear head girth and 1000 grain weight, whereas, non-additive genetic variance for days to 50 per cent flowering, days to maturity, number of

effective tillers per plant, fodder yield per plant, harvest index and grain yield per plant, while, both were equally important for number of nodes, ear head weight and threshing index.

Kumhar and Singhania (2007) studied combining ability variances and effects of eight male sterile lines, nine diverse restorers and their 144 crosses in line $\times$ tester design in pearl millet for grain yield and component characters. Hybrid combinations ICMA 92444A₁ $\times$ IPC 655, ICMA 92333A₁ $\times$ IPC 655, 81A₄ $\times$ IPC 1518, 81A₁ $\times$ IPC 821, ICMA 92333A₁ $\times$ CZI/E 88, ICMA 92333A₄ $\times$ IPC 655, ICMA 98111A₄ $\times$ IPC 1518 and ICMA 92444A₁ $\times$ CZI/E 88 showed high sca effects for grain yield per plant. A₁ cytoplasmic male sterility system was found comparatively better except earliness but both the sources have produced better hybrids for grain yield and component characters.

Vaghasiya *et al.* (2008) studied combining ability in a line $\times$ tester fashion using 12 newly developed B-lines as females and seven broad based restorer lines as males for final selection of superior B-lines before embarking for their conversion into male sterile version 'A' lines in pearl millet. Both GCA and SCA variances were significant for all the characters. Female (B-lines) parents B₁₂, B₁₁, B₁₀ and B₈ and male parents R₁ and R₂ were identified as the best general combiners for grain yield and some important yield components.

Chotaliya *et al.* (2010) studied combining ability in a 10 $\times$ 10 diallel set, excluding reciprocals, for yield and 11 yield components in pearl millet. The study revealed the importance of non-additive gene action in the inheritance of traits viz., grain yield per plant, fodder yield per plant, 1000 grain weight and harvest index; while, additive gene action was preponderant for plant height, ear head length, ear head girth and ear head weight. Both additive and non-additive gene actions were found in days to 50 per cent flowering, days to maturity, number of effective tillers per plant and number of nodes. The parents like D-23, J-2480 and J-2467 could be used in hybridization programme to exploit their GCA effects for grain yield and some important yield attributing traits.

Godasara *et al.* (2010) studied four pearl millet crosses (ICMB 95222 $\times$ J 2372, ICMB 95444 $\times$ J 2340, ICMB 94555 $\times$ J 2290 and JSMB- 101 $\times$ J 2405) comprised of six basic generations, viz., P₁, P₂, F₁, F₂, BC₁ and BC₂. The individual and joint scaling tests indicated the presence of epistasis for all the characters studied, except for number of productive tillers per plant and fodder yield per plant. The nature and

magnitude of gene effects indicated, that the nature and magnitude of gene action varied from cross to cross. Their results also indicated the role of either higher order gene interaction or tight linkage for the expression of grain yield per plant, 1000 grain weight and days to maturity.

Velu *et al.* (2011) studied ten inbred lines and their full diallel crosses to analyze the nature of gene action and heterosis for these micronutrients in pearl millet. Highly significant positive correlation between mid-parent values and hybrid performance, and no correlation between mid-parent values and mid-parent heterosis confirmed again the predominant role of additive gene action for iron and zinc content.

Bhadalia *et al.* (2012) studied the nature of gene action for grain yield and eleven component traits in pearl millet using 8×8 diallel fashions. The preponderance of non-additive gene action was observed in the inheritance of days to flowering, days to maturity and 1000-grain weight. Whereas, the importance of both additive and non-additive gene action were noticed for grain yield per plant, ear head length, ear head weight, plant height, number of grains per square cm, dry fodder yield per plant length, ear head weight and harvest index. However, the magnitude of dominant gene action (H_1) was greater than their corresponding additive gene effects (D) for all the traits.

Rai *et al.* (2012) investigated factors that can enhance breeding efficiency showed large variability for and high levels of both Fe and Zn content in breeding lines and populations (>80 ppm Fe and >60 ppm Zn). variance due to general combining ability (σ^2_{gca}) as the more predominant component and predictability ratio closer to unity, implying a larger role of additive gene action in controlling both micronutrients.

Yadav *et al.* (2012) studied combining ability for maturity traits in pearl millet. Ten parents selected through a field screening technique for their different response to supra-optimal temperature tolerance were crossed in a diallel manner. Forty-five F_1 hybrids along with their 10 parents were tested for their performance under supra-optimal temperature exposure at seedling stage with an objective to understand the nature of gene action and to identify parents for breeding programme. Variances due to general combining ability and specific combining ability for all the characters studied, viz., Seedling Thermo-tolerance Index (STI), Seed to Seedling Thermo-tolerance Index (SSTI), panicle emergence, effective

tillers, plant height, ear length, ear weight, dry fodder yield, grain yield per plant and total biological yield per plant were highly significant in all the three environments (two stress and one normal) and on pooled basis indicating the importance of both additive and non-additive gene actions. Preponderance of non-additive (dominance component) was recorded for all the characters suggested the success of hybrid breeding by making use of the expected heterosis.

Kumar *et al.* (2013) carried out experiment to identify good general combiners and good specific cross combinations in pearl millet. They observed ear weight, grain yield and harvest index was largely controlled by additive gene action. On the other hand, for days to 50 per cent flowering, total tillers, effective tillers, biological yield and protein content where there was predominance of non-additive gene action, recurrent selection for specific combining ability would be quite effective. For plant height, ear length, ear girth and dry fodder yield both additive and non-additive gene effects were important.

Patel *et al.* (2014) Studied inheritance of grain yield and component characters in pearl millet using ten restorer lines and their 45 F_1 s developed through half diallel mating design. The analysis of variance for combining ability revealed that mean squares due to parents and F_1 s were significant for all characters studied except number of effective tillers per plant, thereby suggesting the importance of both additive and non additive gene effects. However, potence ratio and predictability ratio depicted preponderance of non-additive gene effect for all the characters except number of effective tillers per plant, average ear head length, average ear head and girth. Among the parents, AIB-34 was only good general combiner for grain yield per plant. While, in case of hybrids, AIB-9 $\times$ AIB-34 and AIB-9 $\times$ AIB-29 were good specific combiners for grain yield per plant, number of effective tillers per plant and average ear head weight.

Jog *et al.* (2016) analyzed the nature and magnitude of gene action in six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) for grain yield and its attributing characters in four crosses of pearl millet. On the basis of individual scaling test A, B and C and joint scaling test, the additive-dominance model was found to be adequate for description of variation in generation means for number of nodes per plant, number of effective tillers per plant, grain yield per plant and biological yield per plant in all the four crosses, days to flowering in ICMB-04999 $\times$ J-2454; days to maturity and ear head length in crosses ICMB-20071 $\times$ J-2480 and ICMB-04999 $\times$

J-2454; while, test weight in crosses ICMB-20071 $\times$ J-2500 and ICMB20071 $\times$ J-2480. They found all the three or any one or any two interaction parameters significant for most of the traits in most of the crosses indicating interaction parameters also played important role in the inheritance of these characters. Their results indicated that grain yield per plant and its component characters were mostly governed by additive and non-additive gene effects but the magnitude of dominance effect was higher for almost all the characters. Duplicate type of epistasis played a greater role than complementary epistasis was observed for most of cases.

Nandaniya *et al.* (2016^a) conducted an experiment with five male sterile lines (female parents) and nine testers (male parents) of pearl millet in line $\times$ tester fashion. The predictability ratio of gca and sca revealed preponderance of non-additive genetic variance for all the characters under studied.

Suryawanshi *et al.* (2016) carried out genetic analysis of six basic generations of each of the four crosses of pearl millet (*Pennisetum glaucum* L.) involving ten characters viz., days to 50% flowering, days to maturity, plant height, number of effective tillers per plant, ear head length, ear head girth, number of grain per cm², 1000 grain weight, grain yield per plant and fodder yield per plant. They found the nature and magnitude of gene action varied from cross to cross. Hence, they handled each cross separately for specific character. Their results also indicated the role of either higher order gene interaction or tight linkage for the expression of grain yield per plant and yield contributing characters. They found additive, dominance and their interactions to play important role in the inheritance of various economic characters.

Jakhar *et al.* (2017) undertook the study with the help of six generations P₁, P₂, F₁, F₂, B₁, and B₂ in three crosses, viz, 863B $\times$ P 7-7 (1), 843B $\times$ P 7-4 (2), and 81B $\times$ ICMP 451 (3) of pearl millet. Simple additive-dominance model failed to explain the genetic variation of most of the characters. They found that all type of digenic interactions were prevalent, the dominance $\times$ dominance gene effects with duplicate epistasis were pronounced. They suggested that cyclic breeding particularly reciprocal recurrent selections should be practiced to improve yield and its attribute traits in Pearl millet rather than going only for simple selections methods.

Kumar *et al.* (2017^a) studied 3 crosses of pearl millet viz., R-16419 $\times$ R-15114, R-15134 $\times$ R-15762, and R-15762 $\times$ ASRT-111 consisting families (P₁, P₂, F₁, F₂, BC₁ and BC₂) of Joint scaling test suggested that nodes per plant and days to

physiological maturity were adequate for 3 parameter model. Six parameter models revealed that both additives (d) as well as additive $\times$ additive (i) type of gene effects were significant for seed setting in cross 'R-15134 $\times$ R-15762'. Duplicate type of epistasis was found for plant height, grain yield per plant in all three crosses of pearl millet, flag leaf length, 1000 seed weight in cross 'R16419 $\times$ R-15114', tillers per plant, panicle length, seed setting, middle leaf temperature, harvest index in cross R-16419 $\times$ R-15114 and tillers per plant, panicle length, flag leaf length, middle leaf temperature, 1000 seed weight in cross of R-15762 $\times$ ASRT-111. Significant role of epistasis revealed that both additive as well non-additive effects involved in the expression of yield and its attributes.

Singh *et al.* (2017^a) conducted experiment based on six generations from three crosses viz., 863B $\times$ P 7-7, 843B $\times$ P 7-4 and 81B $\times$ ICMP 451 of pearl millet. There was all type of digenic interactions was prevalent, the dominance $\times$ dominance gene effects with duplicate epistasis was pronounced. They suggested that cyclic breeding particularly reciprocal recurrent selections should be practiced to improve yield and its attribute traits in pearl millet rather than going only for simple selections methods.

Goah *et al.* (2020) used generation mean analysis to study epistasis and estimate gene effects for grain iron and zinc contents along with the agronomic and morphological traits in pearl millet. Six generations P₁, P₂, F₁, F₂, BC₁ and BC₂ were generated and were evaluated during the 2018-19 off season. Analysis of variance showed significant variability for all the traits in both generations. Six parameter model revealed predominance of additive gene effects for inheritance of grain iron concentration, and additive $\times$ additive type of non-allelic interactions. For grain zinc concentration additive gene effects were preponderant compared to non-additive gene effects, and only additive $\times$ dominance gene effects were significant among the three types of epistasis. Grain weight per plant was predominantly under non-additive gene effects and additive $\times$ additive and additive $\times$ dominance gene effects type of epistasis. Likewise, for flowering non-additive gene effects were most important with the presence of dominance $\times$ dominance type of epistasis. For plant height, panicle circumference and length, additive $\times$ additive genes effects were the most important among the three type of non-allelic gene action.

Patel *et al.* (2021) crossed four cytoplasmic male sterile lines with nine restorers to develop 36 hybrids using line $\times$ tester design to study combining ability in pearl

millet for twelve different characters and evaluated at Main Pearl millet Research Station, JAU, Jamnagar in *kharif* 2018. Their estimates of σ^2_{sca} were greater than the corresponding σ^2_{gca} for ear head girth, ear head weight, 1000-grain weight, dry fodder yield per plant, grain yield per plant and harvest index, indicated the preponderance of non-additive gene effects. While for rest of the characters, the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ was found greater than unity, suggested the preponderance of additive gene effects for the express of these traits.

2.2 Heterosis

Heterosis the term as defined by Shull (1914) refers to the increased vigour, growth, yield or function of a hybrid progeny over the parents that result from crossing genetically diverse individuals. The terms relative heterosis and heterobeltiosis refer to the heterosis over mid and superior parental value, respectively (Fonseca and Patterson, 1968). Burton (1951) was the first to report heterosis in pearl millet.

Murty *et al.* (1967) used a group of 184 randomly chosen elite inbreds of pearl millet belonging to advanced generations of diverse crosses as male parents in crosses with two male sterile lines and examined for the magnitude and nature of heterosis. Out of the 93 inbreds crossed with Tift. 23A, there was an increase of 6.7 per cent for tiller number and 10.2 per cent for ear length in the hybrids as compared to the inbreds. There was a decrease of 4.8 per cent in ear head girth. The overall analysis, on the other hand, has revealed a reduction of 7.1 per cent in the tiller number and an increase of 36.9 per cent for ear length and 1.6 per cent for ear girth.

Lal and Singh (1968) studied heterosis by obtaining hybrid from two S_7 lines, viz., 200 and 424 of pearl millet. They observed highly significant increase or heterosis for plant height, number of internodes, number of branches, number of spike bearing branches, days to flower.

Rai *et al.* (1985) studied the effects of one generation of selfing on grain yield, plant height, head length, 1000 seed weight and days to flowering in the base populations as well as in three successive full sib recurrent selection cycle bulks of the medium maturity composite and serere composite-I of pearl millet [*Pennisetum americanum* (L.) Leeke]. Their results showed that average inbreeding depressions in both the composites were highest for grain yield (25 % and 36 %) followed by 1000 seed weight (12% and 14%). Plant height, days to flowering and ear head

length were least affected by selfing, with the average inbreeding depressions for these characters ranging from 4 % to 7 %. They concluded that there were no indications that the extent of inbreeding depressions in the advanced cycle bulks and were less than those in the base populations or initial cycle bulks which might have resulted, in part due to the relatively large number of progenies (24-46) recombined in each cycle of recurrent selection.

Sagar (1990) studied plant height in six crosses of pearl millet using six generations at two stages of crop growth, *i.e.* seedling to panicle initiation and anthesis. The F_1 of all the crosses exhibited heterosis over better parent.

Presterl and Weltzien (2003) used six populations developed by ICRISAT to study heterosis in pearl millet for population breeding in arid environments. They observed that the elite populations generally showed higher grain yield than the landraces; stover yield (SY) was similar in both population types. The landraces flowered earlier, had a higher tillering potential, and smaller seeds. Mean level of mid-parent heterosis was generally low, ranging from 0.85 % for time to flowering (TF) to 6.57 % for stover yield. For grain yield, expression of heterosis for individual population crosses was between -14 % and 30 % under drought stress, and between -9 % and 17 % in the favorable environments. For stover yield, mean heterosis was always positive and higher than for grain yield.

Pethani *et al.* (2004) conducted experiment in line $\times$ tester fashion using eight male sterile lines and eight restorer lines on yield and some component traits in pearl millet. Their results revealed that estimates of heterosis over mid parent and better parent for various traits indicated high heterotic effects for grain yield and ear head weight. The hybrid MS 2072 $\times$ J 2338 expressed the highest heterotic values for grain yield over mid parent (152.92 %) and better parent (121.45 %).

Yadav (2006) evaluated 12 crosses between selected landraces and elite composites along with 7 parental populations for two years in arid zone environments in pearl millet. Crosses produced almost as high biomass as landraces but their better partitioning resulted into highest grain yield in them. Manifestation of heterosis in crosses varied for different characters. Grain yield was the most heterotic trait with mean heterosis of 17 % and other traits *viz.*, days to flowering, plant height, panicle length and harvest index were far less heterotic with mean heterosis ranging between 2-4 %.

Davda *et al.* (2008) carried out study to estimate the nature and magnitude of heterosis for grain yield and its attributing traits through line $\times$ tester fashion involving 8 CMS lines and 10 pollinators in pearl millet. The magnitude of heterosis varied from cross to cross for all the characters studied. The high level of heterosis was observed for grain yield per plant, fodder yield per plant, ear heads weight per plant, ear head length and number of effective tillers per plant, while moderate heterosis was found for 1000 seed weight and harvest index. Ear head girth exhibited the least heterosis. Maximum positive heterosis for grain yield per plant over better parent and standard check (GHB-558) was observed to be 262.15 and 41.05 per cent, respectively. They suggested that the cause of heterosis in grain yield might be due to its component traits, mainly, ear head weight, number of effective tillers per plant, harvest index and 1000 seed weight.

Vetriventhan *et al.* (2008) conducted an experiment comprised of five male sterile lines and 30 inbred testers of pearl millet and their 150 hybrids of pearl millet for studying the extent of hybrid vigour in F_1 for grain yield and its components. Highest and significant negative relative heterosis, heterobeltiosis and standard heterosis was observed in the cross ICMA 94111A $\times$ PT 5259 and the same combination showed negative relative heterosis, heterobeltiosis and standard heterosis for the trait plant height. The cross combination ICMA 94111A $\times$ PT 5423 showed higher magnitude of positive relative heterosis and heterobeltiosis for the trait total number of tillers. Highest and significant positive standard heterosis was recorded in ICMA 88004A $\times$ PT 5164 for total number of tillers. The cross combination ICMA 94111A $\times$ PT 5423 showed highest and significant relative heterosis, heterobeltiosis and standard heterosis for total productive tillers. The hybrid ICMA 88004A $\times$ PT 5181 recorded highest and significant positive standard heterosis for ear head length and 100 grain weight, ICMA 88004A $\times$ PT 5200 for ear head girth. 13 hybrids recorded highly significant standard heterosis for grain yield per plant. Among 150 hybrids studied, seven hybrids namely ICMA 88004 A $\times$ PT 5164, ICMA 88004 A $\times$ PT 5200, ICMA 88004 A $\times$ PT 5232, ICMA 88004 A $\times$ PT 5130, ICMA 88004 A $\times$ PT 5173, ICMA 732 A $\times$ PT 5172 and ICMA 88004 A $\times$ PT 5809 were selected as best crosses since they expressed high standard heterosis over standard hybrid (MBH 163) for many of the traits studied.

Vagadiya *et al.* (2010) crossed four cytoplasmic genic male sterile lines with 12 diverse pollinators in line $\times$ tester design to study the nature and magnitude of

heterosis for grain yield and its seven component traits in pearl millet. The high magnitude of heterosis was observed for grain yield per plant, fodder yield per plant and ear heads weight per plant; medium level of heterosis was exhibited for days to 50 % flowering, days to maturity, node number per plant and 1000-grain weight. While, low amount of heterosis was recorded only for threshing index. Among 48 crosses, 36 and four hybrids exhibited significant and positive heterosis over better parent (heterobeltiosis) and standard check (GHB 719) (standard heterosis), respectively for grain yield. The maximum positive heterosis of 105.71 and 11.30 per cent over better parent and standard check, respectively, for grain yield per plant.

Jethva *et al.* (2012) carried out the heterosis study for grain yield and its attributes in pearl millet (*Pennisetum glaucum* (L.) R. Br.) They found that the degree of heterobeltiosis and average heterosis varied for all the hybrids and for all the characters studied. In general, it was inferred that the magnitude of heterosis effect was high for grain yield per plant, fodder yield per plant, 1000-seed weight, ear head weight, harvest index and number of effective tillers per plant; moderate for ear head length and threshing index and low for ear head girth. The hybrids ICMA 95222 $\times$ J 2372 and JMSA 101 $\times$ J 2296 exhibited the highest, significant and positive heterotic effect and mean performance for grain yield per plant and some of its important component traits.

Govindaraj *et al.* (2013) conducted study on two sets of line $\times$ tester in pearl millet. Their results showed that the underlying physiological processes determining the grain Fe and Zn densities were largely under additive genetic control, and Fe and Zn densities of the inbred lines *per se* and their general combining ability (gca) were positively and highly significantly correlated. Lack of better-parent heterosis indicated that to breed hybrids with high Fe and Zn densities would require high levels of these micronutrients in both parental lines.

Shinde and Mehetre (2014) conducted study to find heterosis in pearl millet. They recorded that the cross combinations viz., Giant bajra $\times$ RHRB-282, PMFT-907 $\times$ RHRB-278, RHRB-259 $\times$ RHRB-260, Giant bajra $\times$ PMFT-905 and PMFT-905 $\times$ PMFT-907 displayed significant and positive heterosis over mid and better parent for green forage yield and other related traits in both the seasons.

Maryam (2015) carried out an experiment using eight varieties of pearl millet using North Carolina Design II. They selected the best parents that give high

heterosis in terms of yield components, yield and downy mildew resistance. Two hybrids PEO5984 × P1449 and PEO5984 × PEO5532 had significant heterosis for 50 % days to flowering, PEO5984 × P1449, PEO5984 × PEO5532, PEO5984 × DMR15 and PEO5984 × SOSATC88 for yield.

Jog *et al.* (2016) observed the highest estimate of heterobeltiosis for grain yield per plant in cross 1 (76.45 %) followed by biological yield in cross 1 (73.76 %), number of effective tillers per plant in cross 1 (40.00 %), plant height in cross 1 (26.84 %), ear head length in cross 4 (11.43 %), test weight in cross 1 (11.23 %), days to flowering in cross 2 (-8.37 %), ear head girth in cross 4 (8.06 %) and days to maturity in cross 2 (-3.42 %). Highly significant heterobeltiosis with low inbreeding depression was observed for number of effective tillers per plant, ear head length, grain yield and biological yield in the cross ICMB94555 × J-2290; ICMB-20071 × J-2500 for grain yield and biological yield; ICMB-20071 × J-2480 for test weight and in ICMB-04999 × J-2454 for ear head girth and biological yield.

Nandaniya *et al.* (2016^b) studied the extent of heterosis in pearl millet for yield and quality traits. Heterosis was observed in both directions for most of the characters. High magnitude of heterosis was observed for plant height, ear head girth, ear head weight, grain yield per plant and harvest index. The heterosis was moderate for Fe content, Zn content and test weight. The heterobeltiosis for grain yield per plant ranged from -26.50 to 200.00 per cent, while the standard heterosis ranged from -53.38 to 37.79 per cent. The highest heterobeltiosis was recorded by cross JMSA1 20141 × 149-SB-14 and JMSA5 20142 × J-2340 followed by JMSA1 20141 × 81-SB-14, ICMA4 10444 × 149-SB-14. The cross JMSA5 20142 × J-2340, ICMA4 10444 × J-2340 and ICMA4 10444 × 149-SB-14 recorded the highest standard heterosis for grain yield per plant. They recorded that these crosses also exhibited desirable heterosis for important yield attributes suggesting that the heterosis for grain yield per plant was associated with heterosis for component character.

Pucher *et al.* (2016) studied the superiority of population hybrids over open-pollinated varieties for agro-morphological and agronomic traits in West Africa pearl millet germplasm and to derive strategies for pearl millet hybrid breeding in West Africa, based on quantitative genetic parameters, combining ability and heterotic patterns among geographically close versus distant pearl millet populations. A 10 × 10 factorial mating design was performed with four parental

OPVs from each of five West African countries. Grain yield showed an average panmictic midparent heterosis of 16.7%, ranging from - 26 to 73%.

Bhasker *et al.* (2017) studied heterosis for grain yield and its component traits in bajra through line $\times$ tester mating design using five lines and eight testers along with two checks, PHB-3 and GHB-558. Heterosis was observed in both directions for most of the characters. Maximum range of standard heterosis was obtained for 1000 grain weight, fodder yield per plot, number of productive tillers per plant, plant height, panicle length, grain yield per plant and panicle diameter. The heterobeltiosis for grain yield per plant ranged from 10.89 to 56.18 per cent, while the standard heterosis ranged from - 12.06 to 17.32 per cent. The cross combinations ICMA99666 $\times$ PLM1454R, ICMA97111 $\times$ PLM15047R and ICMA97444 $\times$ PLM15627R had higher grain yield *per se* ranging from 48.07 (ICMA97444 $\times$ PLM15627R) to 48.77 (ICMA99666 $\times$ PLM1454R) and recorded significant positive standard heterosis of 17.32, 15.86, 15.80 and 15.62 respectively for grain yield per plant.

Chittora and Patel (2017) conducted experiment to study extent of hybrid vigour in F₁ for grain yield and its components. The cross JMSA-9904 $\times$ AIB-15 showed highest and significant standard heterosis for total effective tillers, ear head girth, grain yield per plant and panicle harvest index. Among 48 hybrids studied, three hybrids namely JMSA-9904 $\times$ AIB-15, JMSA-9904 $\times$ AIB-30 and ICMA99555 $\times$ AIB-30 selected as best crosses since they expressed high standard heterosis over standard hybrid for many of the traits studied for high grain yield.

Karvar *et al.* (2017) produced 48 hybrids by line (4) $\times$ tester (12) crossing programme and found maximum positive standard heterosis for grain yield per plant over hybrid check, Aadishakti was observed in DHLB-16A $\times$ S-16/08 followed by DHLB-14A $\times$ S-16/06 and DHLB-16A $\times$ S-16/07. The range of standard heterosis over check Aadishakti was -49.28 per cent (DHLB-14A $\times$ S-16/10) to 36.88 per cent (DHLB-16A $\times$ S-16/08). Among ten top performing hybrids, three hybrids viz., DHLB-16A $\times$ S-16/08, DHLB-14A $\times$ S-16/06 and DHLB-16A $\times$ S-16/07 exhibited significant favorable heterobeltiosis, standard heterosis, gca and sca effects for yield and most of the related traits could be utilized for commercial cultivation after extensive testing in state and national trails.

Kumar *et al.* (2017^b) conducted experiment to study the extent of heterosis in pearl millet for yield and its component traits. Highest and significant positive

heterosis for grain yield per plant was recorded in ICMA 04999 $\times$ BIB-76 (355.96) followed by JMSA 20042 $\times$ BIB-40 (315.26), ICMA 04999 $\times$ BIB-40 (300.7) and ICMA 04999 $\times$ BIB-65 (294.91). Among 60 hybrids studied, they selected eighteen hybrids namely RMS 6A $\times$ BIB-65, RMS 7A $\times$ BIB-40, RMS 7A $\times$ BIB-75, RMS 21A $\times$ BIB-186, ICMA 832-22 $\times$ BIB- 65, ICMA 832-22 $\times$ BIB-186, ICMA 92777 $\times$ BIB- 66, ICMA 971111 $\times$ BIB-186, ICMA 93333 $\times$ BIB-66, ICMA 93333 $\times$ BIB-75, ICMA 93333 $\times$ BIB-186, ICMA 04999 $\times$ BIB-65, ICMA 04999 $\times$ BIB-76, ICMA 04999 $\times$ BIB-186, JMSA 20042 $\times$ BIB-40, JMSA 20042 $\times$ BIB-65, JMSA 20042 $\times$ BIB-66 and JMSA 20042 $\times$ BIB-76 as best crosses.

Kanfany *et al.* (2018) crossed a set of 17 inbred lines with Sosat C 88 and Souna 3 following a line $\times$ tester mating design. They observed best parent heterosis for grain yield across the two locations varied from -44% to 60% and 17 hybrids displayed positive best parent heterosis. The mid-parent heterosis varied from -16% for IBL 106-B-1 $\times$ Sosat C 88 to 125% for IBL 119-B-1 $\times$ Souna 3 which was not among the ten best hybrids. All the crosses displayed positive mid-parent heterosis for grain yield except IBL 106-B-1 $\times$ Sosat C 88 (-16%) and IBL 179-2-1 $\times$ Souna 3 (-12%). The standard heterosis values for grain yield across the experimental sites varied from -57% for IBL 179- 2-1 $\times$ Souna 3 to 20% for IBL 206-1-1 $\times$ Souna 3. The crosses IBL 206-1-1 $\times$ Souna 3, IBL 091-1-1 $\times$ Sosat C 88, IBL 206-1-1 $\times$ Sosat C 88, IBL 001-4-1 $\times$ Souna 3, and IBL 003-B-1 $\times$ Sosat C 88 exhibited positive standard heterosis for grain yield.

Ladumor *et al.* (2018) conducted an experiment comprised of four females, seven inbred testers of pearl millet, their 28 hybrids and two standard checks (GHB 732 and Dhanshakti) at Pearl Millet Research Station, Junagadh Agricultural University, Jamnagar in *kharif* 2017 for studies extent and magnitude of heterotic effects of hybrids over better parent and standard check. They observed that crosses JMSA5 20171 $\times$ 153-SB-17, ICMA1 10222 $\times$ 127-SB-17 and JMSA5 20171 $\times$ 54-SB-17 displayed high magnitude of standard heterosis for grain yield per plant and some of its components.

Reshma Krishnan *et al.* (2019) studied the magnitude of heterosis of 35 hybrids resulted from Line $\times$ Tester mating design of seven CMS lines and five restorer tester parents along with the standard check (GHB 558). The degree of heterosis varied from the cross to cross for all 10 characters. Considerable high heterosis in certain crosses and low in others revealed that the nature of gene action varied with

the genetic makeup of the parents. The hybrids viz., ICMA 07777 $\times$ 18488 R, ICMA 06777 $\times$ 18805 R and ICMA 96222 $\times$ 18488 R showed high *per se* performance with highly significant positive heterobeltiosis, standard heterosis for grain yield per plant.

Zakari *et al.* (2019) carried out diallel analysis using six parents and 30 F_1 's in pearl millet to identify the nature of gene action, and improve the restorer gene pool. The cross ICMX 1770192, ICMX 1770197 and ICMX 1770193 exhibited high grain yield with early days to 50% flowering and medium plant height. Nine crosses exhibited significant positive mid parent heterosis (MPH) and better parent heterosis (BPH), while six crosses exhibited significant positive MPH for grain yield. The crosses ICMX 1770202, ICMX 1770206, and ICMX 1770217 exhibited significant negative MPH and BPH for grain yield. For biomass yield, six crosses showed significant positive heterosis simultaneously over MPH and BPH and seven crosses exhibited significant positive MPH. The crosses ICMX 1770206 and ICMX 1770217 had significant positive MPH and BPH for both grain Fe and Zn content. The cross ICMX 1770200 exhibited significant positive MPH for both grain Fe and Zn content. The crosses ICMX 1770205 and ICMX 1770192 had significant positive MPH for grain Fe and Zn, respectively.

Chaudhary *et al.* (2022) carried out experiment using 83 genotypes consisting of 12 parental lines, 35 hybrids resulting from Line $\times$ Tester mating design, their 35 F_2 's and a standard check (GHB 558). Hybrids exhibited significant moderate to high heterosis over mid parent, better parent and standard check in desired direction for all the traits except standard heterosis in days to flowering. The significant economic heterosis in desirable direction was observed in high heterotic hybrids of a grain yield per plant. Out of these hybrids, two hybrids viz., ICMA 92333 $\times$ 15388 R and ICMA 05888 $\times$ 15403 R were possess significant economic heterosis for component characters like number of effective tiller per plant, ear head girth, ear head length, dry fodder yield per plant and test weight.

2.3 Inbreeding depression

Inbreeding means mating together of individuals which are related to each other by ancestry. Inbreeding depression was notice as early as 1876 by Darwin (Rai, 1978). It is measured as coefficient of inbreeding, which is the 'probability that two genes at any locus in individual are identical by decent'. Wright (1922) symbolized

coefficient of inbreeding as F and defined as the correlation between uniting gametes. Theory of inbreeding has been advocated by East and Jones (1919).

The work carried out on inbreeding depression in pearl millet is briefly reviewed as under:

Lal and Singh (1968) evaluated six generations viz., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of cross two S_7 lines, viz., 200 and 424 of pearl millet. They recorded that highly significant inbreeding depression was found in all the characters under observation except for days to flower.

Khadr and El-Rouby (1978) in selection programme from S lines from the the local variety Ex-Borno and from varieties World Composite and Nigerian Composite studied in 1973-75 at two localities in Nigeria, the inbreeding depression for yield was between 17.8 and 36.0%. In experiments in 1975-76 using S_1 , S_2 , S_3 , S_4 and S_5 bulk populations of Nigerian Composite they observed grain yield and head weight and four other characters exhibited high and intermediate inbreeding depression respectively, but pollen shedding date increased with inbreeding.

Shinde *et al.* (1984) studied on heterosis and inbreeding depression for yield and seven related characters in F_1 and F_2 crosses among six varieties of *Pennisetum americanum* (L.). They observed non-significant inbreeding depression for days to flowering and significant inbreeding depression for plant height, number of effective tiller per plant, earhead length, test weight and grain yield per plant.

Rai *et al.* (1985) investigated the effects of one generation of selfing on grain yield, plant height, head length, 1000 seed weight, and days to flowering in the base populations as well as in three successive full sib recurrent selection cycle bulks of the Medium Maturity Composite and Serere Composite-I of pearl millet. The experimental materials consisted of random mated bulks and single generation selfed bulks from 400 random plants corresponding to each cycle (cycle 0 to 3) of both the composites. Results showed that average inbreeding depressions in both the composites were highest for grain yield (25 % and 36 %) followed by 1000 seed weight (12 % and 14 %). Plant height, days to flowering and head length were least affected by selfing, with the average inbreeding depressions for these characters ranging from 4 % to 7 %.

Shanmuganathan (2010) studied six crosses of F_2 population (IP 20381 $\times$ PT 5665, IP 20381 $\times$ GP15071, IP 20381 $\times$ IP 19125, IP 20381 $\times$ IP20350, IP 20334 $\times$

IP 20350 and IP 19125 $\times$ GP 16239. The comparison of F_2 mean in relation to F_1 mean revealed that there was substantial amount of inbreeding depression in all the crosses for both grain and fodder yield except in the cross IP 19125 $\times$ GP 16239. This cross recorded low inbreeding depression for green fodder yield. The cross IP 20381 $\times$ PT 5665 possessed high inbreeding depression for both grain yield and fodder yield.

Jog *et al.* (2016) studied six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) for grain yield and its attributing characters in four crosses of pearl millet. They recorded highly significant heterobeltiosis with low inbreeding depression for number of effective tillers per plant, earhead length, grain yield and biological yield in the cross ICMB94555 $\times$ J-2290; ICMB-20071 $\times$ J-2500 for grain yield and biological yield; ICMB-20071 $\times$ J-2480 for test weight and in ICMB-04999 $\times$ J-2454 for earhead girth and biological yield.

Chaudhary *et al.* (2022) evaluated 35 hybrids, out of this hybrids two hybrids viz., ICMA 92333 $\times$ 15388 R and ICMA 05888 $\times$ 15403 R were possess significant economic heterosis for component characters like number of effective tiller per plant, ear head girth, ear head length, dry fodder yield per plant and test weight and also exhibited significant and positive inbreeding depression for those traits, which indicating that the maximum contribution of this character towards grain yield heterosis. The hybrid ICMA 91777 $\times$ 15041 R was exhibited significant inbreeding depression for all the traits except dry fodder yield per plant. None of the cross showed significant and positive high heterosis with low inbreeding depression in desirable direction in all traits except days to maturity.

2.4 Heritability and Genetic Advance

Heritability is a good index of the transmission of characters from parent to their offspring (Falconer, 1989). Lush (1940) defined heritability in both broad and narrow sense. Heritability in broad sense is the ratio of “Total genotypic variance to the total phenotypic variance” and it provide a measure of the overall importance of hereditary determination of a trait. Heritability in narrow sense is the ratio of “Additive genetic variance to the total phenotypic variance” and measures the portion of the total variance which can be utilized for improvement of given population with respect to that trait by selection. Genetic advance is the improvement in the mean genotypic value of the selected families over the base population.

The utility of the estimates of heritability is increased, when they are used in conjunction with the genetic advance. According to Allard (1960), heritability of yield alone is less and that of yield components is more. However, the gain from selection for a particular character is function of its heritability, selection pressure and the variance existing in the base population. So, genetic gain was expressed as the product of heritability, phenotypic standard deviation and selection differential. Johnson *et al.*, (1955) observed that heritability value indicates the relative effectiveness of selection based on phenotypic expression of a trait, the genetic advance is more useful in predicting the actual value of selection. Genetic advance under selection depends upon the genetic variability among different plants or families in the base population, the heritability of the character under selection and the intensity of selection. The availability of literature on heritability and genetic advance is reviewed as under.

Lal and Singh (1970) studied six genetic populations of a pearl millet cross during 1965-66 at Government Agricultural College, Kanpur, for the study of heritability, genetic advance and minimum number of genes for the expression of 15 grain and fodder yield components. Stem thickness, number of spike bearing branches, leaf length, leaf breadth, days to flowering, peduncle length, peduncle thickness, spike length and 250-grain weight showed high heritability in broad sense, while, other characters showed medium to low heritability. In narrow sense, only leaf length, days to flower, peduncle length and spike length showed high heritability and other characters showed medium to low heritability. Genetic advance in percentage of mean was found maximum for number of spike bearing branches, number of spike bearing tillers, 250-grain weight, number of tillers; intermediate for peduncle length, spike length, days to flowering, stem thickness, leaf breadth and peduncle thickness; minimum for plant height, leaf length, number of internodes, number of branches and for stem thickness.

Sandhu and Phul (1984) examined the genetic components of variance in a pearl millet population of PSB-3 by using the North Carolina Design-II in respect of grain yield and other morphological traits under normal and wide spacing. The heritability estimates were 15 and 20 per cent under wide and normal spacing respectively. The expected genetic advance expressed as percentage of mean for grain yield, ranged from 10.78 to 13.32 per cent under full-sib and half-sib selection schemes. High heritability estimates were obtained in case of ear length, days to 50

per cent flowering and plant height in the two environments. The genetic advance in respect of these traits was also high except in case of days to 50 per cent flowering, where it was low probably due to less variability for this trait among the plants used for mating.

Ghorpade and Metta (1993) used WC-C75 population to develop 100 families each of S_1 , full-sibs and half-sibs. All the three types of families were grown for evaluation in three intermixed 10×10 simple lattice design in rainy season during 1986. They observed heritability estimates on progeny mean basis were high for all characters in all families and moderate for grain yield/plant (0.31) in half-sib families. Expected genetic advance for 51 family selection was high for most traits, particularly for grain yield per plant (25.7%), indicating that S_1 family selection was superior method for population improvement.

Shekhawat *et al.* (1993) conducted an experiment in pearl millet composite JOB GT-1 to estimate the components of genetic variance and heritability for yield and related characters using NCD-I. The dominance variation was very high for number of ears per plot and ear weight per plot, while the same estimate attained a negative value for plant height and ear length, indicating the preponderance of additive gene action in their inheritance. The heritability in narrow sense was high for ear length. Among the various methods of selection for which theoretical responses were calculated, mass selection appeared suitable for all characters.

Tomar *et al.* (2008) carried out an investigation to study of genetic parameters in pearl millet (*Pennisetum glaucum* (L.) R.Br.) with the objective to collect the information on variability, heritability, genetic advance among 45 F_1 s and 10 parents in pearl millet. The high estimates of heritability were observed for all the characters taken under study except number of effective tillers per plant. The genetic gain was observed for grain yield followed by 1000 seed weight, panicle girth, panicle length and least for effective tillers. Grain yield per plant and 1000 seed weight recorded high amount of genetic advance. High heritability with high genetic advance may be attributed to the action of additive genes.

Lakshmana *et al.* (2009) evaluated the 105 (61 restorers and 44 maintainers) diverse pearl millet germplasm lines of pearl millet. They recorded high heritability for 12 characters over two years except days to flowering and days to maturity. However, the values of genetic advance suggested that real progress could be made

only for a few characters such as ear head length, ear head girth and grain yield per plant.

Shanmuganathan (2010) studied six crosses of F_2 population (IP 20381 $\times$ PT 5665, IP 20381 $\times$ GP15071, IP 20381 $\times$ IP 19125, IP 20381 $\times$ IP20350, IP 20334 $\times$ IP 20350 and IP 19125 $\times$ GP 16239). Their result indicated that the high estimates of heritability and genetic advance for almost all characters indicated the presence of additive gene action and hence selection for these traits could be effective in improving stover and grain yield of pearl millet.

Govindaraj *et al.* (2011) conducted an experiment using 61 accessions of pearl millet. They observed high estimates of genetic co-efficient of variation, heritability and genetic advance for iron and crude fat content. High heritability was observed for all the traits under study except seed weight which had moderate heritability. High value of heritability coupled with high genetic advance as per cent of mean were recorded for number of productive tillers, crude protein, crude fat, phosphorus, calcium, iron and zinc content, indicating the important role of additive gene action for the expression of these characters.

Bhadalia *et al.* (2012) studied the nature of gene action for grain yield and eleven component traits in pearl millet using 8×8 diallel fashions. They observed that the narrow sense heritability estimates was high for ear head weight, number of grains per square cm, grain yield per plant, dry fodder yield per plant and harvest index, whereas they were moderate for ear head length. The rest of the characters showed low heritability.

Manga (2013) investigated genetic variation, heritability, genetic advance and association among various traits in a set of 47 inbred restorer lines of pearl millet developed under inbred development programme at CAZRI, Jodhpur. They observed high estimates of heritability for 500 grain weight, grain yield, ear head weight, biomass and plant height. Genetic advance as percent of mean were found to be high for grain yield, ear head weight and biomass.

Vagadiya *et al.* (2013) studied a set of 64 genotypes comprising of 48 F_1 s along with four male sterile lines and 12 pollinators for genetic variability, heritability and genetic advance of grain yield and its nine components in pearl millet at Jamnagar during *kharif* 2009. The analysis of variance revealed highly significant differences among the genotypes for all the ten characters studied. The estimates of heritability (broad sense) ranged from 36.00 to 97.50 per cent. High heritability estimates were

recorded for the traits viz., ear head weight, ear head length, fodder yield per plant and grain yield per plant. Moderate heritability estimate was observed for days to 50 % flowering, days to maturity, ear head girth and 1000-grain weight. While, the remaining two characters viz., number of nodes per plant and plant height recorded low heritability. The estimates of genetic advance as percentage of mean ranged between 6.79 (days to maturity) to 52.50 (fodder yield per plant). The characters like ear head weight, ear head length, fodder yield per plant and grain yield per plant exhibited high heritability coupled with high genetic advance expressed as percentage of mean. Moderate heritability estimates with low to medium genetic gain was manifested for days to 50% flowering, days to maturity, ear head girth and 1000 grain weight. Characters like number of nodes per plant and plant height showed low heritability and genetic advance as percentage of mean, which indicated the predominance of additive and non-additive gene action in controlling these traits.

Dapke *et al.* (2014) conducted study to assess the genetic variability and character association among the twenty advanced hybrids, twelve R line and twelve B lines of pearl millet for ten quantitative traits. Heritability in narrow sense ranged from 65.0% (harvest index) to 95.0% (grain yield/plant) in pooled environment. High GA% observed for grain yield (111.5%) coupled with high heritability (95.0%), indicating the preponderance of the additive gene action.

Kumar *et al.* (2014^a) studied a total of 97 pearl millet genotypes in a randomized block design (RBD) with two replications for genetic variability, correlation and path analysis for eight characters. Estimates of heritability ranged from 18.15 per cent for effective tillers to 94.80 per cent for plant height, while grain yield showed 88.75 per cent heritability. High heritability coupled with high genetic advance as per cent of mean was observed for days to 50 per cent flowering, plant height, panicle length, panicle diameter and grain yield indicating the importance of these traits in selection and crop improvement.

Kumar *et al.* (2014^b) evaluated a set of 26 pearl millet hybrids to estimate the genetic parameters. Estimates of heritability in broad sense ranged from 26 per cent for plant population to 99 per cent for 1000-seed weight, while grain yield showed 75 per cent heritability. Moderate to high heritability coupled with high genetic advance as per cent of mean was observed for 1000-seed weight, grain yield, dry

fodder yield, plant height, productive tillers per plant and ear length indicating the importance of these traits in selection and crop improvement.

Manga (2014) studied genetic variability, heritability and genetic advance for yield and yield contributing traits in pearl millet in 20 newly developed male sterile lines of pearl millet, developed at the Central Arid Zone Research Institute, Jodhpur, during the rainy season of the year 2013. High heritability estimates were observed for grain yield per plot, ear head weight per plot, plant height and days to flowering. High genetic advance as percentage, was recorded for grain yield per plot and ear head weight per plot. Greater magnitude of heritability coupled with higher genetic advance for grain yield per plot and ear head weight/plot revealed additive genetic effects for inheritance of these traits, while, high heritability estimates with low genetic advance indicated the presence of non-additive gene action for days to flowering, plant height and ear head length.

Sathya *et al.* (2014) developed a RIL mapping population by crossing PT 6029 × PT 6129 and evaluated for various genetic variability parameters in pearl millet. The high heritability was recorded for all the traits except for days to 50% flowering, days to maturity and ear head girth. High heritability coupled with high genetic advance as per cent of mean was observed for 1000 grain weight, number of productive tillers, single ear head grain weight, single ear head weight, single plant yield and plant height. These characters were controlled by additive gene effect. Transgressive segregants were observed for all the 11 traits. They suggested the mapping population could be used for mapping of genes for important traits.

Ezeaku *et al.* (2015) evaluated twenty-four parental lines of pearl millet A/B pairs developed jointly by Lake Chad Research Institute (LCRI), Maiduguri and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Kano during 1997 to 1999 along with a seed parent (ZATIB) to determine yield and yield component relationships, heritability estimates as well as genetic advance. The parental lines under study showed high to moderate broad-sense heritability; with panicle length expressing the highest heritability (78.95%), followed by grain yield (75.43%) and head weight (73.30%). The rest characters expressed moderate heritability values. Panicle length and head weight displayed high heritability and high genetic advance indicating that the two traits might be controlled by additive gene effects.

Dhedhi *et al.* (2016) studied 29 forage pearl millet hybrids for genetic variability, heritability, genetic advance and character association of green fodder yield and its components at Jamnagar and Dhari centers of Junagadh Agricultural University, Gujarat under rainfed conditions during *kharif* 2014. The analysis of variance revealed highly significant differences among the hybrids for all the characters studied except lodging score and harvest index. Broad sense heritability ranged from 37.00 % (lodging score) to 81.60 % (plant height). The high heritability coupled with high to moderate genetic advance expressed as percentage of mean was observed for days to maturity, plant height, harvest index, dry fodder yield per plant and grain yield per plant which showed that these traits were controlled by additive gene effects and phenotypic selection were for these traits were likely to be effective.

Singh and Singh (2016) studied 27 accessions of pearl millet of African origin to assess the magnitude of presence of genetic variability and associations among characters. The broad sense heritability (%) and genetic advance (% of mean) estimates were also high for all studied characters. The presence of genetic variability, high heritability and genetic advance and association with grain yield of number of tillers per plant, panicle length (cm), panicle diameter (cm) and days to 50% flowering amenable them for selection and enhancement of grain yield.

Basavaraj *et al.* (2017) carried out an investigation at Regional Agricultural Research Station, Vijayapur, Karnataka with 75 restorer (R) lines of pearl millet in a randomized block design with two replications to estimate the genetic variability, heritability and genetic advance for nine quantitative traits. High heritability coupled with high genetic advance as per cent of mean was observed for characters viz., panicle girth, panicle weight and stover weight per plot, grain yield per plot and 1000 seed weight and indicating predominance of additive gene action for these characters.

Nehra *et al.* (2017) estimated the genotypic and phenotypic variability, heritability, genetic advance, correlation and path coefficient for yield and its contributing quantitative characters. High heritability coupled with high genetic advance for number of productive tillers per plant, 1000 grain weight, dry fodder yield, green fodder yield and grain yield indicated the scope of improvement through direct phenotypic selection. High heritability coupled with high genetic advance for these traits may be because of additive gene effect. High heritability

with moderate to low genetic advance in days to 50% flowering, number of nodes per plant, leaf blade length, spike girth at maximum point, spike length and plant height may be due to dominant and epistatic gene action.

Ramya *et al.* (2017) carried out an investigation to study genetic variability, heritability and genetic advance among 182 restorer (R) lines of pearl millet for twelve characters viz., days to 50% flowering, plant height, ear length, ear diameter, productive tillers per plant, head yield per plant, grain yield per plant, panicle harvest index, fresh stover yield per plant, dry matter yield per plant, 1000 grain weight and grain harvest index. High estimates of heritability along with genetic advance (% mean) were observed for plant height, ear length, ear diameter, productive tillers per plant, and 1000 grain weight indicating that the selection for these traits would be more effective.

Shanthi *et al.* (2017) studied genetic variability with forty-two maintainer inbred lines of pearl millet developed at ICRISAT, Patancheru, Hyderabad, India to assess the magnitude of variability, heritability and genetic advance as per cent of mean for thirteen yield and yield contributing characters at Agricultural Research Station (Dry Land Agriculture), ANGRAU, Ananthapuram, Andhra Pradesh during *rabi* 2011-12. High to moderate estimates of broad sense heritability coupled with high estimates of genetic advance as per cent of mean was noticed for the traits single panicle weight (Main tiller panicle), grain yield per single panicle, fodder yield per plant, weight of total panicles per plant and grain yield per plant, suggesting to go for simple direct selection for the improvement of the genotypes for these characters.

Singh *et al.* (2017^a) studied six generations from three crosses viz., 863B $\times$ P 7-7, 843B $\times$ P 7-4, and 81B $\times$ ICMP 451, of pearl millet. They observed broad sense heritability estimates were generally high for all the characters for all the three crosses. Low narrow sense heritability estimates support the prevalence of epistatic effects as also noted from the generations means. Estimates of expected genetic advance expressed as percentage of mean were low to medium for all the characters including grain yield. But very high gain was obtained for number of effective tillers (191.36%) for cross 863B $\times$ P7-7 and high estimates for gain yield (55.24%) for cross 843B $\times$ P7-4.

Singh *et al.* (2017^b) evaluated 150 seed and restorer parents for grain yield and its component traits at two diverse agro-ecologies CCSHAU-Hisar and ICRISAT-

Patancheru in pearl millet. All the traits exhibited high heritability (>60 %) along with high genetic advance as per cent of mean (19.05 to 74.12 %) except grain yield, indicating most of these yield component traits under the influence of additive genes.

Solanki *et al.* (2017) estimated genetic variability, heritability and genetic advance among 50 hybrids in pearl millet. Plant height, ear head length, test weight, biological and seed yield had moderate to high estimates of GCV, PCV and moderate to high heritability. Moderate heritability and genetic advance as per cent of mean was observed for days to 50% flowering, plant height, ear head length and ear head diameter. Joint consideration of GCV, heritability along with high genetic advance as per cent mean indicated that biological yield per plant (g) and seed yield per plant was mainly under the control of additive gene action.

Subbulakshmi *et al.* (2018) conducted experiment to study the genetic variability present among the newly effected fifty-four hybrids of pearl millet. They studied yield parameters viz., days to 50 per cent flowering, plant height, number of productive tillers, ear head length, ear head girth, test weight, single head grain weight, single plant yield and quality traits such as crude protein, crude fiber, beta carotene, iron and zinc. Highest heritability (h^2) conjunction with genetic advance (GA) was observed for all the characters studied and moderate for number of productive tillers per plant and earhead girth Therefore, the presence of high variability among the genotypes can be utilized for nutritional enrichment in future millet breeding programs.

Thomas *et al.* (2018) evaluated 22 pearl millet genotypes during *kharif* 2017. They found high heritability with high genetic advance as per cent of mean for green fodder yield per plant, dry matter yield per plant, fat content, crude protein content and ash content.

Kumar *et al.* (2019) conducted a field experiment in pearl millet (*Pennisetum glaucum* (L.) R. Br.) to study genetic variability, heritability and genetic advance for grain iron, zinc, yield and its component traits. The observations were recorded on individual plant basis for each replication for days to 50% flowering, plant height, panicle length, panicle girth, total tillers, productive tillers, grain yield per plant, iron content in grain and zinc content in grain. Highest heritability was recorded for grain zinc content (95.0%) followed by total tillers (94.8%), grain iron content (93.8%), plant height (84.9%) and grain yield (80.5%). Highest genetic

advance as per cent of mean was observed to be 118.12 per cent for grain yield per plant followed by 99.19 per cent for total tillers and 43.96 per cent for grain zinc content. Genetic advance as per cent of mean ranged from 0.86 to 118.12 per cent.

Kumawat *et al.* (2019) conducted experiment for variability parameters and character association in 50 pearl millet single cross hybrids which were generated by crossing five male sterile lines with 10 genetically diverse restorers in line $\times$ tester mating design at ICRISAT, Hyderabad. Very high heritability (broad sense) estimates was observed for plant height and days to maturity while moderately high for ear head diameter and ear head length. The expected genetic advance as percentage of mean was high for grain yield per plant followed by number of effective tillers per plant, plant height and ear head length.

Mahendrakar *et al.* (2019) used a bi-parental recombinant inbred lines (RIL) mapping population representing F_2 phenotypic variance. A total of 317 RILs were evaluated for grain iron and zinc content in two seasons. The result from the analysis of variance exhibited a large variability for grain Fe and Zn content across the two environments. They observed that the heritability (h^2) estimated were high as 0.83 (Zn) and 0.83 (Fe). Genetic advance in percentage mean (GAM) was also high for both traits. High heritability and high GAM indicates the preponderance of additive gene effect which responds to selection of the line.

Priyanka *et al.* (2019) studied forty-two genotypes of pearl millet in randomized block design for twenty-two physiological, nutritional and yield related traits to estimates genetic variability, heritability and genetic advance as a percentage of mean. Among the 22 characters studied, the genetic advance as percent of mean along with higher values of heritability estimates were maximum for grain yield per plot, green fodder yield per plot, iron content, leaf area duration, green fodder yield per plant and zinc content indicating that the genetic variances for these traits are probably owing to their high additive gene effects.

Sattler *et al.* (2019) crossed 17 open-pollinated varieties (OPVs) in a diallel mating design and tested together with their offspring. They observed broad-sense heritability estimates were within expectancy range. Most heritable traits were panicle length and plant height ($H^2 = 0.94$ and 0.82). Days to 50% flowering had heritability as a little lower than expected ($H^2 = 0.68$). The heritability estimate for the target trait panicle yield, which is largely influenced by environmental effects, was still adequate ($H^2 = 0.53$).

Zakari *et al.* (2019) carried out diallel analysis using six parents and 30 F_1 's, to identify the nature of gene action, and improve the restorer gene pool. They recorded narrow sense heritability for days to 50% flowering, panicle length, plant height, panicle circumference, biomass yield and grain Fe and Zn content was high indicated the predominance of additive gene action in inheritance of these traits.

Kumar *et al.* (2020^a) conducted experiment for 48 diverse pearl millet genotypes in two replications in randomized complete block design (RCBD) for genetic variability, heritability, genetic advance as per cent of mean along with path analysis of grain micronutrients concentration, yield and its component traits. The analysis of variance showed highly significant differences among the genotypes for most of the characters studied, indicating the presence of adequate variability. High to moderate heritability coupled with moderate to high genetic advance as per cent of mean were observed for the plant height, panicle length, panicle girth, panicle weight, grain yield per plant, grain iron (Fe) and zinc (Zn) content revealed the characters are predominantly governed by additive gene. Characters like dry fodder yield per plant, panicle weight, plant height and panicle length were shown high positive direct effect on grain yield per plant can be directly used for improvement of pearl millet.

Kumar *et al.* (2020^b) carried out investigation to analyze the genetic variability parameters such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability, expected genetic advance and genetic advance as per cent of mean for ten agronomic traits among ninety heterotic gene pools of pearl millet. Analysis of variance revealed highly significant differences among the genotypes for all the traits. High heritability coupled with low expected genetic advance as percentage of mean was observed for test weight is the evidence that this plant trait was under the control of non-additive genetic effects for inheritance of this trait.

Pujar *et al.* (2020) evaluated 281 advanced breeding lines of pearl millet bred at ICRISAT to determine the extent of variability, heritability and diversity for grain Fe, Zn and protein, along with key agronomic traits. High heritability was observed for grain Fe, Zn and protein, along with all the agronomic traits studied, which suggests that simple selection and advancement would increase the genetic gain of these traits. Further, for most of these traits (including Fe and Zn) the high heritability was due to additive gene control, therefore, they suggested that high heritability traits are likely to respond to direct selection.

Sharma *et al.* (2020) studied twenty pearl millet genotypes to explore and evaluate the diversity of antinutritional factors along with establishing their relationship with protein content and yield that contributes to its quality and farmers interest, respectively. High heritability associated with high genetic advance as the percentage of mean observed for grain yield, phytic acid, total phenol and protein content indicates that these are mostly governed by additive gene action and the selection could be beneficial. All genotypes had high heritability and genetic advance as per cent of mean for all five traits.

IV. RESULTS AND DISCUSSION

The results of present investigation on “**Generation mean analysis in pearl millet [*Pennisetum glaucum* (L.) R. Br.]**” are presented and discussed under the following headings.

- 4.1 Analysis of variance for experimental design
- 4.2 *Per se* performance of progenies
- 4.3 Scaling tests and estimation of gene effects
- 4.4 Magnitude of heterosis and inbreeding depression
- 4.5 Heritability and genetic advance

4.1 Analysis of variance for experimental design

Analysis of variance for generation means comprising six generations viz., P₁, P₂, F₁, F₂, BC₁ and BC₂ was computed for fifteen characters for each six crosses of pearl millet [*Pennisetum glaucum* (L.) R. Br.] is presented in Table 4.1. The analysis of variance between generations revealed that the mean squares due to generations were significant for all the characters under study except plant height for cross 5, ear head length for cross 2, ear head girth for cross 1, 5 and 6, days to maturity for cross 1 and 2 and oil content for all six crosses were recorded with non-significant differences. Significant differences suggested presence of sufficient variation for generation mean values of all the crosses for different traits, there by revealing existence of sufficient variation to analyze and interpret the results in terms of objectives under investigation. The significant variation for all the characters under study might be due to more diversity between the parents of all the six crosses which resulted in high variability among its generations.

4.2 *Per se* performance of progenies

The mean value of character of generation within family is important to understand the variation present and also to understand primarily gene effect viz., non-additive, additive, partial dominance, dominant or over-dominant. The mean values of P₁, P₂, F₁, F₂, BC₁ and BC₂ generations for various characters in six crosses of pearl millet viz., cross 1 (05888 B × 15001 R), cross 2 (02889 B × 16317 R), cross 3 (01555 B × 15990 R), cross 4 (98222 B × 15550 R), cross 5 (1202 B × 16317 R) and cross 6 (05888 B × 16066 R) are presented and discussed character wise as below.

Table 4.1: Analysis of variance for six generations in six crosses of pearl millet for grain yield and its contributing characters

Mean sum of squares									
Source of variation	d f.	Days to flowering	Plant height	Number of effective tiller per plant	Earhead length	Earhead girth	Days to maturity	Test weight	Grain yield per plant
Analysis of variance between generations within cross									
Cross 1 (05888 B × 15001 R)									
Replications	2	2.42	34.32	0.04*	3.94	4.92	2.65	0.11*	1.09
Generations	5	16.28**	975.76**	0.16**	16.13**	2.53	1.62	0.54**	82.22**
Error	10	0.87	9.75	0.00	1.05	2.69	1.24	0.02	1.56
Cross 2 (02889 B × 16317 R)									
Replications	2	0.71	52.26*	0.09**	2.13	0.00	0.26	0.19	1.10
Generations	5	8.80**	464.19**	0.19**	5.12	7.31**	1.35	0.35*	16.13**
Error	10	1.38	12.07	0.01	1.80	0.88	0.87	0.06	1.55
Cross 3 (01555 B × 15990 R)									
Replications	2	0.86	1.37	0.05	2.51*	7.89*	0.03	0.15	0.58
Generations	5	50.18**	548.88**	0.15**	1.93*	10.88**	18.65**	0.19*	70.78**
Error	10	0.36	11.93	0.01	0.45	1.36	0.66	0.04	2.19
Cross 4 (98222 B × 15550 R)									
Replications	2	0.25	111.42	0.05	4.30	4.12*	0.02	0.09*	1.53
Generations	5	16.09**	393.92**	0.35**	5.55*	5.60**	14.14**	0.19**	58.68**
Error	10	0.07	33.45	0.01	1.48	0.88	1.19	0.01	1.68
Cross 5 (1202 B × 16317 R)									
Replications	2	0.02	227.51	0.04	7.23*	4.00	1.93	0.07	1.65
Generations	5	19.24**	162.43	0.09**	12.60**	1.09	14.62**	0.29*	86.74**
Error	10	0.45	63.30	0.01	1.06	1.09	1.05	0.06	1.94
Cross 6 (05888 B × 16066 R)									
Replications	2	0.01	22.92	0.01	4.70	0.44	0.26	0.39	2.06
Generations	5	19.19**	191.28**	0.23**	25.71**	0.84	17.08**	0.87**	65.03**
Error	10	0.25	12.97	0.03	1.46	0.62	1.04	0.10	1.98

* and **, significant at 5% and 1% level of significance, respectively

Table 4.1: Continue....

Mean sum of squares								
Source of variation	d.f.	Harvest index	Carbohydrate	Tannin	Iron content	Zinc content	Oil content	Protein content
Analysis of variance between generations within cross								
Cross 1 (05888 B × 15001 R)								
Replications	2	0.02	2.79	0.42	1.41	0.09	0.48	0.16
Generations	5	9.86**	234.98**	3554.82**	869.16**	13.08**	0.55	9.03**
Error	10	0.58	0.90	20.04	2.23	0.27	0.17	0.23
Cross 2 (02889 B × 16317 R)								
Replications	2	0.87	3.05	10.66	1.25	0.18	0.38	0.44
Generations	5	26.07**	54.34**	3917.26**	326.78**	104.47**	0.07	3.83**
Error	10	0.72	2.85	4.68	1.74	0.12	0.16	0.16
Cross 3 (01555 B × 15990 R)								
Replications	2	1.67	8.07	11.05	0.68	0.56	0.39	0.09
Generations	5	47.21**	51.35**	7279.58**	849.70**	56.84**	0.21	9.18**
Error	10	0.88	3.31	6.68	0.44	0.41	0.13	0.19
Cross 4 (98222 B × 15550 R)								
Replications	2	4.85	0.05	4.52	0.97	0.25	0.04	0.37
Generations	5	26.86**	47.46**	3395.72**	581.72**	39.19**	0.15	2.47**
Error	10	1.46	4.39	6.41	3.11	0.19	0.14	0.27
Cross 5 (1202 B × 16317 R)								
Replications	2	2.58	1.99	5.64	0.74	0.31	0.55	0.04
Generations	5	6.02**	40.69**	2594.36**	591.46**	17.58**	0.26	7.95**
Error	10	0.85	4.57	3.35	0.56	0.89	0.13	0.28
Cross 6 (05888 B × 16066 R)								
Replications	2	0.61	0.56	10.72	0.66	0.32	0.20	0.07
Generations	5	6.03**	88.81**	5454.00**	281.62**	8.17**	0.17	13.88**
Error	10	0.33	3.44	5.99	1.57	1.10	0.17	0.20

* and **, significant at 5% and 1% level of significance, respectively

4.2.1 Days to flowering

For days to flowering character, the earliness is desirable for the improvement of crop. Among the parents, mean value of 15001 R observed earliest with 48.83 days in cross 1, followed by 01555 B (50.90) in cross 3. In cross 5, female parent 1202 B was recorded maximum days to flowering with mean value of 56.83 days followed by 16317 R with 55.33 days in cross 2. In all crosses, F_1 recorded significantly higher than their respective parents except cross 1 with indicative of expression of hybrid vigour with over dominance. Among all hybrids, F_1 of cross 1 was early compared to other with mean value of 46.37 days, followed by F_1 of cross 2 (52.70 days). The mean value of F_2 in all crosses was significantly lower than mean value of their respective F_1 's except cross 1 and 2 which suggested inbreeding depression.

The performance of back cross generations was related to their respective recurrent parents in the sense that the use of late or early parent had shifted the days to flowering to their back cross progenies. BC_1 of all the crosses recorded lower days to open first flower than their respective recurrent parents except cross 1, 5 and 6. While in BC_2 the crosses 1, 3, 4 and 6 recorded higher days to open first flower except cross 2 and 5. Similar results for significant variation for mean value of days to flowering of generations within family was also supported by Godasara *et al.* (2010), Jog *et al.* (2016), Suryawanshi *et al.* (2016), Kumar *et al.* (2017^a) and Goah *et al.* (2020).

4.2.2 Plant height (cm)

Lowest mean value of plant height was observed for 15001 R (126.60 cm) in cross 1 followed by 01555 B in cross 3 with 136.93 cm. Highest plant height was recorded for the male parent of cross 3 (15990 R) having 176.97 cm. F_1 of all crosses found differed significantly in the plant height than their respective parents. The highest plant height was observed in F_1 of cross 4 (186.10 cm). The mean value of F_1 's for plant height of cross 1, 2 and 4 exceeded in respect to their respective parents which indicate the hybrid vigour and over dominance while cross 3, 5 and 6 exhibit partial dominance. F_2 generation of cross 1, 2, 3, 5 and 6 significantly higher than their respective F_1 's. In cross 4, mean value of F_2 was slightly lower than their F_1 which indicated the inbreeding depression.

The performance of back cross generations was related to their respective recurrent parents in the sense that the use of parent having higher or lower height was shifted to their back cross progenies. The mean value of BC_1 in all crosses higher value than their respective recurrent parent. While in BC_2 in all crosses higher value than their respective recurrent parent except cross 3 and 4.

Table 4.2.1: *Per se* performance of six generations for days to flowering and plant height in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)			Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Days to flowering																		
Generations	Mean	SE		Mean	SE		Mean	SE		Mean	SE		Mean	SE		Mean	SE	
P ₁	50.97	± 0.34		52.63	± 0.43		50.90	± 0.54		52.63	± 0.44		56.83	± 0.59		53.87	± 0.46	
P ₂	48.83	± 0.40		55.33	± 0.38		54.10	± 0.55		54.50	± 0.53		55.27	± 0.58		54.73	± 0.44	
F ₁	46.37	± 0.53		52.70	± 0.40		54.50	± 0.45		55.17	± 0.49		54.93	± 0.56		55.37	± 0.48	
F ₂	50.64	± 0.43		54.59	± 0.52		45.68	± 0.31		56.60	± 0.31		50.31	± 0.37		50.74	± 0.42	
BC ₁	53.22	± 0.70		51.95	± 0.61		48.67	± 0.50		50.12	± 0.57		57.57	± 0.48		58.33	± 0.30	
BC ₂	51.03	± 0.77		50.68	± 0.89		56.60	± 0.43		55.23	± 0.38		55.22	± 0.38		56.17	± 0.44	
Over all mean	50.18	± 0.54		52.98	± 0.67		51.74	± 0.34		54.04	± 0.15		55.02	± 0.39		54.86	± 0.29	
C.D. (P=0.05)	1.70			2.13			1.09			0.49			1.23			0.91		
Plant height (cm)																		
Generations	Mean	SE		Mean	SE		Mean	SE		Mean	SE		Mean	SE		Mean	SE	
P ₁	143.33	± 1.92		142.77	± 2.21		136.93	± 1.98		153.63	± 1.96		165.80	± 1.97		144.13	± 2.03	
P ₂	126.60	± 1.20		142.60	± 1.73		176.97	± 2.83		165.13	± 2.84		147.70	± 1.83		154.30	± 1.54	
F ₁	167.13	± 1.08		157.27	± 2.07		144.67	± 1.61		186.10	± 2.42		156.70	± 2.70		144.53	± 1.68	
F ₂	166.48	± 2.00		166.51	± 2.27		156.87	± 1.76		160.44	± 2.11		166.16	± 2.31		160.05	± 1.78	
BC ₁	173.20	± 3.25		158.80	± 3.18		153.10	± 2.20		166.77	± 3.26		165.98	± 3.50		158.82	± 2.91	
BC ₂	164.77	± 3.53		173.43	± 3.22		154.37	± 2.49		157.37	± 3.45		158.82	± 4.19		162.48	± 4.54	
Over all mean	156.92	± 1.80		156.90	± 2.00		153.81	± 1.99		164.90	± 3.33		160.19	± 4.59		154.05	± 2.08	
C.D. (P=0.05)	5.68			6.32			6.28			10.52			14.47			6.55		

Similarly, Wilson *et al.* (1990) reported expression of over dominance for this trait. Such results were also in accordance with Sagar (1990), Wilson *et al.* (1990), Godasara *et al.* (2010), Jog *et al.* (2016), Suryawanshi *et al.* (2016), Jakhar *et al.* (2017) and Kumar *et al.* (2017). Singh *et al.* (2017^a) observed similar results for mean value of plant height of different generations within family. They recorded F_1 's higher than their respective parents in all three cross and F_2 's was lower than their respective F_1 's while backcross generations exceeded the mean value of parental mean value.

4.2.3 Number of effective tiller per plant

In crop improvement, effective tiller are important contributing trait for the seed yield. The highest mean for number of effective tillers was recorded in female parent namely 1202 B (2.00) of cross 5 followed by male parent 15990 R (1.63) of cross 3. In crosses 1, 3, 4 and 5, F_1 was found significantly higher mean value of than their both parents indicated the over dominance for this trait while F_1 was found significantly intermediate mean value of their respective parents in cross 2 and 6 indicated the partial dominance for this trait. Mean value of F_2 generations recorded significantly higher than their respective F_1 's which indicated the inbreeding depression. In cross 1 and 4, mean value of BC_1 was recorded significantly higher than their respective recurrent parent but at par with BC_2 .

For number of tillers similar results were also observed by Godasara *et al.* (2010), Suryawanshi *et al.* (2016), Jakhar *et al.* (2017), Kumar *et al.* (2017^a) and Singh *et al.* (2017^a).

4.2.4 Earhead length (cm)

Among parents, female parent 1202 B in cross 5 (25.97 cm) and male parent in cross 1 (23.69 cm) was recorded maximum earhead length and female parent 01555 B in cross 3 (18.03 cm) and male parent 16066 R in cross 6 (18.57 cm) was recorded minimum earhead length. Female parent of cross 4 was significantly higher than each other but at par with F_1 , BC_1 and BC_2 . Female parent of cross 5 was significantly higher than each other but at par with F_2 and BC_1 . Mean of F_1 in cross 1, 2 and 4 was found between mean of both parents indicated partial dominance while in cross 3 F_1 was higher and cross 4 and 5 was lower than both parents suggested the presence of over dominance for this trait. The F_2 of cross 5 and 6 recorded more ear head length and F_2 of other crosses possessed lower ear head length than their respective hybrid indicating presence of inbreeding depression. BC_2 was possessed significantly higher and lower mean value than their respective recurrent parent P_2 in cross 3 and cross 6, respectively.

Singh *et al.* (1974) reported influence of partial dominance for inheritance of this character. similarly, such results for variation in mean value of different generations within family also

recorded by Godasara *et al.* (2010), Jog *et al.* (2016), Suryawanshi *et al.* (2016), Jakhar *et al.* (2017), Kumar *et al.* (2017^a), Singh *et al.* (2017^a) and Goah *et al.* (2020).

4.2.5 Earhead girth (mm)

Ear head girth was recorded the highest by female parent 05888 B (26.63 mm) and male parent 15550 R (26.39 mm) while it was minimum for female parent 01555 B (22.87 mm) and male parent 16317 R (24.00 mm). Female parent 05888 B of cross 1 was found significantly higher but at par with all other generations. The F_1 was significantly exhibited higher and lower ear head girth than both of the parents in cross 4 and 6, respectively indicating over dominance effect for ear head girth. Mean of F_1 and BC_1 was significantly superior but at par with all other generations in cross 6 and cross 5, respectively. Mean of BC_1 was significantly superior but at par with F_1 and F_2 in cross 2 as well as F_2 and BC_2 in cross 3. Mean value of BC_2 was significantly higher than their respective recurrent parent in cross 5 and lower than recurrent parent in cross 2 and cross 3 for ear head girth.

Godasara *et al.* (2010) and Suryawanshi *et al.* (2016) also found results in accordance with present results. Goah *et al.* (2020) observed similar results for earhead girth that mean value of F_2 's was lower than their respective hybrid.

4.2.6 Days to maturity

Similar to days to flowering, for days to maturity earliness also considered desirable. Among the parents, the mean value of 05888 B in cross 1 recorded earliest with 76.37 days followed by 1202 B in cross 5 with 76.43 days. The highest mean value for days to maturity was observed in female parent of cross 6 named 05888 B (82.33 days) followed by 16317 R (82.03 days) in cross 2. The F_1 of all the six crosses exhibited lower mean value than both of their parents indicating over dominance for early maturity. The F_1 of cross 1 recorded the lowest mean (75.80) followed by cross 3 (76.50). The mean value of F_2 's in all six crosses observed significantly higher than their respective F_1 's showed inbreeding depression.

Backcross generations of all the crosses were shifted towards to their recurrent parent. BC_1 of all the crosses exhibited lower days to maturity than their respective recurrent parents except cross 4 and 5. While in BC_2 of all the crosses exhibited higher days to maturity than their respective recurrent parents.

For days to maturity, similar results for significant difference for mean value of different generation within family also supported by Wilson *et al.* (1990), Godasara *et al.* (2010), Jog *et al.* (2016), Jakhar *et al.* (2017), Kumar *et al.* (2017^b) and Singh *et al.* (2017^a).

Table 4.2.2: *Per se* performance of six generations for number of effective tiller per plant and earhead length in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)			Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Number of effective tiller per plant																		
Generations	Mean		SE	Mean		SE	Mean		SE	Mean		SE	Mean		SE	Mean		SE
P ₁	1.17	±	0.07	1.17	±	0.06	1.47	±	0.10	1.50	±	0.09	2.00	±	0.31	1.40	±	0.09
P ₂	1.20	±	0.07	1.40	±	0.12	1.63	±	0.12	1.57	±	0.14	1.57	±	0.10	1.50	±	0.09
F ₁	1.30	±	0.08	1.23	±	0.09	1.93	±	0.13	1.40	±	0.09	1.50	±	0.10	1.47	±	0.11
F ₂	1.44	±	0.05	1.55	±	0.08	1.98	±	0.12	1.98	±	0.11	1.69	±	0.08	1.83	±	0.08
BC ₁	1.73	±	0.11	1.58	±	0.10	2.03	±	0.13	2.20	±	0.16	1.72	±	0.10	1.93	±	0.14
BC ₂	1.63	±	0.12	1.87	±	0.12	1.90	±	0.14	2.12	±	0.15	1.83	±	0.12	2.07	±	0.15
Over all mean	1.41	±	0.05	1.47	±	0.06	1.82	±	0.06	1.79	±	0.07	1.71	±	0.07	1.7	±	0.10
C.D. (P=0.05)	0.16			0.20			0.21			0.22			0.23			0.33		
Earhead length (cm)																		
Generations	Mean		SE	Mean		SE	Mean		SE	Mean		SE	Mean		SE	Mean		SE
P ₁	19.01	±	0.74	23.21	±	0.52	18.03	±	0.56	24.40	±	0.81	25.97	±	0.93	19.27	±	0.60
P ₂	23.69	±	0.91	20.12	±	0.56	19.86	±	0.49	20.97	±	0.56	21.58	±	0.55	18.57	±	0.82
F ₁	25.01	±	0.82	23.68	±	0.77	20.12	±	0.67	23.21	±	0.49	20.67	±	0.76	17.26	±	0.50
F ₂	24.33	±	0.48	23.19	±	0.45	19.87	±	0.40	21.66	±	0.63	24.74	±	0.50	22.01	±	0.44
BC ₁	24.82	±	0.57	22.16	±	0.57	19.60	±	0.43	23.96	±	0.80	24.79	±	0.70	23.06	±	0.57
BC ₂	24.96	±	0.88	23.17	±	0.62	20.18	±	0.72	23.64	±	0.58	23.63	±	0.99	24.86	±	0.97
Over all mean	23.64	±	0.59	22.59	±	0.77	19.60	±	0.38	22.97	±	0.70	23.56	±	0.59	20.83	±	0.69
C.D. (P=0.05)	1.86			2.44			1.22			2.21			1.87			2.20		

Table 4.2.3: *Per se* performance of six generations for earhead girth and days to maturity in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)			Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Earhead girth (mm)																		
Generations	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE				
P ₁	26.18	± 0.80	25.28	± 0.64	22.87	± 0.77	25.05	± 0.52	24.65	± 0.47	26.63	± 0.51						
P ₂	25.17	± 0.40	26.07	± 0.79	24.66	± 0.37	26.39	± 0.70	24.00	± 0.51	25.86	± 0.55						
F ₁	25.62	± 0.86	28.86	± 0.51	23.81	± 0.68	28.93	± 0.56	25.14	± 0.51	26.91	± 0.56						
F ₂	25.57	± 0.39	27.71	± 0.33	26.26	± 0.61	25.37	± 0.48	24.87	± 0.39	26.61	± 0.34						
BC ₁	23.55	± 0.50	29.33	± 0.47	27.94	± 0.77	26.25	± 0.52	25.78	± 0.45	26.60	± 0.64						
BC ₂	25.75	± 0.50	27.32	± 0.49	26.62	± 0.74	26.21	± 0.66	24.54	± 0.44	25.55	± 0.52						
Over all mean	25.31	± 0.94	27.43	± 0.54	25.35	± 0.67	26.36	± 0.54	24.83	± 0.60	26.35	± 0.45						
C.D. (P=0.05)	2.98		1.70		2.12		1.71		1.90		1.44							
Days to maturity																		
Generations	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE				
P ₁	76.37	± 0.45	82.10	± 0.62	81.67	± 0.58	76.57	± 0.45	76.43	± 0.50	82.33	± 0.63						
P ₂	76.50	± 0.55	82.03	± 0.53	77.40	± 0.65	77.57	± 0.60	77.27	± 0.64	81.83	± 0.62						
F ₁	75.80	± 0.48	82.27	± 0.48	76.50	± 0.55	76.90	± 0.61	77.00	± 0.62	76.87	± 0.67						
F ₂	75.88	± 0.31	81.77	± 0.39	76.97	± 0.44	81.64	± 0.38	78.14	± 0.51	78.28	± 0.56						
BC ₁	75.82	± 0.37	80.68	± 0.58	76.98	± 0.55	81.12	± 0.49	82.50	± 0.49	78.23	± 0.64						
BC ₂	77.72	± 0.50	82.65	± 0.33	81.85	± 0.44	78.90	± 0.61	79.02	± 0.75	81.95	± 0.59						
Over all mean	76.35	± 0.64	81.92	± 0.54	78.56	± 0.47	78.78	± 0.63	78.39	± 0.59	79.91	± 0.59						
C.D. (P=0.05)	2.02		1.70		1.48		1.99		1.86		1.86							

4.2.7 Test weight (g)

Among parents, the highest test weight was observed in 16066 R (10.75 g) followed by 16317 R (10.69 g) and 15550 R (10.50 g), while the lowest value observed in 05888 B (8.39 g). The F_1 was exhibited higher average value than both of their parent in cross 2 and cross 3 indicating presence of over dominance while F_1 of cross 5 and 6 exhibited average value in between of their parents indicating partial dominance for test weight. The F_2 of all the crosses recorded lower test weight than their respective hybrids indicating inbreeding depression for this trait. Backcross generation BC_1 was found significantly higher than recurrent parent in cross 1, 3, 4 and 6 but at par with P_2 and BC_2 of cross 1, P_1 and F_1 of cross 3, P_2 and BC_2 of cross 4 as well as P_2 and F_1 of cross 6 whereas BC_2 was also found significantly superior than respective recurrent parent in cross 2, 3 and 5 but at par with F_1 and BC_1 of cross 2 and F_1 of cross 5.

Godasara *et al.* (2010), Jog *et al.* (2016), Suryawanshi *et al.* (2016) and Kumar *et al.* (2017^a) also supported the finding of significant difference between generations with family of cross.

4.2.8 Grain yield per plant (g)

Grain yield is the dependent and complex character so increasing yield is challenging task. Understanding the expression pattern of genes can be rewarding. Among all the parents, the highest grain yield was recorded in 15001 R (33.42 g) followed by 02889 B (29.09 g) and 15990 R (27.01 g) while it was recorded minimum in 01555 B (17.22 g). The highest average value was observed in F_1 of cross 1 (40.33 g) followed by cross 3 (27.15 g), cross 4 (25.15 g) and cross 2 (25.13 g). The F_1 of all the crosses recorded significantly higher mean value except for cross 2 than both the parents indicating over dominance while cross 2 suggested presence of partial dominance for higher grain yield per plant. The F_2 generation of all the crosses recorded higher mean value except for cross 1 than their respective hybrids but F_2 was at par with BC_1 in cross 4 indicating inbreeding depression. Average value of backcross generations BC_1 and BC_2 recorded significantly higher in all the crosses than their respective recurrent parent except for cross 1 (05888 B $\times$ 15001 R).

Similarly, Singh *et al.* (1974) reported similar over dominant gene action in expression of this trait. Godasara *et al.* (2010), Suryawanshi *et al.* (2016), Jakhar *et al.* (2017), Kumar *et al.* (2017^a) and Goah *et al.* (2020) recorded results in agreement with present results for grain yield per plant for different generations.

Table 4.2.4: *Per se* performance of six generations for test weight and grain yield per plant in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)			Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Test weight (g)																		
Generations	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE		
P ₁	8.39	± 0.07	8.99	± 0.19	9.93	± 0.28	10.34	± 0.34	10.00	± 0.27	9.68	± 0.24						
P ₂	9.26	± 0.16	9.40	± 0.19	9.63	± 0.27	10.50	± 0.32	10.64	± 0.35	10.76	± 0.32						
F ₁	8.99	± 0.13	9.60	± 0.35	9.97	± 0.27	10.33	± 0.27	10.51	± 0.27	10.61	± 0.29						
F ₂	8.98	± 0.15	9.38	± 0.12	9.88	± 0.15	9.89	± 0.16	10.07	± 0.17	9.98	± 0.19						
BC ₁	9.54	± 0.17	9.83	± 0.18	10.29	± 0.22	10.61	± 0.22	10.10	± 0.29	11.16	± 0.27						
BC ₂	9.50	± 0.18	9.94	± 0.17	10.29	± 0.22	10.51	± 0.26	10.70	± 0.26	10.57	± 0.26						
Over all mean	9.11	± 0.09	9.52	± 0.14	9.99	± 0.11	10.36	± 0.07	10.33	± 0.14	10.46	± 0.18						
C.D. (P=0.05)	0.28		0.46		0.37		0.23		0.45		0.57							
Grain yield per plant (g)																		
Generations	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE		
P ₁	26.30	± 0.28	29.09	± 0.59	17.22	± 0.48	23.47	± 0.28	22.27	± 0.37	22.36	± 0.39						
P ₂	33.42	± 0.32	24.81	± 0.43	27.01	± 0.40	20.13	± 0.27	20.16	± 0.35	20.82	± 0.29						
F ₁	40.33	± 0.33	25.13	± 0.41	27.15	± 0.54	25.15	± 0.30	24.33	± 0.42	25.06	± 0.34						
F ₂	28.85	± 0.71	27.09	± 0.71	28.42	± 0.69	31.35	± 0.70	30.16	± 0.56	32.71	± 0.65						
BC ₁	28.06	± 1.04	29.38	± 1.13	30.17	± 1.27	30.59	± 1.02	32.87	± 1.00	29.44	± 0.87						
BC ₂	28.00	± 1.06	30.32	± 1.06	30.27	± 1.19	28.93	± 0.54	31.89	± 0.94	29.63	± 0.66						
Over all mean	30.83	± 0.72	27.63	± 0.71	26.70	± 0.85	26.60	± 0.75	26.94	± 0.80	26.66	± 0.81						
C.D. (P=0.05)	2.27		2.26		2.69		2.36		2.53		2.56							

4.2.9 Harvest index (%)

Harvest index is the good presentation of ratio of biological yield and grain yield. Optimum value of harvest index indicated the good grain as well as fodder yield which is very beneficial. Highest mean value among parents for harvest index (%) was observed for 15990 R (44.93 %) in cross 3 followed 05888 B (43.57 %) in cross 1 and 01555 B (43.15 %) for cross 3. The F_1 of cross 3 had maximum harvest index (47.01 %) followed by cross 1 (46.51 %) and cross 4 (42.42 %). Male parent was found significantly higher in cross 2 and cross 4 than all other generations but at par with F_1 of cross 4. The F_1 was recorded higher harvest index than both the parents in cross 1, 3 and 5 indicating over dominance effect. The F_2 of all crosses recorded lower harvest index than their respective hybrids except for cross 6 indicating inbreeding depression for this trait. Back cross generation of all crosses showed lower harvest index than their respective recurrent parents for this trait except for BC_1 of cross 6 and BC_2 of cross 1. Kumar *et al.* (2017^a) also referred similar results for significant variation in different generations.

4.2.10 Carbohydrate (g/100 g)

The highest carbohydrate content was observed for 02889 B (68.96 g/100 g) in cross 2 followed by 1202 B (66.32 g/100 g) in cross 5. Mean of female parent of cross 2, 4 and 5 was significantly superior than all other generations. Mean of male parent of cross 1 and cross 3 was found significantly higher than other generations but male parent of cross 3 was at par with P_1 , F_1 and BC_2 . Average value of F_1 was lower in all crosses than their respective parents except for cross 6 suggesting influence of over dominance. F_2 mean value was significantly lower than their respective F_1 but at par with male parent in cross 6 indicating inbreeding depression and the presence of additive gene action. Average value of backcross generation was lower than their respective recurrent parent except for BC_1 of cross 1 and BC_2 of cross 2 and 4.

4.2.11 Tannin (mg/100 g)

Tannins (commonly known as tannic acid) are polyphenols which are water soluble. It is known that foods with rich in tannin content are considered to be of low nutritional value. The lowest mean value was observed in 15990 R (100.51 mg/100 g) in cross 3, followed by 98222 B (107.56 mg/100 g) in cross 4. Female parent of cross 4 and male parent of cross 3 were found significantly lower than all other generations. In case of cross 2 and cross 6, F_1 was significantly lower than both parents which suggested the expression of over dominance. The F_2 was found lower than their respective F_1 's in crosses 1, 4 and 5 while it was higher in crosses 2, 3 and 6 than their respective F_1 's. The mean value of BC_1 of cross 5 and BC_2 of

Table 4.2.5: *Per se* performance of six generations for harvest index and carbohydrate in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)			Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Harvest index (%)																		
Generations	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE		
P ₁	43.57	± 0.28	41.98	± 0.39	43.15	± 0.35	38.06	± 0.26	36.51	± 0.41	35.98	± 0.50						
P ₂	41.02	± 0.44	42.45	± 0.39	44.93	± 0.42	42.81	± 0.39	36.31	± 0.31	39.50	± 0.46						
F ₁	46.51	± 0.42	41.85	± 0.46	47.01	± 0.46	42.42	± 0.63	38.45	± 0.56	38.57	± 0.40						
F ₂	43.56	± 0.57	41.06	± 0.45	40.94	± 0.60	37.44	± 0.50	36.10	± 0.51	40.03	± 0.52						
BC ₁	42.44	± 0.57	41.89	± 0.55	39.52	± 0.88	35.88	± 0.77	34.32	± 0.73	38.72	± 0.84						
BC ₂	43.05	± 0.59	34.71	± 0.66	35.96	± 0.72	36.63	± 0.74	35.03	± 0.57	39.19	± 0.62						
Over all mean	43.36	± 0.44	40.66	± 0.49	41.91	± 0.54	38.87	± 0.70	36.11	± 0.53	38.66	± 0.33						
C.D. (P=0.05)	1.38		1.55		1.71		2.20		1.68		1.06							
Carbohydrate (g/100g)																		
Generations	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE		
P ₁	47.64	± 0.32	68.96	± 0.35	62.83	± 0.39	59.23	± 0.35	66.32	± 0.53	48.92	± 0.35						
P ₂	63.16	± 0.60	60.07	± 0.50	63.94	± 0.63	51.71	± 0.34	60.04	± 0.34	55.88	± 0.33						
F ₁	37.14	± 0.37	61.93	± 0.36	62.34	± 0.52	49.47	± 0.36	55.19	± 0.22	56.05	± 0.49						
F ₂	54.34	± 0.64	57.07	± 0.65	58.39	± 0.61	53.28	± 0.66	60.40	± 0.53	57.22	± 0.53						
BC ₁	56.66	± 0.66	58.49	± 0.69	52.75	± 1.01	59.12	± 0.76	62.20	± 0.93	44.09	± 1.06						
BC ₂	52.54	± 0.47	63.56	± 0.61	61.39	± 1.03	53.56	± 0.76	58.89	± 0.65	47.76	± 0.55						
Over all mean	51.91	± 0.54	61.68	± 0.97	60.27	± 1.05	54.39	± 1.21	60.50	± 1.23	51.65	± 1.07						
C.D. (P=0.05)	1.72		3.07		3.31		3.81		3.88		3.37							

cross 1 was significantly lower than all other generations but BC₁ of cross 5 was at par with F₂ generation.

4.2.12 Iron content (mg/kg)

Maximum iron content among parents was found in 16066 R (89.34 mg/kg) in cross 6, followed by 05888 B (85.58 mg/kg) in same cross and 05888 B (85.43 mg/kg) in cross 1 while the lowest was recorded in male parent of cross 4 namely 15550 R (59.28 mg/kg). Female parent of cross 1, 2, 3 and 5 was significantly higher than other generations while male parent of cross 6 was significantly higher than other generations. The mean value of F₁ was lower than respective parents in cross 2, 4, 5 and 6 which suggest the over dominance except cross 1 and 3 in which F₁ hybrid mean value was in between two parents suggested the partial dominance. Average value of F₂ generations lowered than their respective F₁ hybrids which indicated the influence of non-additive gene action except cross 2 and 5 in which it is higher than mean of F₁ generation, so it suggested the additive gene action. Backcross generation BC₁ was significantly lower than their recurrent parent in cross 4. Goah *et al.* (2020) also observed similar results of significant variation between mean values of generations within family.

4.2.13 Zinc content (mg/kg)

Highest mean value was observed in 02889 B (51.29 mg/kg) in cross 2, while lowest mean value was observed in 16317 R (33.01 mg/kg) in cross 2. Female and male parent of cross 2 and cross 1 was found significantly superior than all other generations but male parent of cross 1 was found at par with female parent. F₁ hybrid mean value of zinc content was observed higher than their respective parents in crosses 3, 4 and 6 as well as lower than their respective parents in cross 1 and 5 which explains the expression of over dominance while in cross 2, it was in between respective parents suggested the influence of partial dominance. In all crosses, mean value of F₂ generations for zinc content was lowered than their respective F₁ hybrid except for cross 3. BC₂ of cross 5 was found significantly higher but at par with P₁ and F₂. Goah *et al.* (2020) also found similar results for zinc content.

4.2.14 Oil content (%)

Maximum mean value of oil content among parents was observed in 01555 B (5.56 %) in cross 3 as well as minimum mean value observed in 15990 R in same genotype cross 3 (4.95 %). The mean value of F₁ hybrid was found significantly superior to their respective parents in all crosses (except for cross 1 and 5) but at par with other generations of cross 2, 4 and 6 which suggested presence of over dominance. Average value of F₂ was observed higher in all crosses except for crosses 1 and 5 than the respective hybrid. Average of BC₁ and BC₂ was observed higher than their respective recurrent parent P₁ and P₂ of cross 5 and cross 1, respectively.

Table 4.2.6: *Per se* performance of six generations for tannin and Iron content in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)			Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Tannin (mg/100g)																		
Generations	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE				
P ₁	194.56	± 0.50	120.69	± 0.49	125.50	± 0.46	107.56	± 0.68	160.07	± 0.56	200.87	± 0.69						
P ₂	211.14	± 0.45	121.23	± 0.45	100.51	± 0.73	194.58	± 0.53	129.71	± 0.61	189.98	± 0.55						
F ₁	201.93	± 0.57	105.49	± 0.62	122.51	± 0.64	194.91	± 0.69	194.69	± 0.70	101.99	± 0.70						
F ₂	192.67	± 2.71	202.32	± 1.25	197.80	± 1.26	181.30	± 2.70	121.33	± 1.63	116.48	± 1.06						
BC ₁	201.69	± 5.14	162.94	± 0.83	208.03	± 1.60	190.10	± 1.79	120.51	± 1.13	118.75	± 2.03						
BC ₂	117.61	± 4.86	125.77	± 1.22	207.56	± 1.64	182.99	± 1.14	128.48	± 4.13	118.87	± 1.18						
Over all mean	186.60	± 2.58	139.74	± 1.24	160.31	± 1.49	175.24	± 1.46	142.46	± 1.05	141.15	± 1.41						
C.D. (P=0.05)	8.14		3.93		4.70		4.60		3.33		4.45							
Iron content (mg/kg)																		
Generations	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE						
P ₁	85.43	± 0.22	77.09	± 0.25	84.66	± 0.36	64.14	± 0.52	82.70	± 0.23	85.58	± 0.28						
P ₂	64.27	± 0.14	75.51	± 0.26	65.98	± 0.25	59.28	± 0.40	77.27	± 0.30	89.34	± 0.45						
F ₁	66.01	± 0.16	64.86	± 0.42	67.75	± 0.39	45.01	± 0.43	50.58	± 0.39	73.11	± 0.26						
F ₂	35.79	± 0.10	65.65	± 0.25	49.00	± 0.68	30.26	± 0.86	56.71	± 0.28	72.31	± 0.33						
BC ₁	67.00	± 0.44	52.32	± 0.87	47.59	± 0.90	66.33	± 0.67	51.63	± 0.67	64.41	± 0.50						
BC ₂	48.97	± 0.37	53.74	± 0.73	38.95	± 0.51	60.54	± 0.61	54.35	± 0.64	69.37	± 0.31						
Over all mean	61.25	± 0.86	64.86	± 0.76	58.98	± 0.38	54.25	± 1.01	62.20	± 0.43	75.68	± 0.72						
C.D. (P=0.05)	2.72		2.40		1.21		3.21		1.37		2.28							

Table 4.2.7: *Per se* performance of six generations for zinc content and oil content in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)			Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Zinc content (mg/kg)																		
Generations	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE		
P ₁	44.13	± 0.26	51.29	± 0.22	47.08	± 0.33	35.81	± 0.17	40.04	± 0.24	41.82	± 0.34						
P ₂	44.78	± 0.28	33.01	± 0.25	42.20	± 0.27	35.97	± 0.20	38.95	± 0.33	41.61	± 0.32						
F ₁	41.22	± 0.20	41.38	± 0.26	51.04	± 0.31	43.87	± 0.22	35.01	± 0.23	43.81	± 0.32						
F ₂	39.54	± 0.25	40.82	± 0.20	40.43	± 0.29	40.58	± 0.33	40.10	± 0.34	41.94	± 0.33						
BC ₁	40.63	± 0.23	39.95	± 0.24	40.43	± 0.37	34.49	± 0.51	35.89	± 0.58	42.05	± 0.41						
BC ₂	40.93	± 0.50	39.21	± 0.32	41.29	± 0.33	40.04	± 0.32	40.79	± 0.51	38.70	± 0.42						
Over all mean	41.87	± 0.30	40.94	± 0.20	43.74	± 0.37	38.45	± 0.25	38.46	± 0.54	41.65	± 0.60						
C.D. (P=0.05)	0.95		0.63		1.16		0.80		1.72		1.90							
Oil content (%)																		
Generations	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE		
P ₁	5.38	± 0.06	5.48	± 0.24	5.56	± 0.17	4.96	± 0.15	5.01	± 0.20	5.05	± 0.19						
P ₂	5.32	± 0.06	5.14	± 0.16	4.95	± 0.19	5.16	± 0.19	4.95	± 0.14	5.33	± 0.14						
F ₁	5.25	± 0.19	5.55	± 0.18	5.66	± 0.19	5.63	± 0.18	5.16	± 0.18	5.60	± 0.13						
F ₂	5.84	± 0.14	5.41	± 0.14	5.39	± 0.11	5.23	± 0.12	5.47	± 0.12	5.51	± 0.12						
BC ₁	5.95	± 0.20	5.29	± 0.18	5.18	± 0.19	5.31	± 0.15	5.70	± 0.18	5.03	± 0.17						
BC ₂	6.32	± 0.24	5.49	± 0.17	5.50	± 0.17	5.44	± 0.15	5.49	± 0.17	5.13	± 0.18						
Over all mean	5.68	± 0.24	5.39	± 0.23	5.37	± 0.21	5.28	± 0.21	5.29	± 0.21	5.27	± 0.24						
C.D. (P=0.05)	0.76		0.73		0.67		0.69		0.67		0.75							

4.2.15 Protein content (%)

Protein is essential for regular metabolic activities. The highest and lowest mean value was observed for 05888 B (11.96 %) in cross 1 and 15990 R (4.51 %) of cross 3. Female parent of cross 1, 3, 4 and 6 was found significantly superior than all other generations. F_1 hybrid mean value was found intermediate of two parents suggested the partial dominance in all crosses. Average of F_2 generation observed higher than respective F_1 except for crosses 1 and 4, which indicated inbreeding depression. BC_1 of cross 2 and BC_2 of cross 5 were found significantly superior than its respective recurrent parent P_1 and P_2 , respectively.

4.3 Scaling tests and estimation of gene effects

The basic set of six generation means for each of the four crosses were used to estimate various gene effects for grain yield and other characters under present study. Individual scaling tests A, B, C and D of Mather (1949) and joint scaling test proposed by Cavalli (1952) were employed to detect the presence of epistasis.

The weighted least square estimates of additive (d) and dominance (h) gene effects were obtained from the simple additive-dominance model (three parameter model) of Cavalli (1952). Wherever this simple model failed to be adequate to explain the variation in generation means, the interaction parameters models were tried. The six parameters perfect fit solution advocated by Hayman (1958) was used to estimate the interaction effects (i), (j) and (l) along with main effects (m), (d) and (h). Since, all the six generation means were used for parameter estimation, the fit of the six parameter model could not be tested by the chi-square test. The significance of the parameters was tested against their corresponding standard errors. Whenever, any non-significant interaction parameter(s) occurred in the six parameter model, four or five parameter models were tried as best fitting model after removal of such interaction effect(s) to estimate the magnitude of the remaining components. The results are presented in Table 4.3.1 to Table 4.3.15 pertaining to estimates of scaling tests for testing adequacy of additive-dominance model, estimates of different genetic parameters and weighted least square procedure for best fitting four, five or six parameter model for different characters of four crosses in pearl millet.

Generation mean analysis provides information about the type of epistasis, which depends on the sign of two component only, viz., h and l. Those crosses in which (h) and (l) have similar signs (either positive or negative) that indicates the presence of complementary epistasis, and those in which (h) and (l) have opposite signs reveals duplicate epistasis (Singh and Narayanan, 2013). The character-wise and cross-wise results of genetic analysis are described in the subsequent paragraphs.

Table 4.2.8: *Per se* performance of six generations for protein content in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)			Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Protein content (%)																		
Generations	Mean	SE		Mean	SE		Mean	SE		Mean	SE		Mean	SE		Mean	SE	
P ₁	11.96	±	0.29	8.00	±	0.28	9.34	±	0.26	10.05	±	0.12	7.05	±	0.15	11.43	±	0.31
P ₂	6.79	±	0.27	5.57	±	0.29	4.51	±	0.29	8.75	±	0.11	4.61	±	0.16	5.13	±	0.18
F ₁	10.74	±	0.21	6.12	±	0.15	8.34	±	0.30	9.71	±	0.12	6.10	±	0.19	7.26	±	0.16
F ₂	9.93	±	0.22	7.85	±	0.16	8.99	±	0.24	8.78	±	0.17	8.35	±	0.20	9.45	±	0.16
BC ₁	9.26	±	0.36	8.41	±	0.21	8.49	±	0.29	7.48	±	0.37	8.54	±	0.33	7.51	±	0.29
BC ₂	9.26	±	0.28	7.43	±	0.30	8.10	±	0.26	8.60	±	0.28	8.68	±	0.40	8.78	±	0.25
Over all mean	9.66	±	0.27	7.23	±	0.23	7.96	±	0.25	8.89	±	0.30	7.21	±	0.31	8.25	±	0.25
C.D. (P=0.05)	0.87			0.74			0.79			0.95			0.97			0.81		

4.3.1 Days to flowering

The results obtained for days to flowering are depicted in Table 4.3.1. The scaling tests A, B, C and D were significant in cross 1, cross 3 and cross 6. Scaling tests B, C and D in cross 2, while A, C and D in cross 4 and cross 5. For all the crosses significance of any scaling test indicated the presence of digenic interaction which implied that the additive-dominance model was inadequate for all crosses. Simple scaling tests as well as χ^2 value of joint scaling test were significant for all the families revealed inadequacy for additive dominance model but there is some negligible amount of gene interaction was present so six parameter model (Hayman, 1958) was found adequate for cross 2 only.

According to six parameter model (Hayman, 1958), additive (d) gene effect was significant and positive in cross 1, 5 and 6. The dominance (h) effect was significant and negative in cross 2 and cross 4. The additive $\times$ additive (i) type of interaction was found significant and negative in cross 2 and cross 4, whereas it was positively significant for crosses 1, 3, 5 and 6. The additive $\times$ dominance (j) type of interaction was found significant and negative in cross 3 and cross 4 but significant and positive in cross 2, 5 and 6, while it was non-significant in cross 1. The dominance $\times$ dominance (l) type of interaction was found significant and negative in cross 1, 3, 5 and 6, while it was significant and positive in cross 2 and cross 4.

On estimation of gene effects on best fitting model, three parameter (additive-dominance) model gets satisfied for cross 4 with significant values of all the components viz., 'm', (d) and (h) for days to flowering. While five parameter model was found sufficient for cross 1, 3 and 5 whereas six parameter model was best fitted for cross 2 (Hayman, 1958) and cross 4. It was found that additive (d) effect was found significant for all crosses as negative significant additive effect was observed for cross 3 and 4 whereas positive significant was recorded for cross 1 and 5, while dominance (h) effect was negative significant for cross 4 while positive significant in crosses 1, 3, 4 and 5. The additive $\times$ additive (i) and additive $\times$ dominance (j) type of interaction was found negative significant for cross 4 only. The dominance $\times$ dominance (l) type of interaction was found negative significant for cross 1 and 6. The significant opposite signs associated with dominance (h) and dominance $\times$ dominance (l) component in cross 1, 4 and 6 suggested duplicate type of epistasis and significant similar signs associated with dominance (h) and dominance $\times$ dominance (l) component in cross 3 and 5 suggested complementary type of epistasis for this cross.

The genetic of this character varied from cross to cross. In six parameter model, dominant gene action was predominant in all crosses except cross 1 which suggest additive as well as non-additive gene action was responsible for inheritance of this trait. Similarly observing the

results of best fitting model, it suggested similar result of influence of additive as well as non-additive gene action with predominance of dominant gene action in all crosses except cross 2. Presence of additive as well as non-additive gene actions indicated that simple selection would not be beneficial in improving this trait, thus population improvement maintaining adequate population size could be used. Also in majority of crosses, influence of dominant gene action observed though heterosis breeding can be implemented to get desirable hybrid.

Similarly, preponderance of non-additive variance also observed by Bhandari *et al.* (2007), Godasara *et al.* (2010), Bhadaliya *et al.* (2012), Kumar *et al.* (2013), Kumar *et al.* (2017^a) and Goah *et al.* (2020) while, all three type of interactions with duplicate gene action was observed by Jog *et al.* (2016) and Suryawanshi *et al.* (2016) but Patel *et al.* (2021) recorded the opposite result with same trait as influence of additive gene effect.

4.3.2 Plant height (cm)

Based on individual scaling test, the failure of additive-dominance model was observed for this trait in four crosses due to significance of all the scaling tests *viz.*, A, B and C in crosses 1, 2 and 6; B and C in cross 4 and the C in cross 2. Simple scaling tests as well as χ^2 value of joint scaling test were significant for all the families revealed inadequacy for additive dominance model but there is some negligible amount of gene interaction was present so six parameter model (Hayman, 1958) was found adequate for cross 3 and 5 only.

According to six parameter model (Hayman, 1958), additive (d) effect was significant and negative in cross 4 only while it was non significant in other crosses. While, the dominance (h) effect was significant and positive in cross 1 and 4; significant and negative in cross 3 and non significant in other crosses. The additive $\times$ additive (i) type of interaction was found non significant for all six crosses. The additive $\times$ dominance (j) type of interaction was found significant and positive in cross 3 and 4; significant and negative in cross 2. The dominance $\times$ dominance (l) type of interaction was found significant and negative in cross 1, 2 and 6.

Thus, the best fit model for five parameter was adequate in cross 2; four parameter was adequate in cross 1, 4 and 6 while six parameter (Hayman, 1958) was adequate in cross 3 and 5. Estimates of additive (d) gene effect were found significant and negative in the cross 3 and 4 as well as significant and positive in the cross 1. While, the estimates of dominance (h) gene effect were found significant and positive in the crosses 1, 2 and 4. The additive $\times$ dominance

Table 4.3.1 Estimation of scaling tests and gene effects for days to flowering in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)	Cross 2 (02889 B × 16317 R)	Cross 3 (01555 B × 15990 R)
Days to flowering			
Scaling tests (Mather, 1949)			
A	9.10** ± 1.54	-1.43 ± 1.35	-8.07** ± 1.23
B	6.87** ± 1.69	-6.67** ± 1.86	4.60** ± 1.11
C	10.03** ± 2.10	5.00* ± 2.34	-31.27** ± 1.72
D	-2.97* ± 1.35	6.55** ± 1.51	13.90** ± 0.90
Gene effects in different models			
Three parameter model (Cavali, 1952)			
m	50.45** ± 0.25	53.94** ± 0.27	50.16** ± 0.33
d	1.08** ± 0.26	-1.26** ± 0.27	-3.40** ± 0.33
h	-1.86** ± 0.54	-1.34** ± 0.49	1.09 ± 0.39
χ^2	55.73**	20.71**	465.85**
Six parameter model (Hayman, 1958)			
m	50.64** ± 0.43	54.59** ± 0.52	45.68** ± 0.31
d	2.18* ± 1.04	1.26 ± 1.08	-7.93** ± 0.66
h	2.40 ± 2.78	-14.38** ± 3.06	29.80** ± 1.91
i	5.93* ± 2.71	-13.10** ± 3.02	27.80** ± 1.81
j	1.11 ± 1.08	2.61* ± 1.11	-6.33** ± 0.77
l	-21.90** ± 4.68	21.20** ± 4.91	-24.33** ± 3.16
Best fitting model (Mather and Jinks, 1982)			
m	43.75** ± 2.72	-	23.19** ± 1.85
d	1.13** ± 0.26	-	-3.21** ± 0.33
h	24.94** ± 7.21	-	58.66** ± 4.82
i	6.13* ± 2.71	-	29.31** ± 1.80
j	-	-	-
l	-22.32** ± 4.67	-	27.35** ± 3.14
χ^2	1.06	-	67.72**
Types of epistasis	Duplicate	-	Complementary

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.1 Continue...

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Days to flowering									
Scaling tests (Mather, 1949)									
A	-7.57**	±	1.32	3.37**	±	1.27	7.43**	±	0.90
B	0.80	±	1.05	0.23	±	1.11	2.23*	±	1.11
C	8.93**	±	1.74	-20.73**	±	2.05	-16.37**	±	2.05
D	7.85**	±	0.93	-12.17**	±	0.97	-13.02**	±	1.00
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	53.91**	±	0.30	55.27**	±	0.36	54.69**	±	0.28
d	-1.55**	±	0.30	0.98**	±	0.34	0.72**	±	0.27
h	1.75**	±	0.58	-1.74*	±	0.67	1.48**	±	0.55
χ ²	85.07**			169.90**			217.18**		
Six parameter model (Hayman, 1958)									
m	56.60**	±	0.31	50.30**	±	0.37	50.74**	±	0.42
d	-5.11**	±	0.68	2.35**	±	0.62	2.16**	±	0.53
h	-14.10**	±	1.96	23.21**	±	2.07	27.10**	±	2.08
i	-15.70**	±	1.86	24.33**	±	1.95	26.03**	±	2.00
j	-4.18**	±	0.77	1.56*	±	0.74	2.60**	±	0.62
l	22.46**	±	3.26	-27.93**	±	3.22	-35.70**	±	2.97
Best fitting model (Mather and Jinks, 1982)									
m	69.26**	±	1.89	32.22**	±	1.98	28.26**	±	2.02
d	-0.93**	±	0.34	1.27**	±	0.34	-0.43	±	0.32
h	-36.56**	±	4.97	49.62**	±	4.92	62.80**	±	4.79
i	-15.70**	±	1.86	23.82**	±	1.93	26.03**	±	2.00
j	-8.36**	±	1.54	-	-		5.20**	±	1.25
l	22.46**	±	3.26	32.22**	±	3.18	-35.70**	±	2.97
χ ²	-			4.39**			-		
Types of epistasis	Duplicate			Complementary			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.2 Estimation of scaling tests and gene effects for plant height in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Plant height									
Scaling tests (Mather, 1949)									
A	35.93**	±	6.88	17.57*	±	7.04	24.60**	±	5.09
B	35.80**	±	7.24	47.00**	±	6.99	-12.90*	±	5.96
C	61.73**	±	8.61	66.13**	±	10.38	24.23**	±	8.49
D	-5.00	±	6.25	0.78	±	6.41	6.27	±	4.84
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	138.54**	±	1.06	146.29**	±	1.31	158.44**	±	1.48
d	9.98**	±	1.09	-0.33	±	1.34	-16.71**	±	1.52
h	31.84**	±	1.56	19.54**	±	2.44	-11.20**	±	2.35
χ ²	91.34**			74.92**			36.80**		
Six parameter model (Hayman, 1958)									
m	166.48**	±	2.00	166.50**	±	2.27	156.86**	±	1.76
d	8.43	±	4.80	-14.63**	±	4.52	-1.26	±	3.32
h	42.16**	±	12.61	13.01	±	13.07	-24.81*	±	9.98
i	10.00	±	12.51	-1.56	±	12.82	-12.53	±	9.69
j	0.06	±	4.93	-14.71**	±	4.74	18.75**	±	3.75
l	-81.73**	±	21.06	-63.00**	±	20.87	0.83	±	15.79
Best fitting model (Mather and Jinks, 1982)									
m	-220.49**	±	3.90	142.68**	±	1.40	-		-
d	24.65**	±	1.10	0.08	±	1.40	-		-
h	421.72**	±	4.37	79.93**	±	7.95	-		-
i	-		-	-		-	-		-
j	-		-	-29.44**	±	9.48	-		-
l	392.62**	±	4.10	-65.34**	±	8.14	-		-
χ ²	-			0.02			-		
Types of epistasis	Complementary			Duplicate			-		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.2 Continue....

Table 13.12 Continued...

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Plant height									
Scaling tests (Mather, 1949)									
A	-6.20	±	7.23	9.47	±	7.76	28.97**	±	6.40
B	-36.50**	±	7.84	13.23	±	8.99	26.13**	±	9.36
C	-49.20**	±	10.33	37.73**	±	11.07	52.70**	±	8.30
D	-3.25	±	6.35	7.52	±	7.16	-1.20	±	6.47
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	155.29**	±	1.57	158.06**	±	1.29	152.73**	±	1.18
d	-2.94	±	1.61	9.08**	±	1.30	-3.66**	±	1.22
h	23.84**	±	2.88	3.92	±	2.78	-2.30	±	2.08
χ ²	35.71**			12.56**			56.11**		
Six parameter model (Hayman, 1958)									
m	160.44**	±	2.11	166.15**	±	2.31	160.05**	±	1.78
d	9.40	±	4.75	7.16	±	5.46	-3.66	±	5.39
h	33.21*	±	13.05	-15.08	±	14.64	-2.28	±	13.11
i	6.50	±	12.71	-15.03	±	14.33	2.40	±	12.94
j	15.15**	±	5.05	-1.88	±	5.62	1.41	±	5.54
l	36.20	±	21.63	-7.66	±	24.49	-57.50*	±	23.12
Best fitting model (Mather and Jinks, 1982)									
m	155.71**	±	1.58	-	-		149.24	±	1.27
d	-4.45**	±	1.71	-	-		-4.97	±	1.23
h	23.16**	±	2.90	-	-		49.14	±	7.18
i	-	-		-	-		-	-	
j	26.53**	±	10.07	-	-		-	-	
l	-	-		-	-		-53.85	±	7.19
χ ²	28.78**			-			0.14		
Types of epistasis	-			-					

* and **, significant at 5% and 1% level of significance, respectively

(j) type of interaction was found significant and positive in cross 4; significant and negative in cross 2. The dominance $\times$ dominance (l) type of interaction was found positively significant and negatively significant in cross 1 and cross 2, respectively. The similar opposite sign of (h) and (l) estimates in cross 1 and cross 2 indicated the role of complimentary and duplicate type of epistasis for this trait, respectively.

Kumar *et al.* (2017^a) observed the same result for plant height with influence of dominant gene action as well as dominant $\times$ dominant epistasis gene action for inheritance of this trait. Mahadevappa (1968), Singh *et al.* (1974), Sagar (1990), Godasara *et al.* (2010) and Nandaniya *et al.* (2016) found that non-additive variance is responsible for inheritance of this trait. Bhadaliya *et al.* (2012), Kumar *et al.* (2013), Patel *et al.* (2014), Jog *et al.* (2016), Suryawanshi *et al.* (2016), Jakhar *et al.* (2017), Singh *et al.* (2017^a) and Goah *et al.* (2020) observed all three type of gene action with duplicate epistasis. Wilson *et al.* (1990), Bhandari *et al.* (2007) and Patel *et al.* (2021) observed additive gene action.

In best fitting model, the influence of dominant gene action as well as dominant $\times$ dominant (l) epistasis interaction collectively non-additive gene action in cross 1 and 2 suggested the heterosis breeding as well as recurrent selection for SCA can be very effective for improvement of this trait. But duplicate epistasis action was found in all crosses as it indicated that variability in segregating generation may be reduced thus which may hinder the selection.

4.3.3 Number of effective tiller per plant

The estimates of gene effects for number of effective tiller per plant were carried out and are tabulated as in Table 4.3.3. All the individual scaling tests A, B, C and D were found significant in cross 1; A, B, C in cross 2, 4 and 6; A in cross 3 and B in cross 5 while χ^2 value of joint scaling test were found non significant in cross 3 and 5 suggested adequacy of simple additive-dominance (Three parameter) model .

According to six parameter model (Hayman, 1958), additive (d) effect was non significant in all six crosses. While, the dominance (h) effect and additive $\times$ additive (i) type of interaction was significant and positive in cross 1 only, otherwise it was found non significant in remaining five crosses. The additive $\times$ dominance (j) type of interaction was found non significant in all six crosses. The dominance $\times$ dominance (l) type of interaction was found significant and negative in cross 1, 2, 4 and 6 while it was found non significant in remaining two crosses.

Based on the outcome of best fitting model, five parameter model was found best for cross 1; four parameter was found best suited for crosses 2, 4 and 6, as well as three parameter (additive-dominance) model was observed best fitted for crosses 3 and 5. Additive (d) effect

was found non significant for all crosses. While dominance (h) effect was found significantly positive for all crosses except cross 3 and 5. The additive $\times$ additive (i) interaction was found significantly positive for cross 1. The dominance $\times$ dominance (l) type of interaction was found significantly negative in all crosses except cross 3 and 5. The significant opposite sign associated with dominance (h) and dominance $\times$ dominance (l) component in all crosses except cross 3 and 5 revealed the role of duplicate type of epistasis for this trait.

Based on the results, it was observed that additive and epistasis gene action was influencing this trait. Murty *et al.* (1967), Singh *et al.* (1974), Bhandari *et al.* (2007), Godasara *et al.* (2010) and Kumar *et al.* (2013) recorded opposite non-additive gene effect. Suryawanshi *et al.* (2016), Jakhar *et al.* (2017) and Singh *et al.* (2017^a) reported all three type of gene actions were predominating for inheritance of this trait. As per the results shown in table 4.3.3, best fitting model for cross 1 indicated that significant positive additive $\times$ additive (i) epistasis was playing major role which suggesting simple selection followed by crossing such parents will improve the character.

4.3.4 Earhead length (cm)

Significance of the scaling tests A, B, C and D was observed in cross 6; scaling test B and C in cross 5; scaling test B and D in cross 4 as well as scaling test A in cross 1 indicated inadequacy of additive-dominance model and thereby indicating importance of digenic interaction effects for this trait (Table 4.3.4). Simple scaling tests as well as χ^2 value of joint scaling test were significant for all the families revealed inadequacy for additive dominance model but there is some negligible amount of gene interaction was present so six parameter model (Hayman, 1958) was found adequate for cross 1 and 5 only.

As per to the six parameter model (Hayman, 1958), additive (d) effect was non significant in all six crosses. While, the dominance (h) effect and additive $\times$ additive (i) type of interaction was significant and positive in cross 4 and 6 otherwise it was found non significant in remaining four crosses. The additive $\times$ dominance (j) type of interaction was found negatively significant in cross 2 and non significant in other crosses. The dominance $\times$ dominance (l) type of interaction was found significant and negative in cross 4 and 6 while it was found non significant in remaining four crosses.

As per the results of best fitting model, six parameter model (Hayman, 1958) was found best fitted for cross 1 and 5, while five parameter model was found best for cross 4 and 6 as well as three parameter (additive-dominance) model was observed best fitted for cross 2 and 3. All five type of parameter was found non significant for cross 4, while dominance (h)

effect, additive $\times$ additive (i) was found significantly positive for cross 6. Whereas dominance $\times$ dominance (l) was found significantly negative for cross 6.

Godasara *et al.* (2010) and Goah *et al.* (2020) observed same result with additive $\times$ additive (i) epistasis interaction influencing this trait for inheritance. Murty *et al.* (1967), Mahadevappa (1968), Singh *et al.* (1974) and Bhadaliya *et al.* (2012) observed that only non-additive gene effect is responsible for this trait. Bhandari *et al.* (2007) and Patel *et al.* (2021) suggested that additive gene effect was responsible for this trait. According to best fitting model, both additive as well dominant gene effect with additive $\times$ additive (i) epistasis interaction found effective for influence of this trait suggested that for improvement of this trait can be done by population improvement while maintaining the sufficient variation in population.

4.3.5 Earhead girth (mm)

Of all the four individual scaling tests viz., A, B, C and D were found non significant for crosses 4, 5 and 6 so three parameter model was adequate for this crosses; scaling test A, B and C was found significant in cross 3 while scaling test A was found significant for cross 1 and 3 suggesting inadequacy of simple additive-dominance model to explain the genetic architecture of earhead girth (Table 4.3.5). It was also supported by the significant chi-square values in joint scaling tests for above said crosses. This clearly indicated the influence of digenic interaction effects. Simple scaling tests as well as χ^2 value of joint scaling test were significant for all the families revealed inadequacy for additive dominance model but there is some negligible amount of gene interaction was present so six parameter model (Hayman, 1958) was found adequate for cross 1 and 4 only.

According to Hayman's six parameter model, additive (d) effect was significant and negative in cross 1 and significant and positive in cross 2 whereas non significant in other crosses. The dominance (h) effect was significant and positive in cross 2 and 4 as well as found non significant in remaining crosses. The additive $\times$ additive (i) type of interaction was non significant in all six crosses. The additive $\times$ dominance (j) component was significant and positive in cross 2 and significant and negative in cross 1. Dominance $\times$ dominance (l) effect was significant and positive in cross 1 but significant and negative in cross 2 and 3.

Looking to the results of best fitting model, four parameter model was found best for crosses 2 and 3. Additive (d) effect was found non significant in crosses 2 and 3. The dominance (h) effect was found positively significant for crosses 2 and 3. The additive $\times$ additive (i) type of interaction was not found for all crosses. The additive $\times$ dominance (j) type of interaction was found significantly positive for cross 2 only. The dominance $\times$ dominance (l) type of interaction was found significant and negative for cross 3 only. The opposite sign of

(h) and (l) estimates in cross 3 suggested the role of duplicate type of epistasis for this character.

Mahadevappa (1968), Nandaniya *et al.* (2016) and Patel *et al.* (2021) recorded similar results suggesting the presence of non-additive gene action for inheritance of this character. Similarly, Murty *et al.* (1967), Bhadaliya *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 crosses 2 and 3, the influence of dominant gene action was observed this exhibited that for this character heterosis breeding would be effective. Presence of non-additive gene action as well as epistasis specifically additive $\times$ dominance (cross 2) and dominance $\times$ dominance (cross 3) interaction which suggested the reciprocal recurrent selection as well as diallel selective mating by maintaining adequate population size this character can be improved.

4.3.6 Days to maturity

All scaling tests A, B, C and D were found significant in cross 4 only, while A, B and D tests were found significant in cross 3 and cross 5. Scaling tests B and D found significant for cross 1 and cross 6. Significance of scaling tests indicted the inadequacy of additive-dominance model in crosses. Simple scaling tests as well as χ^2 value of joint scaling test were significant for all the families revealed inadequacy for additive dominance model but there is some negligible amount of gene interaction was present so six parameter model (Hayman, 1958) was found adequate for cross 1 only.

According to three parameter model of Cavalli (1952), besides significance of 'm' parameter in all the six crosses, additive (d) gene effect was found non significant in all crosses.

As per Hayman's six parameter model, additive (d) effects were found significant and negative in crosses 1, 2, 3 and 6, while dominance (h) effects were found significant and negative in cross 4 only. The additive $\times$ additive (i) type of interaction was significant and positive in crosses 1, 3, 5 and 6. The additive $\times$ dominance (j) type of interaction was significant and positive in both the crosses 4 and 5. Dominance $\times$ dominance (l) effect was significant and negative in crosses 1, 3, 5 and 6. Based on best fitting model, additive (d) effects were found non significant for all crosses and dominance (h) effects were found significant for crosses 3, 4 and 5. Six parameter model was best fitted for cross 1 (Hayman, 1958) and 6. Five parameter model was found best for crosses 3, 4 and 5 while three parameter (additive-dominance) model was found adequate for cross 2 only.

Table 4.3.3 Estimation of scaling tests and gene effects for number of effective tiller per plant in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Number of effective tiller per plant									
Scaling tests (Mather, 1949)									
A	1.00**	±	0.24	0.77**	±	0.24	0.67*	±	0.32
B	0.77**	±	0.27	1.10**	±	0.28	0.23	±	0.34
C	0.80**	±	0.29	1.17**	±	0.41	0.97	±	0.59
D	-0.48*	±	0.19	-0.35	±	0.23	0.03	±	0.32
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	1.26**	±	0.04	1.43**	±	0.06	1.61**	±	0.07
d	-0.00	±	0.05	-0.19**	±	0.06	-0.05	±	0.07
h	0.26**	±	0.09	0.03	±	0.11	0.48**	±	0.14
χ ²	23.21**			23.46**			5.64		
Six parameter model (Hayman, 1958)									
m	1.44**	±	0.05	1.55**	±	0.08	1.98**	±	0.12
d	0.10	±	0.16	-0.28	±	0.16	0.13	±	0.20
h	1.08**	±	0.41	0.65	±	0.48	0.31	±	0.66
i	0.96*	±	0.39	0.70	±	0.47	-0.06	±	0.64
j	0.11	±	0.17	-0.16	±	0.17	0.21	±	0.21
l	-2.73**	±	0.73	-2.56**	±	0.77	-0.83	±	0.99
Best fitting model (Mather and Jinks, 1982)									
m	0.18	±	0.39	1.29**	±	0.07	-		-
d	-0.00	±	0.05	-0.14*	±	0.06	-		-
h	3.90**	±	1.09	1.42**	±	0.32	-		-
i	0.99*	±	0.39	-		-	-		-
j	-		-	-		-	-		-
l	-2.79**	±	0.72	-1.49**	±	0.32	-		-
χ ²	0.44			2.90	±		-		
Types of epistasis	Duplicate			Duplicate			-		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.3 Continue....

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)			
Number of effective tiller per plant										
Scaling tests (Mather, 1949)										
A	1.50**	±	0.34		-0.07	±	0.39		1.00** ± 0.32	
B	1.27**	±	0.35		0.60*	±	0.29		1.17** ± 0.34	
C	2.03**	±	0.52		0.20	±	0.51		1.50** ± 0.44	
D	-0.37	±	0.31		-0.17	±	0.23		-0.33 ± 0.27	
Gene effects in different models										
Three parameter model (Cavali, 1952)										
m	1.74**	±	0.07		1.78**	±	0.10		1.55** ± 0.06	
d	-0.10	±	0.08		0.13	±	0.10		-0.05 ± 0.06	
h	-0.09	±	0.12		-0.21	±	0.16		0.24* ± 0.12	
χ ²	36.56**				4.47				22.98**	
Six parameter model (Hayman, 1958)										
m	1.97**	±	0.11		1.69**	±	0.08		1.83** ± 0.08	
d	0.08	±	0.22		-0.11	±	0.16		-0.13 ± 0.20	
h	0.60	±	0.65		0.05	±	0.50		0.68 ± 0.56	
i	0.73	±	0.63		0.33	±	0.46		0.66 ± 0.55	
j	0.11	±	0.24		-0.33	±	0.23		-0.08 ± 0.21	
l	-3.50**	±	1.03		-0.86	±	0.83		-2.83** ± 0.94	
Best fitting model (Mather and Jinks, 1982)										
m	1.52**	±	0.08		-		-		1.45** ± 0.06	
d	-0.01	±	0.08		-		-		-0.05 ± 0.06	
h	2.28**	±	0.42		-		-		1.79** ± 0.35	
i	-		-		-		-		-	
j	-		-		-		-		-	
l	-2.41**	±	0.40		-		-		-1.77** ± 0.38	
χ ²	1.53				-				1.55	
Types of epistasis	Duplicate				-				Duplicate	

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.4 Estimation of scaling tests and gene effects for earhead length in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Earhead length									
Scaling tests (Mather, 1949)									
A	5.62**	±	1.60	-2.57	±	1.48	1.05	±	1.23
B	1.22	±	2.15	2.53	±	1.56	0.37	±	1.67
C	4.60	±	2.79	2.07	±	2.50	1.36	±	2.22
D	-1.12	±	1.42	1.05	±	1.24	-0.03	±	1.16
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	21.97**	±	0.51	21.74**	±	0.36	19.07**	±	0.34
d	-1.71**	±	0.50	1.09**	±	0.35	-0.82*	±	0.33
h	4.54**	±	0.97	2.12**	±	0.75	1.42*	±	0.69
χ ²	12.37**			8.55*			0.79		
Six parameter model (Hayman, 1958)									
m	24.33**	±	0.48	23.18**	±	0.45	19.87**	±	0.40
d	-0.13	±	1.05	-1.00	±	0.84	-0.57	±	0.84
h	5.90	±	3.03	-0.10	±	2.63	1.22	±	2.45
i	2.24	±	2.85	-2.11	±	2.48	0.05	±	2.33
j	2.20	±	1.21	-2.55**	±	0.93	0.34	±	0.92
l	-9.09	±	5.07	2.15	±	4.22	-1.47	±	4.05
Best fitting model (Mather and Jinks, 1982)									
m	-		-	-		-	-		-
d	-		-	-		-	-		-
h	-		-	-		-	-		-
i	-		-	-		-	-		-
j	-		-	-		-	-		-
l	-		-	-		-	-		-
χ ²	-			-			-		
Types of epistasis	-			-			-		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.4 Continue....

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Earhead length									
Scaling tests (Mather, 1949)									
A	0.31	±	1.86	2.94	±	1.85	9.58**	±	1.39
B	3.09*	±	1.38	5.01*	±	2.20	13.89**	±	2.18
C	-5.15	±	2.88	10.08**	±	2.75	15.66**	±	2.28
D	-4.28**	±	1.60	1.07	±	1.58	-3.90**	±	1.44
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	22.65**	±	0.43	24.59**	±	0.47	21.35**	±	0.44
d	1.34**	±	0.44	2.44**	±	0.47	-0.02	±	0.45
h	0.67	±	0.69	-2.13*	±	0.90	-1.64*	±	0.71
χ ²	10.36*			15.45**			97.20**		
Six parameter model (Hayman, 1958)									
m	21.66**	±	0.63	24.74**	±	0.50	22.00**	±	0.44
d	0.32	±	0.99	1.16	±	1.22	-1.80	±	1.13
h	9.08**	±	3.28	-5.23	±	3.30	6.15*	±	2.97
i	8.55**	±	3.21	-2.13	±	3.17	7.80**	±	2.88
j	-1.38	±	1.10	-1.03	±	1.33	-2.15	±	1.24
l	-11.95*	±	4.90	-5.82	±	5.61	-31.27**	±	5.07
Best fitting model (Mather and Jinks, 1982)									
m	13.33	±	3.18	-	-		12.96**	±	2.72
d	1.44	±	0.44	-	-		-0.01	±	0.46
h	23.41	±	7.73	-	-		31.87**	±	7.15
i	9.24	±	3.16	-	-		6.06*	±	2.70
j	-	-		-	-		-	-	
l	-13.54	±	4.74	-	-		-27.57**	±	4.60
χ ²	1.57			-			2.99		
Types of epistasis	-			-			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

The sign of (h) and (l) parameters being opposite in crosses 3, 5 and cross 6 showed influence of duplicate type of interaction for this trait, so suitable breeding method which create sufficient variation should be used like population improvement method or diallel selective mating. Wilson *et al.* (1990), Godasara *et al.* (2010), Jog *et al.* (2016), Jakhar *et al.* (2017), Kumar *et al.* (2017^a), Singh *et al.* (2017^a) observed similarly all three type of gene effects with duplicate epistasis, but Bhandari *et al.* (2007), Bhadaliya *et al.* (2012) observed more influence of non-additive gene action whereas Patel *et al.* (2021) suggested the additive gene action for inheritance of days to maturity trait. All three genetic components were of equal magnitude, either composite or population improvement programme should be taken up for development of superior lines with several desirable genes.

4.3.7 Test weight (g)

Adequacy of simple additive-dominance model was evident from non-significance of all the individual scaling tests viz., tests A, B, C and D in crosses 3 and 5 (Table 4.3.7). Whereas, failure of simple additive-dominance model was found from the significance of one or more scaling tests as well as joint scaling tests in the crosses 1, 2, 4 and 6 suggesting the presence of digenic interaction for this trait but there is some negligible amount of gene interaction was present so six parameter model (Hayman, 1958) was found adequate for cross 2 only.

According to three parameter model of Cavalli (1952), additive (d) gene effect was found significant and negative in cross 1. However, dominance (h) gene effect was found significant and positive in both the crosses 1 and 2. According to Hayman's six parameter model additive (d) gene effect was non significant for all six crosses. The dominance (h) and additive $\times$ additive (i) gene effects were significant and positive in crosses 1, 2, 4 and 6. Additive $\times$ dominance (j) was significant and positive in cross 6 only. While, dominance $\times$ dominance (l) gene effect was significant and negative in all crosses except cross 5.

The perusal of table 4.3.7 indicated that six parameter model was found best for cross 2 (Hayman, 1958) and cross 6; five parameter for crosses 1 and 4 whereas three parameter was found best for cross 3 and 5. Additive (d) effect was found significantly negative for cross 1 and 6. While dominance (h) and additive $\times$ additive (i) effect was found significant and positive for crosses 1, 4 and 6. The additive $\times$ dominance (j) type of interaction was found significant and positive for cross 6 only. The dominance $\times$ dominance (l) type of interaction was found significant and negative for crosses 1, 4 and 6. The opposite sign of (h) and (l) parameter in crosses 1, 4 and 6 suggested the role of duplicate type of epistasis for this character.

Godasara *et al.* (2010), Suryawanshi *et al.* (2016), Jog *et al.* (2016), and Kumar *et al.* (2017^a) observed similar result as influence of non-additive gene effect with presence of epistasis with duplicate epistasis. Mahadevappa (1968), Singh *et al.* (1974), Rasal and Patil (2003), Bhadaliya *et al.* (2012), Patel *et al.* (2014), Nandaniya *et al.* (2016^a) and Patel *et al.* (2021) reported that only non-additive gene action was having influence on inheritance of this trait. For test weight, observing the best fitting model it was found that influence of dominant gene action in crosses 1, 4 and 6 with presence of additive $\times$ additive (i) and dominance $\times$ dominance (l) epistasis interaction. This suggested that for exploitation of non-additive variance heterosis breeding or recurrent selection for SCA would improve the character significantly while exploitation of epistasis the appropriate population improvement method can be used to get desired recombinants for test weight.

4.3.8 Grain yield per plant (g)

The results manifested grain yield per plant is depicted in Table 4.3.8. All types of scaling test A, B, C and D found significant in cross 5 and cross 6. The significance of scaling tests A, B and C in cross 1, 3 and 4; while B and D significant in cross 2 indicated the inadequacy of additive-dominance model. Simple scaling tests as well as χ^2 value of joint scaling test were significant for all the families revealed inadequacy for additive dominance model. Three parameter m, d, h and χ^2 test found significant in all crosses. According to Hayman's six parameter model, additive (d) effect was non significant in all crosses. The dominance (h) effect was significant and positive in crosses 2, 3 and 5. The additive $\times$ additive (i) type of interaction was positively significant in cross 2 and cross 5. The additive $\times$ dominance (j) component was positively significant in cross 1 and cross 3. Dominance $\times$ dominance (l) effect was significant and positive in cross 1 while it was significant and negative in cross 2, 3, 4, 5 and cross 6. The significant opposite sign associated with dominance (h) and dominance $\times$ dominance (l) component in all crosses except cross 6 suggested duplicate type of epistasis for this trait.

Based on the results of best fitting model, five parameter model was found best for crosses 1, 2 and 6, while four parameter best suited for crosses 3 and 4. Additive (d) effect was found significant and positive for cross 2, 4, 5 and 6 while it was observed negatively significant for crosses 1 and 3. The dominance (h) effect was found significant and positive for crosses 2, 3, 4 and 5. The additive $\times$ additive (i) type of interaction was found significantly positive for cross 5 only, while it was negatively significant for cross 6. The additive $\times$ dominance (j) type of interaction was found significantly positive for cross 1 only and it was negatively significant for cross 2, while it was absent for crosses 3, 4, 5 and 6. The dominance

Table 4.3.5 Estimation of scaling tests and gene effects for earhead girth in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Earhead girth									
Scaling tests (Mather, 1949)									
A	- 4.70**	±	1.55	4.52**	±	1.25	9.20**	±	1.85
B	0.70	±	1.39	-0.29	±	1.36	4.78**	±	1.68
C	-0.31	±	2.50	1.79	±	1.97	9.89**	±	2.95
D	1.84	±	1.05	-1.22	±	0.95	-2.05	±	1.63
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	25.09**	±	0.39	26.08**	±	0.41	24.73**	±	0.39
d	-0.32	±	0.37	0.41	±	0.40	-0.14	±	0.39
h	0.08	±	0.81	3.37**	±	0.72	1.21	±	0.76
χ ²	13.78**			13.68**			31.74**		
Six parameter model (Hayman, 1958)									
m	25.57**	±	0.39	27.71**	±	0.33	26.25**	±	0.61
d	-2.19**	±	0.71	2.00**	±	0.67	1.31	±	1.07
h	-3.73	±	2.32	5.62**	±	2.04	4.13	±	3.37
i	-3.68	±	2.11	2.44	±	1.90	4.09	±	3.27
j	-2.69**	±	0.84	2.40**	±	0.85	2.21	±	1.15
l	7.68*	±	3.78	-6.67*	±	3.36	-18.07**	±	5.21
Best fitting model (Mather and Jinks, 1982)									
m	-	-		26.19**	±	0.41	23.95**	±	0.41
d	-	-		-0.49	±	0.50	-0.58	±	0.39
h	-	-		3.19**	±	0.72	11.61**	±	2.15
i	-	-		-	-		-	-	
j	-	-		5.10**	±	1.69	-	-	
l	-	-		-	-		-11.76**	±	2.28
χ ²	-			4.60			5.13		
Types of epistasis	-			-			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.5 Continue.....

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Earhead girth									
Scaling tests (Mather, 1949)									
A	-1.47	±	1.29	1.77	±	1.14	-0.33	±	1.50
B	-2.90	±	1.60	-0.06	±	1.14	-1.68	±	1.32
C	-7.80**	±	2.41	0.55	±	2.00	0.14	±	1.93
D	-1.71	±	1.28	-0.58	±	1.00	1.08	±	1.08
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	25.09**	±	0.39	24.42**	±	0.31	26.15**	±	0.33
d	-0.41	±	0.38	0.52	±	0.30	0.53	±	0.34
h	2.83**	±	0.70	0.98	±	0.59	0.58	±	0.64
χ ²	11.29*			2.55			1.98		
Six parameter model (Hayman, 1958)									
m	25.37**	±	0.48	24.87**	±	0.39	26.61**	±	0.34
d	0.04	±	0.84	1.24	±	0.63	1.05	±	0.83
h	6.63*	±	2.66	1.98	±	2.10	-1.48	±	2.27
i	3.42	±	2.56	1.16	±	2.01	-2.15	±	2.16
j	0.71	±	0.95	0.91	±	0.72	0.67	±	0.91
l	0.94	±	4.14	-2.87	±	3.23	4.16	±	3.86
Best fitting model (Mather and Jinks, 1982)									
m	-		-	-		-	-		-
d	-		-	-		-	-		-
h	-		-	-		-	-		-
i	-		-	-		-	-		-
j	-		-	-		-	-		-
l	-		-	-		-	-		-
χ ²	-		-	-		-	-		-
Types of epistasis	-			-			-		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.6 Estimation of scaling tests and gene effects for days to maturity in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Days to maturity									
Scaling tests (Mather, 1949)									
A	-0.53	±	0.99	-3.00*	±	1.41	-4.20**	±	1.37
B	3.13*	±	1.25	1.00	±	0.98	9.80**	±	1.23
C	-0.97	±	1.74	-1.60	±	2.02	-4.20	±	2.27
D	-1.78*	±	0.88	0.20	±	1.03	-4.90**	±	1.14
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	76.54**	±	0.31	81.87**	±	0.35	80.09**	±	0.38
d	-0.46	±	0.30	-0.52	±	0.34	0.02	±	0.37
h	-0.68	±	0.58	0.24	±	0.62	-3.07**	±	0.69
χ ²	8.94*			6.93			100.68**		
Six parameter model (Hayman, 1958)									
m	75.87**	±	0.31	81.76**	±	0.39	76.96**	±	0.44
d	-1.90**	±	0.63	-1.96**	±	0.67	-4.86**	±	0.71
h	2.93	±	1.87	-0.20	±	2.16	6.76**	±	2.38
i	3.56*	±	1.77	-0.40	±	2.07	9.80**	±	2.28
j	-1.83*	±	0.72	-2.00*	±	0.78	-7.00**	±	0.83
l	-6.16*	±	3.05	2.40	±	3.37	-15.40**	±	3.64
Best fitting model (Mather and Jinks, 1982)									
m	-	-		-	-		67.74**	±	2.31
d	-	-		-	-		0.22	±	0.37
h	-	-		-	-		28.14**	±	5.69
i	-	-		-	-		12.01**	±	2.26
j	-	-		-	-		-	-	
l	-	-		-	-		-19.38**	±	3.61
χ ²	-			-			70.22**		
Types of epistasis	-			-			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.6 Continue....

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Days to maturity									
Scaling tests (Mather, 1949)									
A	8.77**	±	1.26	11.57**	±	1.27	-2.73	±	1.58
B	3.33*	±	1.49	3.77*	±	1.75	5.20**	±	1.50
C	18.63**	±	2.11	4.87	±	2.52	-4.80	±	2.76
D	3.27**	±	1.10	-5.23**	±	1.36	-3.63*	±	1.42
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	78.31**	±	0.34	77.71**	±	0.37	82.07**	±	0.40
d	-0.24	±	0.34	0.45	±	0.36	-0.58	±	0.39
h	2.33**	±	0.67	1.91**	±	0.70	-5.19**	±	0.77
χ ²	95.29**			84.39**			23.81**		
Six parameter model (Hayman, 1958)									
m	81.64**	±	0.38	78.14**	±	0.51	78.27**	±	0.56
d	2.21**	±	0.78	3.48**	±	0.90	-3.71**	±	0.87
h	-6.70**	±	2.32	10.61**	±	2.82	2.05	±	2.95
i	-6.53**	±	2.20	10.46**	±	2.72	7.26*	±	2.84
j	2.71**	±	0.87	3.90**	±	0.99	-3.96**	±	0.98
l	-5.56	±	3.80	-25.80**	±	4.40	-9.73*	±	4.46
Best fitting model (Mather and Jinks, 1982)									
m	86.54**	±	0.98	63.65**	±	2.66	74.81**	±	2.87
d	-0.53	±	0.38	0.24	±	0.37	0.25	±	0.44
h	-9.35**	±	1.45	44.61**	±	6.60	11.78	±	7.06
i	-9.36**	±	1.05	13.04**	±	2.64	7.26*	±	2.84
j	5.88**	±	1.72	-	-		-7.93**	±	1.96
l	-	-		-31.26**	±	4.18	-9.73*	±	4.46
χ ²	2.14			15.52 **			-		
Types of epistasis	-			Duplicate			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.7 Estimation of scaling tests and gene effects for test weight in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Test weight									
Scaling tests (Mather, 1949)									
A	1.69**	±	0.38	1.08	±	0.54	0.68	±	0.59
B	0.76	±	0.42	0.87	±	0.54	0.98	±	0.59
C	0.29	±	0.71	-0.09	±	0.92	0.02	±	0.91
D	-1.08**	±	0.40	-1.02**	±	0.36	-0.82	±	0.44
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	8.88**	±	0.08	9.24**	±	0.13	9.87**	±	0.17
d	-0.44**	±	0.08	-0.19	±	0.12	0.11	±	0.16
h	0.34*	±	0.15	0.69*	±	0.28	0.28	±	0.32
χ ²	21.33**			9.26*			4.60		
Six parameter model (Hayman, 1958)									
m	8.97**	±	0.15	9.37**	±	0.12	9.87**	±	0.15
d	0.03	±	0.25	-0.10	±	0.25	-0.002	±	0.31
h	2.32**	±	0.82	2.44**	±	0.81	1.83	±	0.94
i	2.16**	±	0.81	2.04**	±	0.72	1.63	±	0.88
j	0.46	±	0.26	0.10	±	0.28	-0.14	±	0.37
l	-4.61**	±	1.24	-3.99**	±	1.37	-3.28*	±	1.55
Best fitting model (Mather and Jinks, 1982)									
m	6.59**	±	0.81	-	-		-	-	
d	-0.38**	±	0.08	-	-		-	-	
h	7.13**	±	2.00	-	-		-	-	
i	2.19**	±	0.81	-	-		-	-	
j	-	-	-	-	-		-	-	
l	-4.74**	±	1.24	-	-		-	-	
χ ²	3.01			-			-		
Types of epistasis	Duplicate			-			-		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.7 Continue....

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Test weight									
Scaling tests (Mather, 1949)									
A	0.55	±	0.62	-0.31	±	0.70	2.03**	±	0.67
B	0.20	±	0.68	0.25	±	0.70	-0.23	±	0.69
C	-1.94	±	0.98	-1.36	±	0.98	-1.75	±	1.06
D	-1.34**	±	0.48	-0.65	±	0.52	-1.78**	±	0.54
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	10.33**	±	0.20	10.23**	±	0.19	10.17**	±	0.18
d	0.01	±	0.19	-0.36	±	0.19	-0.30	±	0.17
h	-0.12	±	0.36	0.12	±	0.35	0.47	±	0.34
χ ²	8.85*			2.93			16.95**		
Six parameter model (Hayman, 1958)									
m	9.89**	±	0.16	10.07**	±	0.17	9.98**	±	0.19
d	0.09	±	0.34	-0.60	±	0.39	0.58	±	0.38
h	2.59*	±	1.02	1.49	±	1.10	3.94**	±	1.15
i	2.67**	±	0.95	1.30	±	1.05	3.55**	±	1.09
j	0.17	±	0.42	-0.28	±	0.45	1.12*	±	0.43
l	-3.42*	±	1.70	-1.24	±	1.87	-5.35**	±	1.86
Best fitting model (Mather and Jinks, 1982)									
m	7.69**	±	0.98	-	-		6.66**	±	1.11
d	-0.02	±	0.19	-	-		-0.54**	±	0.20
h	6.14*	±	2.56	-	-		9.29**	±	2.86
i	2.72**	±	0.95	-	-		3.55**	±	1.09
j	-	-		-	-		2.25**	±	0.86
l	-3.50*	±	1.68	-	-		-5.35**	±	1.86
χ ²	0.18			-			-		-
Types of epistasis	Duplicate			-			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

× dominance (l) type of interaction was found significantly positive for cross 1 only and significantly negative for remaining crosses 2, 3, 4, 5 and cross 6. The significant opposite sign associated with dominance (h) and dominance × dominance (l) component in all crosses except for cross 6 indicated the presence of duplicate type of epistasis for this trait.

Suryawanshi *et al.* (2016), Jakhar *et al.* (2017), Kumar *et al.* (2017^a), Singh *et al.* (2017^a) and Goah *et al.* (2020) observed similar results for the grain yield per plant that presence of all three type of gene action with duplicate epistasis. While Singh *et al.* (1974), Pethani and dave (1989), Bhandari *et al.* (2007), Godasara *et al.* (2010), Bhadaliya *et al.* (2012), Patel *et al.* (2014), Nandaniya *et al.* (2016^a) and Patel *et al.* (2021) found the expression of non-additive gene action with presence of epistasis but Mahadevappa (1968) and Kumar *et al.* (2013) recorded the trait governed additive gene action. Prevalence of all three type of gene action for inheritance with predominance of dominant gene action of this trait suggested that for the line development the cyclic population improvement such as reciprocal recurrent selection can be used as well as the heterosis breeding suggested for hybrids with high yielding capacity.

4.3.9 Harvest index (g)

The results manifested harvest index (%) is depicted in Table 4.3.9. The significance of scaling tests A, B, C and D in cross 3 and 5; A, B and C in cross 4; B and D in cross 2; A in cross 1 and C in cross 6 indicated the inadequacy of three parameter (additive-dominance) model. Simple scaling tests as well as χ^2 value of joint scaling test were significant for all the families revealed inadequacy for additive dominance model but there is some negligible amount of gene interaction was present so six parameter model (Hayman, 1958) was found adequate for cross 6 only.

According to Hayman's six parameter model, additive (d) effect was significant and positive in cross 2 and 3 while dominance (h) effect was significant and negative in cross 2 and 3. The additive × additive (i) type of interaction was negatively significant in cross 2, 3 and 5. The additive × dominance (j) component was positively significant in cross 2 and 3, while it was negatively significant in cross 1 only. Dominance × dominance (l) effect was significant and positive in all crosses except cross 6.

As per the results of best fitting model, six parameter model (Hayman, 1958) was found best for cross 6, Five parameter model was found best for cross 2 and 3 and four parameter model was found best for cross 1, 4 and 5. Additive (d) effect was significant and positive in cross 1 while significant and negative in cross 3 and 4. The dominance (h) effect was significant and negative in crosses 2, 3, 4 and 5. The additive × dominance (j) type of interaction was found significant and positive only for cross 2 and significant and negative in

cross 3. The dominance $\times$ dominance (l) type of interaction was found positively significant for all crosses except cross 6. The significant opposite sign associated with dominance (h) and dominance $\times$ dominance (l) component in crosses 2, 3, 4 and 5 suggested the role of duplicate type of epistasis for this trait.

Scientists Rasal and Patil (2003), Bhanderi *et al.* (2007), Nandaniya *et al.* (2016^a) and Patel *et al.* (2021) reported the presence of only non-additive gene action in their experiment for this trait.

4.3.10 Carbohydrate (g/100 g)

The results indicated carbohydrate (g/100g) is depicted in Table 4.3.10. The significance of all scaling tests in cross 2 and 6; A, B, and C in cross 1; A, B and D in cross 4; A and C in cross 3 and scaling test C in cross 5 indicated the inadequacy of additive-dominance model. Simple scaling tests as well as χ^2 value of joint scaling test were significant for all the families revealed inadequacy for additive dominance model but there is some negligible amount of gene interaction was present so six parameter model (Hayman, 1958) was found adequate for cross 6 only.

In connection to Hayman's six parameter model, additive (d) effect was significant and positive in cross 1, 4 and 5 while it was observed negatively significant in crosses 2, 3 and 6. The dominance (h) effect was positively significant in cross 2 only whereas it was negatively significant for crosses 1, 5 and 6. The additive $\times$ additive (i) type of interaction was positively significant in all crosses 2 and 4 while significant and negative in cross 6. The additive $\times$ dominance (j) component was positively significant in cross 1 and negatively significant for crosses 2 and 3. Dominance $\times$ dominance (l) effect was significantly negative in cross 1 and 4 while significantly positive in crosses 3 and 6.

Best fitting model indicated that Six parameter model (Hayman, 1958) was found best for cross 5 and four parameter model was found best for cross 1 and 3, whereas five parameter model was found best for cross 2, 4 and 6. Additive (d) effect was found significant and positive in crosses 2 and 4 and negatively significant in crosses 1, 3 and 6. Dominant (h) effect was observed positively significant for crosses 1 and 4 while it was negatively significant in all remaining crosses 2, 3 and 6. The additive $\times$ additive (i) type of interaction was found significantly positive for cross 4 and negatively significant for cross 6, while it was absent in other crosses. The additive $\times$ dominance (j) type of interaction was found significant and negative for cross 2 only and for other crosses it was found absent. The dominance $\times$ dominance (l) type of interaction was found positively significant in crosses 2, 3 and 6 while in crosses 1 and 4 it was found significantly negative. The significant opposite sign associated

with dominance (h) and dominance $\times$ dominance (l) component in all crosses except cross 5 revealed the role of duplicate type of epistasis for this trait.

Duplicate type of epistasis was present in all crosses except cross 5 suggested that variation in segregating generation may get reduced which might hinder selection process, thus population improvement method may be used to get desirable recombinants that can be used in breeding programmes in improvement of this trait.

4.3.11 Tannin (mg/100 g)

The results manifested tannin content (mg/100 g) is depicted in Table 4.3.11. The significance of scaling tests A, B, C and D in cross 2 and 3 while A, B and C in cross 4, 5 and 6 as well as B, C and D in cross 1 indicated the inadequacy of three parameter (additive-dominance) model. Individual scaling tests as well as χ^2 value of joint scaling test were significant for all the families revealed inadequacy for additive dominance model.

According to the Hayman's six parameter model, additive (d) effect was positively significant in crosses 1, 2 and 4 where found non significant in other crosses. The dominance (h) effect was significant and negative in crosses 1, 2 and 6, while in crosses 3, 4 and 5 it was positively significant. The additive $\times$ additive (i) type of interaction was negatively significant in crosses 1 and 2, while in cross 3 it was positively significant. The additive $\times$ dominance (j) component was found negatively significant in crosses 3, 5 and 6 as well as in crosses 1, 2 and 4 it was positively significant. Dominance $\times$ dominance (l) effect was significant and positive in crosses 1, 2, 5 and 6 whereas in crosses 3 and 4 it was negatively significant.

As per to the results of best fitting model, five parameter model was found best for all crosses. The additive effect (i) was significantly negative for crosses 1 and 4 while significantly positive in crosses 3, 5 and 6. The dominance (h) effect was found significant and negative for crosses 1, 5 and 6 while found positively significant for 2, 3 and 4. The additive $\times$ additive (i) type of interaction was found significantly negative for crosses 1 and 5 as well as significantly positive for cross 3. The additive $\times$ dominance (j) type of interaction was found significantly negative for cross 6 only while it was positive for cross 2 and 4. The dominance $\times$ dominance (l) type of interaction was found significant and negative for crosses 2, 3 and 4 and significantly positive for cross 1, 5 and 6. The significant opposite sign associated with dominance (h) and dominance $\times$ dominance (l) component in all six crosses depicted the role of duplicate type of epistasis for this trait.

Table 4.3.8 Estimation of scaling tests and gene effects for grain yield per plant in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Grain yield per plant									
Scaling tests (Mather, 1949)									
A	-10.51**	±	2.13	4.53	±	2.38	15.98**	±	2.65
B	-17.75**	±	2.18	10.70**	±	2.22	6.39*	±	2.48
C	-24.99**	±	2.95	4.18	±	3.06	15.15**	±	3.04
D	1.64	±	2.06	-5.52*	±	2.11	-3.61	±	2.23
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	29.34**	±	0.21	27.34**	±	0.34	22.69**	±	0.30
d	-3.43**	±	0.21	2.07**	±	0.35	-4.66**	±	0.31
h	9.78**	±	0.39	-1.63**	±	0.55	6.09**	±	0.60
χ ²	150.29**			26.86**			59.02**		
Six parameter model (Hayman, 1958)									
m	28.84**	±	0.71	27.08**	±	0.71	28.41**	±	0.69
d	0.06	±	1.49	-0.94	±	1.56	-0.10	±	1.75
h	7.19	±	4.14	9.23*	±	4.26	12.25**	±	4.50
i	-3.27	±	4.12	11.04*	±	4.23	7.22	±	4.46
j	3.61*	±	1.50	-3.08	±	1.60	4.79**	±	1.77
l	31.53**	±	6.65	-26.27**	±	6.95	-29.59**	±	7.63
Best fitting model (Mather and Jinks, 1982)									
m	29.86**	±	0.21	26.94**	±	0.36	22.13**	±	0.31
d	-3.55**	±	0.21	2.14**	±	0.36	-4.74**	±	0.31
h	-16.07**	±	2.18	7.39**	±	2.41	22.65**	±	2.43
i	-		-	-		-	-		-
j	7.19*	±	3.01	-6.54*	±	3.20	-		-
l	26.54**	±	2.20	-9.21**	±	2.38	-17.65**	±	2.50
χ ²	0.63			6.81**			9.46**		
Types of epistasis	Duplicate			Duplicate			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.8 Continue....

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Grain yield per plant									
Scaling tests (Mather, 1949)									
A	12.57**	±	2.09	19.14**	±	2.09	11.47**	±	1.81
B	12.58**	±	1.15	19.28**	±	1.97	13.38**	±	1.39
C	31.52**	±	2.90	29.55**	±	2.48	37.56**	±	2.74
D	3.19	±	1.82	-4.43*	±	1.79	6.36**	±	1.70
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	22.46**	±	0.19	22.28**	±	0.24	22.61**	±	0.23
d	1.46**	±	0.19	1.08**	±	0.25	0.90**	±	0.24
h	4.36**	±	0.35	4.93**	±	0.47	4.50**	±	0.41
χ ²	246.25**			277.44**			283.55**		
Six parameter model (Hayman, 1958)									
m	31.35**	±	0.70	30.16**	±	0.56	32.71**	±	0.65
d	1.66	±	1.16	0.98	±	1.38	-0.18	±	1.09
h	-3.01	±	3.66	11.98**	±	3.61	-9.24**	±	3.43
i	-6.37	±	3.64	8.86*	±	3.58	-12.71**	±	3.40
j	-0.00	±	1.17	-0.07	±	1.40	-0.95	±	1.11
l	-18.77**	±	5.47	-47.28**	±	6.06	-12.12*	±	5.15
Best fitting model (Mather and Jinks, 1982)									
m	21.79**	±	0.19	12.34**	±	3.58	33.80**	±	3.36
d	1.69**	±	0.19	1.05**	±	0.25	0.72**	±	0.24
h	30.54**	±	1.71	59.29**	±	9.49	4.39	±	8.23
i	-		-	8.87*	±	3.57	-12.22**	±	3.35
j	-		-	-		-	-		-
l	-27.18**	±	1.74	-47.30**	±	6.05	-13.13**	±	5.02
χ ²	3.50			-			0.72		
Types of epistasis	Duplicate			Duplicate			-		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.9 Estimation of scaling tests and gene effects for harvest index in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Harvest index									
Scaling tests (Mather, 1949)									
A	-5.20**	±	1.26	-0.05	±	1.27	-11.12**	±	1.86
B	-1.43	±	1.33	-14.88**	±	1.46	-20.01**	±	1.58
C	-3.41	±	2.49	-3.91	±	2.11	-18.36**	±	2.63
D	1.61	±	1.41	5.51**	±	1.25	6.39**	±	1.66
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	42.08**	±	0.25	41.74**	±	0.26	42.96**	±	0.26
d	1.20**	±	0.25	0.38	±	0.26	-0.35	±	0.27
h	3.69**	±	0.48	-1.27*	±	0.52	1.19*	±	0.52
χ ²	17.89**			106.00**			208.24**		
Six parameter model (Hayman, 1958)									
m	43.55**	±	0.57	41.05**	±	0.45	40.93**	±	0.60
d	-0.61	±	0.82	7.18**	±	0.86	3.56**	±	1.14
h	0.98	±	2.86	-11.39**	±	2.55	-9.80**	±	3.35
i	-3.22	±	2.82	-11.02**	±	2.49	-12.77**	±	3.31
j	-1.88*	±	0.86	7.41**	±	0.90	4.44**	±	1.17
l	9.86*	±	4.14	25.95**	±	4.04	43.91**	±	5.27
Best fitting model (Mather and Jinks, 1982)									
m	42.36**	±	0.26	42.21**	±	0.27	58.39**	±	3.30
d	1.10**	±	0.25	-0.23	±	0.27	-0.64*	±	0.26
h	-1.56	±	1.60	-10.02**	±	1.57	-58.46**	±	8.33
i	-	-		-	-		-	-	
j	-	-		13.94**	±	1.80	-14.40**	±	3.28
l	5.71**	±	1.66	9.65**	±	1.65	47.07**	±	5.20
χ ²	6.11*			19.48**			14.31**		
Types of epistasis	-			Duplicate			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.9 Continue...

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Harvest index									
Scaling tests (Mather, 1949)									
A	-8.73**	±	1.69	-6.32**	±	1.63	2.90	±	1.81
B	-11.96**	±	1.66	-4.70**	±	1.31	0.32	±	1.40
C	-15.97**	±	2.42	-5.30*	±	2.40	7.50**	±	2.36
D	2.36	±	1.47	2.86*	±	1.38	2.15	±	1.49
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	39.87**	±	0.23	36.07**	±	0.25	38.09**	±	0.31
d	-2.09**	±	0.23	0.02	±	0.25	-1.62**	±	0.32
h	-1.10	±	0.58	0.80	±	0.55	0.98	±	0.52
χ ²	87.84**			24.91**			11.54**		
Six parameter model (Hayman, 1958)									
m	37.43**	±	0.50	36.10**	±	0.51	40.03**	±	0.52
d	-0.75	±	1.07	-0.71	±	0.93	-0.46	±	1.05
h	-2.73	±	3.01	-3.69	±	2.84	-3.45	±	3.03
i	-4.72	±	2.94	-5.72*	±	2.77	-4.29	±	2.98
j	1.61	±	1.10	-0.80	±	0.96	1.29	±	1.10
l	25.41**	±	4.93	16.75**	±	4.44	1.07	±	4.84
Best fitting model (Mather and Jinks, 1982)									
m	40.40**	±	0.23	36.40**	±	0.26	-		-
d	-2.29**	±	0.23	0.05	±	0.25	-		-
h	-16.16**	±	1.75	-6.25**	±	1.65	-		-
i	-		-	-		-	-		-
j	-		-	-		-	-		-
l	18.18**	±	1.99	8.29**	±	1.83	-		-
χ ²	4.89			4.51			-		
Types of epistasis	Duplicate			Duplicate			-		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.10 Estimation of scaling tests and gene effects for carbohydrate in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Carbohydrate									
Scaling tests (Mather, 1949)									
A	28.53**	±	1.41	-13.90**	±	1.48	-19.66**	±	2.12
B	4.78**	±	1.17	5.11**	±	1.36	-3.49	±	2.23
C	32.27**	±	2.77	-24.62**	±	2.78	-17.89**	±	2.78
D	-0.52	±	1.52	-7.92**	±	1.60	2.63	±	1.90
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	57.01**	±	0.30	64.06**	±	0.28	62.51**	±	0.34
d	-7.57**	±	0.30	3.76**	±	0.28	-0.60	±	0.35
h	-16.90**	±	0.50	-3.25**	±	0.47	-2.36**	±	0.62
χ ²	498.23**			181.17**			114.50**		
Six parameter model (Hayman, 1958)									
m	54.34**	±	0.64	57.06**	±	0.65	58.38**	±	0.61
d	4.12**	±	0.81	-5.06**	±	0.92	-8.63**	±	1.44
h	-17.22**	±	3.09	13.24**	±	3.24	-6.31	±	3.86
i	1.03	±	3.05	15.83**	±	3.20	-5.26	±	3.80
j	11.87**	±	0.88	-9.50**	±	0.97	-8.08**	±	1.49
l	-34.34**	±	4.27	-7.04	±	4.63	28.41**	±	6.42
Best fitting model (Mather and Jinks, 1982)									
m	54.39**	±	0.33	64.51**	±	0.30	63.60**	±	0.36
d	-5.92**	±	0.31	4.44**	±	0.30	-1.05**	±	0.36
h	12.85**	±	1.75	-16.66**	±	1.80	-21.97**	±	2.24
i	-		-	-		-	-		-
j	-		-	-19.72**	±	1.94	-		-
l	-30.11**	±	1.70	14.07**	±	1.79	20.70**	±	2.27
χ ²	184.31**			24.40			31.40**		
Types of epistasis	Duplicate			Duplicate			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.10 Continue....

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Carbohydrate									
Scaling tests (Mather, 1949)									
A	9.54**	±	1.61	2.89	±	1.96	-16.79**	±	2.21
B	5.94**	±	1.61	2.56	±	1.36	-16.40**	±	1.26
C	3.27	±	2.80	4.88*	±	2.27	11.99**	±	2.38
D	-6.11**	±	1.71	-0.29	±	1.56	22.59**	±	1.60
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	55.82**	±	0.23	63.51**	±	0.29	52.00**	±	0.23
d	3.85**	±	0.24	3.23**	±	0.30	-3.04**	±	0.23
h	-5.59**	±	0.43	-8.14**	±	0.38	2.30**	±	0.51
χ ²	46.42**			9.23*			282.21**		
Six parameter model (Hayman, 1958)									
m	53.28**	±	0.66	60.40**	±	0.53	57.22**	±	0.53
d	5.56**	±	1.08	3.31**	±	1.14	-3.67**	±	1.20
h	6.21	±	3.46	-7.41*	±	3.15	-41.53**	±	3.25
i	12.21**	±	3.43	0.57	±	3.12	-45.18**	±	3.20
j	1.79	±	1.11	0.16	±	1.18	-0.19	±	1.22
l	-27.69**	±	5.17	-6.03	±	5.10	78.379**	±	5.37
Best fitting model (Mather and Jinks, 1982)									
m	43.26**	±	3.44	-	-		97.36**	±	2.91
d	3.84**	±	0.24	-	-		-3.48**	±	0.24
h	33.89**	±	8.46	-	-		-119.25**	±	7.37
i	12.21**	±	3.43	-	-		-44.96**	±	2.91
j	-	-		-	-		-	-	
l	-27.68**	±	5.17	-	-		77.94**	±	4.64
χ ²	2.61			-			0.02		
Types of epistasis	Duplicate			-			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

In majority of crosses, negative value of additive and dominant gene action with more influence of dominant gene action with presence of all three type of gene action suggested that to fix trait through population improvement method to improve the pearl millet seed quality. Heterosis breeding can also be very useful as additive as well dominant gene has a negative significant value in most of the crosses.

4.3.12 Iron content (mg/kg)

The estimates of gene effects for iron content out and tabulated as in Table 4.3.12. All six crosses showed significance of scaling tests A, B, C and D which indicated the inadequacy of three parameter (additive-dominance) model. Simple scaling tests as well as χ^2 value of joint scaling test were significant for all the families revealed inadequacy for additive dominance model.

According to Hayman's six parameter model, additive (d) effect was found significantly positive in cross 1, 3 and 4 while significantly negative in cross 5. The dominance (h) effect was found significant and positive in crosses 1 and 4 while, in crosses 2, 3 and 5 it was observed significantly negative. The additive $\times$ additive (i) type of interaction was also positively significant in crosses 1 and 4 whereas found negatively significant in crosses 2, 3 and 5. The additive $\times$ dominance (j) component was found positive and significant in crosses 1 and 4 and negatively significant in cross 5 only. Negative and significant dominance $\times$ dominance (l) effect was found in crosses 1 and 4 as well as crosses 2, 3 and 5 showed positively significant effects.

The perusal of table 4.3.12 indicated that six parameter model was best fitted for cross 4 and 6; five parameters was best fitted for crosses 1, 3 and 5; while four parameter model was best fitted for cross 2 only. The additive effect (i) was significantly positive for all crosses except cross 6. Dominance effect (h) was found significantly positive for crosses 1 and 4 but negatively significant for remaining crosses 2, 3, 5 and 6. The additive $\times$ additive (i) type of interaction was also found significantly positive in crosses 1 and 4 as well as significantly negative in crosses 3, 5 and 6. The additive $\times$ dominance (j) type of interaction was showed significantly positive for cross 4 while negatively significant for cross 6 only and other crosses showed non significant effect. Crosses 2, 3, 5 and 6 showed positively significant effect and crosses 1 and 4 showed negatively significant effect for dominance $\times$ dominance (l) type of interaction. The significant opposite sign associated with dominance (h) and dominance $\times$ dominance (l) parameter in all six crosses proposed that role of duplicate type of epistasis for this trait.

Velu *et al.* (2011), Rai *et al.* (2012) and Goah *et al.* (2020) observed additive gene action for inheritance of this trait while Nandaniya *et al.* (2016^a) recorded the non-additive gene action. In crosses 4 and 6, all three type of gene action was present with predominance of non-additive gene action which suggested the cyclic method of breeding can be used keeping population size would be advisable to pool the desirable genes to develop elite line by utilizing additive and non-additive component of inheritance.

4.3.13 Zinc content (mg/kg)

The results on zinc content (mg/kg) showed in table 4.3.13 which indicates the significance of scaling tests A, B, C and D in cross 1, 2 and 5; A, B, C in cross 3; B, C and D in cross 6; while significance of scaling test A and D in cross 4 indicated the inadequacy of additive-dominance model. Scaling tests as well as χ^2 value of joint scaling test for three parameter model were significant for all the families revealed inadequacy for additive dominance model.

As par the Hayman's six parameter model, additive (d) effect was significantly negative in crosses 4 and 5, while in cross 6, it was positively significant. The dominance (h) effect was significant and negative in 2, 4, 5 and 6 crosses while significant and positive for cross 3. The additive $\times$ additive (i) type of interaction was significantly negative in crosses 2, 4, 5 and 6; while in case of cross 1 it was found significantly positive for this parameter. The additive $\times$ dominance (j) component was negatively significant in cross 2, 3, 4 and 5 whereas positively significant in cross 6 only. Dominance $\times$ dominance (l) effect was significant and positive in crosses 2, 3, 4 and 6 but none of cross possessed significant and negative interaction.

Looking to the results of best fitting model, six parameter model was best fitted for crosses 4 and 6, five parameter best fitted for cross 2 only whereas four parameter model was best fitted for crosses 1, 3 and 5. The additive effect (i) was significantly positive for crosses 2 and 3, while it was significantly negative for cross 1 only. Dominance effect (h) was found significant and negative for all crosses except cross 1, it was found significantly positive. The additive $\times$ additive (i) type of interaction was found significantly positive for cross 1 and significantly negative for cross 4, 5 and 6. The additive $\times$ dominance (j) type of interaction was found significantly positive for cross 6 while it was observed negatively significant for cross 2 and 4. The dominance $\times$ dominance (l) type of interaction was found significant and positive for crosses 2, 3, 4 and 6. The significant opposite sign associated with dominance (h) and dominance $\times$ dominance (l) component in all crosses except for cross 1 and 5 indicated that role of duplicate type of epistasis for this trait.

Velu *et al.* (2011), Rai *et al.* (2012) and Goah *et al.* (2020) observed additive gene action for inheritance of this trait while Nandaniya *et al.* (2016^a) recorded the non-additive gene action. In cross 1 and 5 significant value of chi-square for best fitting model suggest that the digenic model is not adequate to describe, there may be presence of higher order gene interactions. In other crosses, all three type of gene action was present which suggested the population improvement can be used to improve this trait.

4.3.14 Oil content (%)

The estimates of gene effects for oil content out and tabulated as in Table 4.3.14. The significance of scaling tests A, B, C in cross 1 and 5 indicated the inadequacy of additive-dominance model. χ^2 value of joint scaling test were significant for cross 1 and 5 revealed inadequacy for additive dominance model. Whereas crosses 2, 3 and 4 are found non significant for scaling tests A, B, C and D indicated that three parameter (additive-dominance) model was adequate for these crosses.

Three parameter model was adequate for crosses 2, 3, 4 and 6. additive effect (d) and was non significant for all crosses while dominance effect (h) was significant for 1, 4 and 6 crosses. In relation to Hayman's six parameter model, additive effect (d) and dominance effect (h) was non significant for all crosses. The additive $\times$ additive (i) type of interaction was negatively significant in cross 6 and non significant in remaining crosses. The additive $\times$ dominance (j) parameter was negatively significant in cross 3 while in other crosses it was observed non significant. Dominance $\times$ dominance (l) effect was negatively significant in cross 1 and 5 and it was found positively significant for cross 6.

Four parameter model best suited for cross 1 and 5. The additive effect was observed non significant for all crosses. The dominance (h) effect was found significant and positive for cross 1 and 5. The additive $\times$ additive (i) type of interaction was found non significant in cross 1 and 5. The additive $\times$ dominance (j) type of interaction was not found for all crosses. The dominance $\times$ dominance (l) type of interaction was found significantly negative for crosses 1 and 5. The significant opposite sign associated with dominance (h) and dominance $\times$ dominance (l) component in crosses 1 and 5 depicted that role of duplicate type of epistasis for governing inheritance of this trait. Duplicate type of epistasis present in crosses 1 and 5 so population improvement can be used while to fix this trait.

Table 4.3.11 Estimation of scaling tests and gene effects for tannin content in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Tannin content									
Scaling tests (Mather, 1949)									
A	6.89	±	10.32	99.70**	±	1.85	168.06**	±	3.31
B	-177.85**	±	9.76	24.83**	±	2.57	192.11**	±	3.43
C	-38.89**	±	10.95	356.40**	±	5.21	320.19**	±	5.28
D	66.04**	±	8.93	115.93**	±	2.91	-19.99**	±	3.42
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	202.59**	±	0.33	126.79**	±	0.32	122.22**	±	0.42
d	-8.10**	±	0.33	2.96**	±	0.32	8.50**	±	0.42
h	-1.45*	±	0.66	-1.75*	±	0.68	20.53**	±	0.76
χ ²	344.05**			6877.50**			8391.57**		
Six parameter model (Hayman, 1958)									
m	192.66**	±	2.71	202.32**	±	1.25	197.80**	±	1.26
d	84.07**	±	7.08	37.16**	±	1.48	0.47	±	2.30
h	-132.99**	±	17.87	-247.33**	±	5.87	49.47**	±	6.88
i	-132.07**	±	17.86	-231.86**	±	5.82	39.97**	±	6.84
j	92.37**	±	7.09	37.43**	±	1.52	-12.02**	±	2.34
l	303.03**	±	30.38	107.33**	±	7.90	-400.13**	±	10.62
Best fitting model (Mather and Jinks, 1982)									
m	345.26**	±	17.84	120.95**	±	0.33	73.79**	±	6.85
d	-8.08**	±	0.33	-0.26	±	0.33	12.08**	±	0.42
h	-467.04**	±	47.70	169.28**	±	2.81	447.31**	±	17.17
i	-142.39**	±	17.84	-	-		39.38**	±	6.83
j	-	-		52.83**	±	2.99	-	-	
l	323.71**	±	30.34	-184.74**	±	2.92	-398.60**	±	10.61
χ ²	169.60**			1582.92**			26.33**		
Types of epistasis	Duplicate			Duplicate			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.11 Continue...

Cross	Cross 4 (98222 B × 15550 R)				Cross 5 (1202 B × 16317 R)				Cross 6 (05888 B × 16066 R)			
Tannin content												
Scaling tests (Mather, 1949)												
A	77.73**	±	3.71		-113.73**	±	2.44		-65.36**	±	4.19	
B	-23.51**	±	2.44		-67.44**	±	8.32		-54.23**	±	2.52	
C	33.23**	±	10.93		-193.85**	±	6.74		-128.90**	±	4.56	
D	-10.50	±	5.80		-6.34	±	5.39		-4.65	±	3.17	
Gene effects in different models												
Three parameter model (Cavali, 1952)												
m	151.90**	±	0.42		140.50**	±	0.41		191.41**	±	0.43	
d	-41.49**	±	0.42		12.49**	±	0.41		5.30**	±	0.43	
h	43.88**	±	0.80		41.01**	±	0.80		-100.06**	±	0.81	
χ ²	561.93**				2833.27**				1298.80**			
Six parameter model (Hayman, 1958)												
m	181.29**	±	2.70		121.32**	±	1.63		116.48**	±	1.06	
d	7.11**	±	2.12		-7.96	±	4.28		-0.12	±	2.35	
h	64.84**	±	11.64		62.47**	±	10.81		-84.12**	±	6.39	
i	20.99	±	11.61		12.67	±	10.78		9.30	±	6.33	
j	50.62**	±	2.167		-23.14**	±	4.30		-5.56*	±	2.39	
l	-75.22**	±	13.84		168.49**	±	18.42		110.28**	±	10.46	
Best fitting model (Mather and Jinks, 1982)												
m	151.06**	±	0.43		171.64**	±	7.90		195.42**	±	0.44	
d	-43.51**	±	0.43		14.95**	±	0.41		5.44**	±	0.44	
h	95.26**	±	4.21		-224.30**	±	18.70		-218.15**	±	3.49	
i	-		-		-26.73**	±	7.90		-		-	
j	100.05**	±	4.28		-		-		-13.68**	±	4.46	
l	-51.41**	±	4.27		247.34**	±	11.13		124.72**	±	3.56	
χ ²	3.27				28.86**				2.15			
Types of epistasis	Duplicate				Duplicate				Duplicate			

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.12 Estimation of scaling tests and gene effects for Iron content in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Iron content									
Scaling tests (Mather, 1949)									
A	-17.44**	±	0.93	-37.32**	±	1.80	-57.24**	±	1.89
B	-32.35**	±	0.79	-32.90**	±	1.54	-55.84**	±	1.13
C	-138.55**	±	0.60	-19.71**	±	1.35	-90.15**	±	2.86
D	-44.38**	±	0.62	25.25**	±	1.24	11.46**	±	1.71
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	61.77**	±	0.11	75.15**	±	0.17	72.37**	±	0.21
d	6.07**	±	0.12	0.90**	±	0.18	9.47**	±	0.21
h	-17.04**	±	0.21	-16.18**	±	0.40	-15.35**	±	0.43
χ ²	53050.50**			882.24**			3700.21**		
Six parameter model (Hayman, 1958)									
m	35.79**	±	0.10	65.65**	±	0.25	48.99**	±	0.68
d	18.03**	±	0.58	-1.42	±	1.13	8.63**	±	1.04
h	79.91**	±	1.26	-61.94**	±	2.52	-30.49**	±	3.46
i	88.76**	±	1.24	-50.50**	±	2.48	-22.92**	±	3.43
j	7.45**	±	0.60	-2.20	±	1.15	-0.70	±	1.06
l	-38.98**	±	2.42	120.72**	±	4.74	136.00**	±	5.07
Best fitting model (Mather and Jinks, 1982)									
m	-11.45**	±	1.23	76.29**	±	0.18	97.55**	±	3.27
d	10.94**	±	0.13	0.82**	±	0.18	9.30**	±	0.21
h	111.52**	±	3.59	-39.42**	±	1.14	-164.41**	±	7.72
i	86.44**	±	1.23	-	-	-	-22.24**	±	3.27
j	-	-	-	-	-	-	-	-	-
l	-34.06**	±	2.39	27.99**	±	1.29	134.61**	±	4.61
χ ²	153.63**			415.66**			0.43		
Types of epistasis	Duplicate			Duplicate			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.12 Continue....

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Iron content									
Scaling tests (Mather, 1949)									
A	23.51**	±	1.50	-30.02**	±	1.43	-29.86**	±	1.08
B	16.79**	±	1.35	-19.15**	±	1.37	-23.72**	±	0.82
C	-92.42**	±	3.64	-34.28**	±	1.43	-31.89**	±	1.53
D	-66.36**	±	1.96	7.44**	±	1.09	10.85**	±	0.89
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	62.41**	±	0.31	78.37**	±	0.18	82.48**	±	0.22
d	2.77**	±	0.31	2.92**	±	0.18	0.71**	±	0.23
h	-16.27**	±	0.53	-34.72**	±	0.39	-14.05**	±	0.37
χ ²	1182.43**			932.77**			1577.28**		
Six parameter model (Hayman, 1958)									
m	30.25**	±	0.86	56.71**	±	0.28	72.31	±	0.33
d	5.78**	±	0.91	-2.72**	±	0.93	-4.95	±	0.59
h	116.02**	±	3.96	-44.29**	±	2.23	-36.04	±	1.83
i	132.71**	±	3.92	-14.88**	±	2.18	-21.69	±	1.79
j	3.35**	±	0.96	-5.43**	±	0.95	-3.07	±	0.65
l	-173.01**	±	5.14	64.05**	±	4.00	75.27	±	2.83
Best fitting model (Mather and Jinks, 1982)									
m	-71.01**	±	3.93	94.38**	±	2.19	109.15**	±	1.81
d	2.42**	±	0.33	2.49**	±	0.18	-1.88**	±	0.27
h	289.04**	±	8.90	-106.86**	±	6.08	-111.32**	±	4.54
i	132.71**	±	3.92	-14.34**	±	2.18	-21.69**	±	1.79
j	6.71**	±	1.93	-	-	-	-6.14**	±	1.30
l	-173.01**	±	5.14	63.06**	±	3.99	75.27**	±	2.83
χ ²	-			32.44**			-		
Types of epistasis	Complementary			Duplicate			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.13 Estimation of scaling tests and gene effects for zinc content in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Zinc content									
Scaling tests (Mather, 1949)									
A	-4.09**	±	0.57	-12.77**	±	0.60	-17.26**	±	0.88
B	-4.13**	±	1.06	4.04**	±	0.73	-10.65**	±	0.79
C	-13.17**	±	1.16	-3.78**	±	1.02	-29.66**	±	1.42
D	-2.48**	±	0.75	2.47**	±	0.57	-0.87	±	0.78
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	43.44**	±	0.17	41.60**	±	0.15	42.33**	±	0.19
d	-0.47**	±	0.17	7.78**	±	0.15	1.64**	±	0.19
h	-3.38**	±	0.28	-1.85**	±	0.29	3.89**	±	0.37
χ ²	154.93**			518.90**			706.41**		
Six parameter model (Hayman, 1958)									
m	39.54**	±	0.25	40.81**	±	0.20	40.42**	±	0.29
d	-0.29	±	0.55	0.73	±	0.40	-0.86	±	0.50
h	1.71	±	1.52	-5.72**	±	1.18	8.13**	±	1.61
i	4.95**	±	1.50	-4.94**	±	1.14	1.74	±	1.56
j	0.02	±	0.58	-8.40**	±	0.44	-3.30**	±	0.54
l	3.26	±	2.49	13.67**	±	1.91	26.17**	±	2.46
Best fitting model (Mather and Jinks, 1982)									
m	37.55**	±	0.50	42.15**	±	0.17	44.53**	±	0.21
d	-0.37*	±	0.17	9.13**	±	0.17	1.91**	±	0.19
h	3.60**	±	0.63	-7.01**	±	0.81	-21.52**	±	1.05
i	6.84**	±	0.55	-	-	-	-	-	-
j	-	-	-	-17.41**	±	0.86	-	-	-
l	-	-	-	6.24**	±	0.84	28.03**	±	1.08
χ ²	2.33			18.65**			38.53**		
Types of epistasis	-			Duplicate			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.13 Continue....

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Zinc content									
Scaling tests (Mather, 1949)									
A	-10.71**	±	1.07	-3.26**	±	1.22	-1.52	±	0.96
B	0.24	±	0.72	7.61**	±	1.11	-8.02**	±	0.96
C	2.81	±	1.43	11.41**	±	1.53	-3.28*	±	1.57
D	6.64**	±	0.90	3.53**	±	1.05	3.13**	±	0.90
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	35.82**	±	0.13	40.10**	±	0.19	41.20**	±	0.21
d	-0.25*	±	0.13	0.03	±	0.19	0.51*	±	0.22
h	7.80**	±	0.25	-4.42**	±	0.31	1.61**	±	0.39
χ ²	107.60**			102.83**			69.32**		
Six parameter model (Hayman, 1958)									
m	40.58**	±	0.33	40.10**	±	0.34	41.93**	±	0.33
d	-5.55**	±	0.61	-4.89**	±	0.78	3.34**	±	0.59
h	-5.29**	±	1.83	-11.53**	±	2.12	-4.16*	±	1.85
i	-13.27**	±	1.81	-7.05**	±	2.10	-6.25**	±	1.80
j	-5.47**	±	0.62	-5.43**	±	0.81	3.24**	±	0.64
l	23.74**	±	2.84	2.71	±	3.49	15.80**	±	2.86
Best fitting model (Mather and Jinks, 1982)									
m	49.16**	±	1.82	45.18**	±	0.69	47.97**	±	1.82
d	-0.08	±	0.13	0.19	±	0.20	0.10	±	0.23
h	-29.03**	±	4.57	-10.16**	±	0.81	-19.96**	±	4.56
i	-13.27**	±	1.81	-5.58**	±	0.73	-6.25**	±	1.80
j	-10.94**	±	1.25	-	-		6.49**	±	1.28
l	23.74**	±	2.84	-	-		15.80**	±	2.86
χ ²	-			44.99**			-		
Types of epistasis	Duplicate			-			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.14 Estimation of scaling tests and gene effects for oil content in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Oil content									
Scaling tests (Mather, 1949)									
A	1.29**	±	0.46	-0.45	±	0.47	-0.85	±	0.46
B	2.08**	±	0.53	0.30	±	0.42	0.40	±	0.43
C	2.19**	±	0.68	-0.09	±	0.75	-0.26	±	0.64
D	-0.59	±	0.42	0.03	±	0.38	0.09	±	0.33
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	5.38**	±	0.04	5.27**	±	0.12	5.23**	±	0.11
d	0.02	±	0.04	0.07	±	0.12	0.18	±	0.11
h	0.45**	±	0.15	0.26	±	0.23	0.34	±	0.22
χ ²	24.03**			1.69			5.12		
Six parameter model (Hayman, 1958)									
m	5.84**	±	0.14	5.40**	±	0.14	5.39**	±	0.11
d	-0.36	±	0.32	-0.20	±	0.25	-0.31	±	0.25
h	1.08	±	0.87	0.17	±	0.80	0.21	±	0.71
i	1.18	±	0.85	-0.06	±	0.77	-0.18	±	0.67
j	-0.39	±	0.32	-0.37	±	0.29	-0.62*	±	0.28
l	-4.55**	±	1.46	0.21	±	1.25	0.63	±	1.20
Best fitting model (Mather and Jinks, 1982)									
m	5.34**	±	0.04	-	-		-	-	
d	0.02	±	0.04	-	-		-	-	
h	2.54**	±	0.48	-	-		-	-	
i	-	-		-	-		-	-	
j	-	-		-	-		-	-	
l	-2.65**	±	0.57	-	-		-	-	
χ ²	3.01			-			-		
Types of epistasis	Duplicate			-			-		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.14 Continue...

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Oil content									
Scaling tests (Mather, 1949)									
A	0.04	±	0.39	1.23**	±	0.45	-0.59	±	0.42
B	0.09	±	0.41	0.86*	±	0.42	-0.67	±	0.42
C	-0.45	±	0.65	1.57*	±	0.66	0.46	±	0.62
D	-0.29	±	0.32	-0.26	±	0.35	0.86*	±	0.35
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	5.04**	±	0.11	5.16**	±	0.11	5.14**	±	0.10
d	-0.10	±	0.10	0.11	±	0.11	-0.14	±	0.11
h	0.55**	±	0.21	0.37	±	0.21	0.40*	±	0.18
χ ²	0.84			11.02*			6.35		
Six parameter model (Hayman, 1958)									
m	5.23**	±	0.12	5.46**	±	0.12	5.51**	±	0.12
d	-0.12	±	0.22	0.21	±	0.25	-0.09	±	0.25
h	1.14	±	0.69	0.70	±	0.75	-1.30	±	0.74
i	0.57	±	0.65	0.52	±	0.71	-1.72*	±	0.71
j	-0.02	±	0.25	0.18	±	0.28	0.03	±	0.28
l	-0.70	±	1.10	-2.61*	±	1.22	2.97*	±	1.19
Best fitting model (Mather and Jinks, 1982)									
m	-		-	4.99**	±	0.12	-		-
d	-		-	0.06	±	0.11	-		-
h	-		-	1.96**	±	0.54	-		-
i	-		-	-		-	-		-
j	-		-	-		-	-		-
l	-		-	-1.79**	±	0.56	-		-
χ ²	-			0.93			-		
Types of epistasis	-			Duplicate			-		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.15 Estimation of scaling tests and gene effects for protein content in six crosses of pearl millet

Cross	Cross 1 (05888 B × 15001 R)			Cross 2 (02889 B × 16317 R)			Cross 3 (01555 B × 15990 R)		
Protein content									
Scaling tests (Mather, 1949)									
A	-4.17**	±	0.80		2.69**	±	0.53		-0.69 ± 0.71
B	1.00	±	0.65		3.17**	±	0.70		3.36** ± 0.68
C	-0.48	±	1.06		5.57**	±	0.82		5.43** ± 1.23
D	1.34*	±	0.63		-0.15	±	0.49		1.38* ± 0.63
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	9.21**	±	0.17		7.72**	±	0.16		7.30** ± 0.18
d	2.19**	±	0.18		1.26**	±	0.17		1.97** ± 0.17
h	1.36**	±	0.29		-1.04**	±	0.25		1.81** ± 0.34
χ ²	30.71**				65.39**				40.74**
Six parameter model (Hayman, 1958)									
m	9.93**	±	0.22		7.84**	±	0.16		8.99** ± 0.24
d	0.001	±	0.45		0.97*	±	0.37		0.39 ± 0.39
h	-1.32	±	1.30		-0.37	±	1.02		-1.35 ± 1.32
i	-2.69*	±	1.27		0.29	±	0.99		-2.76* ± 1.27
j	-2.58**	±	0.49		-0.24	±	0.42		-2.02** ± 0.44
l	5.86**	±	2.11		-6.15**	±	1.71		0.09 ± 2.01
Best fitting model (Mather and Jinks, 1982)									
m	-	-			6.78**	±	0.20	-	-
d	-	-			1.16**	±	0.17	-	-
h	-	-			4.97**	±	0.78	-	-
i	-	-			-	-	-	-	-
j	-	-			-	-	-	-	-
l	-	-			-5.64**	±	0.70	-	-
χ ²	-				0.35			-	
Types of epistasis	-			Duplicate			-		

* and **, significant at 5% and 1% level of significance, respectively

Table 4.3.15 Continue....

Cross	Cross 4 (98222 B × 15550 R)			Cross 5 (1202 B × 16317 R)			Cross 6 (05888 B × 16066 R)		
Protein content									
Scaling tests (Mather, 1949)									
A	-4.81**	±	0.77	3.93**	±	0.72	-3.68**	±	0.67
B	-1.25*	±	0.58	6.66**	±	0.84	5.18**	±	0.55
C	-3.09**	±	0.76	9.55**	±	0.94	6.72**	±	0.81
D	1.48*	±	0.58	-0.52	±	0.66	2.61**	±	0.50
Gene effects in different models									
Three parameter model (Cavali, 1952)									
m	9.25**	±	0.08	6.22**	±	0.10	8.64**	±	0.15
d	0.60**	±	0.08	1.17**	±	0.11	2.64**	±	0.16
h	0.14	±	0.14	1.10**	±	0.21	-0.75**	±	0.23
χ ²	54.02**			159.83**			194.60**		
Six parameter model (Hayman, 1958)									
m	8.77**	±	0.17	8.34**	±	0.20	9.45**	±	0.16
d	-1.12*	±	0.46	-0.14	±	0.52	-1.27**	±	0.38
h	-2.65*	±	1.18	1.31	±	1.35	-6.24**	±	1.03
i	-2.96*	±	1.17	1.04	±	1.33	-5.22**	±	1.01
j	-1.77**	±	0.47	-1.36*	±	0.53	-4.42**	±	0.42
l	9.02**	±	2.02	-11.63**	±	2.30	3.71*	±	1.73
Best fitting model (Mather and Jinks, 1982)									
m	12.36**	±	1.17	5.82**	±	0.11	13.50**	±	1.02
d	0.65**	±	0.08	1.16**	±	0.11	3.15**	±	0.18
h	-11.67**	±	3.15	10.04**	±	0.75	-9.95**	±	2.71
i	-2.96*	±	1.17	-	-		-5.22**	±	1.01
j	-3.55**	±	0.95	-	-		-8.85**	±	0.84
l	9.02**	±	2.02	-9.77**	±	0.79	3.71*	±	1.73
χ ²	-			6.66*			-		
Types of epistasis	Duplicate			Duplicate			Duplicate		

* and **, significant at 5% and 1% level of significance, respectively

4.3.15 Protein content (%)

The results manifested protein content (%) is depicted in Table 4.3.15. The significance of scaling tests A, B, C and D in cross 4 and 6; A, B and C in cross 2 and 5; B, C and D in cross 3, while A and D scaling tests were significant in cross 1 which leads to the inadequacy of three parameter (additive-dominance) model. Simple scaling tests as well as χ^2 value of joint scaling test were significant for all the families revealed inadequacy for additive dominance model but there is some negligible amount of gene interaction was present so six parameter model (Hayman, 1958) was found adequate for cross 1 and 3 only.

In relation to Hayman's six parameter model, additive (d) effect was significant and positive in cross 2 while significant and negative in crosses 4 and 6. The dominance (h) effect was negatively significant in crosses 4 and 6 while other crosses remain non significant. The additive $\times$ additive (i) type of interaction was significant and negative in crosses 1, 3, 4 and 6 whereas it was found non significant in cross 2 and 5. The additive $\times$ dominance (j) component was negatively significant in all crosses except cross 2. While crosses 1, 4 and 6 was positively significant as well as cross 2 and 5 was negatively significant for dominance $\times$ dominance (l) effect.

As per the results of best fitting model, six parameter model was found best for crosses 4 and 6; four parameter was found best suited for cross 2 and 5. Additive (d) effect was found significantly positive for all crosses. While dominance (h) effect was found significantly negative for cross 2 and 5 whereas it was significantly negative for cross 4 and 6. The additive $\times$ additive (i) and additive $\times$ dominance (j) type of interaction was found significantly negative in cross 4 and 6. The dominance $\times$ dominance (l) type of interaction was found significantly negative in cross 2 and 4 whereas significantly positive for crosses 4 and 6.

Kumar *et al.* (2013) and Patel *et al.* (2014) observed similar results that influence of additive and non-additive gene action for inheritance of this trait. In cross 4 and 6, dominance $\times$ dominance (l) type of interaction present this suggested the heterosis breeding for this trait.

4.4 Magnitude of heterosis and inbreeding depression

The extent of heterotic effects i.e. relative heterosis (RH) and heterobeltiosis (HB) as well as inbreeding depression (ID) were estimated for all the characters under study. The relative heterosis was estimated over mid-parent and heterobeltiosis over better parent in F_1 hybrid value and inbreeding depression in F_2 generation for seed yield and its component characters in six crosses of Pearl millet are presented in Table 4.4. The character-wise results are presented and discussed as under.

4.4.1 Days to flowering

For the purpose of estimation of heterosis, parent having less number of days to flowering was considered as better parent. The results in table 4.4 showed that the magnitude of heterosis over mid parent and better parent.

The estimates of relative heterosis (RH) for days to flowering in six crosses ranged from -7.08 per cent in cross 1 (05888 B $\times$ 15001 R) to 3.81 per cent in cross 3 (01555 B $\times$ 15990 R). Two crosses namely 05888 B $\times$ 15001 R and 02889 B $\times$ 16317 R depicted significant and negative relative heterosis, which is desired for earliness. Heterobeltiosis calculated by taking early flowering parent as better parent. Similar to relative heterosis only one cross 05888 B $\times$ 15001 R depicted negative and significant heterobeltiosis.

The crosses 05888 B $\times$ 15001 R (-9.22 per cent), 02889 B $\times$ 16317 R (-3.59) and 98222 B $\times$ 15550 R (-2.60 per cent) showed negatively significant inbreeding depression, While cross 3, 5 and 6 showed positively significant inbreeding depression.

Similar results for significant relative heterosis and heterobeltiosis for days to flowering was also observed by Lal and Singh (1968), Presterl and Weltzien (2003), Pethani *et al.* (2004), Yadav (2006), Vetriventhan *et al.* (2008), Vagadiya *et al.* (2010), Maryam (2015), Jog *et al.* (2016), Pucher *et al.* (2016), Ladumor *et al.* (2018) and Zakari *et al.* (2019). Lal and Singh (1968), Shinde *et al.* (1984), Rai *et al.* (1985), Shanmuganathan (2010) and Jog *et al.* (2016) showed similar negative inbreeding depression for this trait.

4.4.2 Plant height (cm)

The crosses 05888 B $\times$ 15001 R (23.83 per cent), 02889 B $\times$ 16317 R (10.22 per cent) and 98222 B $\times$ 15550 R (16.76 per cent) exhibited significant and positive relative heterosis whereas cross 3 (01555 B $\times$ 15990 R) and cross 6 (05888 B $\times$ 16066 R) exhibited significant and negative relative heterosis. It was ranged from -7.83 per cent for cross 3 (01555 B $\times$ 15990 R) to 23.83 per cent for cross 1 (05888 B $\times$ 15001 R).

All crosses showed significant and positive heterobeltiosis except cross 6 (05888 B $\times$ 16066 R). Heterobeltiosis ranged from 0.28 per cent for cross 6 (05888 B $\times$ 16066 R) to 32.02 per cent for cross 1 (05888 B $\times$ 15001 R). Cross 1 (05888 B $\times$ 15001 R) exhibited the highest significant and positive heterobeltiosis effect (32.02 %) followed by cross 4 (98222 B $\times$ 15550 R) (16.76 %) and cross 2 (02889 B $\times$ 15001 R) (10.22 %). The estimates of inbreeding depression was significant and positive for the cross 4 (98222 B $\times$ 15550 R) (13.79 %). It ranged from -10.74 per cent in cross 6 (05888 B $\times$ 16066 R) to 13.79 per cent in cross 4 (98222 B $\times$ 15550 R).

These results were in agreement with those obtained by Lal and Singh (1968), Pethani *et al.* (2004), Yadav (2006), Vetriventhan *et al.* (2008), Maryam (2015), Jog *et al.* (2016), Pucher *et al.* (2016), Karvar *et al.* (2017), Ladumor *et al.* (2018) and Zakari *et al.* (2019). Lal and Singh (1968), Shinde *et al.* (1984) and Rai *et al.* (1985) also observed similar significant and negative inbreeding depression for plant height.

4.4.3 Number of effective tiller per plant

A significant and positive relative heterosis was estimated for cross 3 (01555 B $\times$ 15990 R) (24.73 %) but positive non-significant for crosses 1 (5888 B $\times$ 15001 R) (9.86 %) and cross 6 (05888 B $\times$ 16066 R) (1.15 %). Positive better parent heterosis is desirable for this character. Better parent heterosis ranged from -25.00 % in cross 5 (1202 B $\times$ 16317 R) to 18.37 % in cross 3 (01555 B $\times$ 15990 R). None of the crosses recorded positive and significant heterobeltiosis, While in the cross 1 (05888 B $\times$ 15001 R) and cross 3 (01555 B $\times$ 15990 R) it was found significant. Values of inbreeding depression were negative for all six crosses. Inbreeding depression ranged from -25.68 % in cross 2 (02889 B $\times$ 16317 R) to -2.59 % in cross 3 (01555 B $\times$ 15990 R).

Similar results for heterosis pertaining to number of tiller per plant were reported by Murty *et al.* (1967), Lal and Singh (1968), Pethani *et al.* (2004), Vetriventhan *et al.* (2008), Jethva *et al.* (2012), Maryam (2015), Jog *et al.* (2016), Pucher *et al.* (2016), Karvar *et al.* (2017) and Ladumor *et al.* (2018). While for inbreeding depression similar negative result was recorded by Lal and Singh (1968) and Jog *et al.* (2016) but Shinde *et al.* (1984) observed the significant inbreeding depression for this character.

4.4.4 Earhead length (cm)

In case of mid parent heterosis it was ranged from -13.03 % in cross 5 (1202 B $\times$ 16317 R) to 17.11 % in cross 1 (05888B $\times$ 15001 R). Cross 1 (05888 B $\times$ 15001 R) (17.11 %) and cross 2 (02889 B $\times$ 16317 R) (9.28 %) exhibit highly significant and positive relative heterosis, while in cross 5 and 6 it was significant and negative relative heterosis. The estimates of better parent heterosis ranged from -20.39 % in cross 5 (12002 B $\times$ 16317 R) to 5.54 % in cross 1 (05888 B $\times$ 15001 R). Significant and positive heterosis over better parent observed in cross 1 (05888 B $\times$ 15001 R) (17.11 %) and cross 2 (02889 B $\times$ 16317 R) (9.28 %). The highest heterobeltiosis reported in cross 1 (05888 B $\times$ 15001 R) (5.54 per cent). The estimates of inbreeding depression was ranged from -27.47 % in cross 6 (05888 B $\times$ 16066 R) to 7.86 % in cross 4 (98222 B $\times$ 15550 R). The cross 4 (98222 B $\times$ 15550 R) (7.86 %) exhibited significant positive inbreeding depression.

Murty *et al.* (1967), Lal and Singh (1968), Pethani *et al.* (2004), Yadav (2006), Vetriventhan *et al.* (2008), Jethva *et al.* (2012), Maryam (2015), Jog *et al.* (2016), Pucher *et al.* (2016), Karvar *et al.* (2017), Ladumor *et al.* (2018) and Zakari *et al.* (2019) also reported similar negative to positive range of heterosis for earhead length. Similar non-significant inbreeding depression was reported by Lal and Singh (1968) and Jog *et al.* (2016).

4.4.5 Earhead girth (mm)

Mid parent heterosis ranged from -0.19 % (05888 B $\times$ 15001 R) to 12.49 % (98222 B $\times$ 15550 R). Crosses 2 and 4 exhibit significant and positive relative heterosis. Significant and positive heterosis over better parent observed in cross 02889 B $\times$ 16317 R (10.67 %) and cross 98222 B $\times$ 15550 R (9.63 %). Better parent heterosis ranged from -2.12 % (05888 B $\times$ 15001 R) to 10.67 % (02889 B $\times$ 16317 R). Inbreeding depression was ranged from -10.30 % (01555 B $\times$ 15990 R) to 12.29 % (98222 B $\times$ 15550 R). The cross 4 (98222 B $\times$ 15550 R) (12.29 %) exhibited significant and positive inbreeding depression, whereas cross 3 (01555 B $\times$ 15990 R) (-7.90 %) exhibited non-significant and negative inbreeding depression.

Murty *et al.* (1967), Lal and Singh (1968), Vetriventhan *et al.* (2008), Jethva *et al.* (2012), Maryam (2015), Jog *et al.* (2016), Pucher *et al.* (2016), Karvar *et al.* (2017), Ladumor *et al.* (2018), Zakari *et al.* (2019) reported the similar significant mid-parent heterosis and better parent heterosis. While, Lal and Singh (1968) and Jog *et al.* (2016)'s findings for inbreeding depression were in agreement with those finding for earhead girth.

4.4.6 Days to maturity

Data presented in table 4.4 revealed that all the two crosses showed negative and highly significant relative heterosis for this trait ranged from -6.36 per cent in cross 6 (05888 B $\times$ 16088 R) to 0.24 per cent in cross 2 (02889 B $\times$ 16317 R). Heterobeltiosis was observed negatively significant in cross 6 (05888 B $\times$ 16088 R) (-6.07 %) while in crosses 1 (05888B $\times$ 15001 R) and 3 (01555 B $\times$ 15990 R) it was observed negative and non-significant. The crosses 05888B $\times$ 15001R (-0.10 per cent), 01555 B $\times$ 15990 R (-0.61 per cent), 98222 B $\times$ 15550 R (-6.17 per cent) and 1202 B $\times$ 16317 R (-1.83 per cent) showed negative non-significant inbreeding depression.

Pethani *et al.* (2004), Vagadiya *et al.* (2010), Jog *et al.* (2016), Karvar *et al.* (2017) and Ladumor *et al.* (2018) also found results in accordance with findings for days to maturity. Jog *et al.* (2016) observed similar inbreeding depression ranging from -2.90 to 1.47 per cent.

4.4.7 Test weight (g)

A mid parent heterosis ranged from 1.15 % (1202 B $\times$ 16317 R) to 6.80 % (02889 B $\times$ 16317 R). Positive mid parent heterosis was estimated for all crosses. Heterobeltiosis for this trait ranged from -1.66 % (1202 B $\times$ 16317 R) to 4.21 % (02889 B $\times$ 16317 R) and positive heterobeltiosis over better parent recorded in all crosses except cross 5 (1202 B $\times$ 16317 R) (-1.66 %). Inbreeding depression ranged from 0.98 % (01555 B $\times$ 15990 R) to 5.91 % (98222 B $\times$ 15550 R). Estimates of inbreeding depression were positive but non-significant for all crosses.

Lal and Singh (1968), Presterl and Weltzien (2003), Pethani *et al.* (2004), Vetriventhan *et al.* (2008), Jethva *et al.* (2012), Vagadiya *et al.* (2010), Jog *et al.* (2016), Pucher *et al.* (2016), Karvar *et al.* (2017), Maryam (2017), Kanfany *et al.* (2018), Ladumor *et al.* (2018) and Zakari *et al.* (2019) also reported similar results for non significant heterosis. Lal and Singh (1968), Shinde *et al.* (1984), Rai *et al.* (1985) and Jog *et al.* (2016) were observed similar non significant inbreeding depression for this character.

4.4.8 Grain yield per plant (g)

An examination of the data presented in Table 4.4 indicated that all the cross combinations showed significant heterotic effect with a range from -6.73 per cent in cross 2 (02889 B $\times$ 16317 R) to 35.06 per cent in cross 1 (05888 B $\times$ 15001 R) for relative heterosis. Highest heterotic values for grain yield per plant was observed in cross 1 (05888 B $\times$ 15001 R) (35.06 %) followed by cross 3 (01555 B $\times$ 15990 R) (22.76 %); cross 6 (05888 B $\times$ 16066 R) (16.08 %), cross 4 (98222 B $\times$ 15550 R) (15.40 %) and cross 5 (1202 B $\times$ 16317 R) (14.68 %). The heterotic effect in relation to better parent revealed that out of six crosses, five crosses differed positively significant. The maximum heterobeltiosis was recorded by cross 1 (05888 B $\times$ 15001 R) (20.69 %) followed by cross 6 (05888 B $\times$ 16066 R) (12.08 %), cross 5 (1202 B $\times$ 16317 R) (9.27 %) and cross 4 (98222 B $\times$ 15550 R) (7.18 %). All the six F₂'s tested for inbreeding depression, showed differed inbreeding depression values ranging from -30.54 per cent in cross 6 (05888 B $\times$ 16066 R) to 28.47 per cent in cross 1 (05888 B $\times$ 15001 R). The highest inbreeding depression was recorded in cross 1 (05888 B $\times$ 15001 R) (28.47 %).

Results recorded by researchers are similar for significant relative heterosis and heterobeltiosis for grain yield per plant, *i.e.*, Presterl and Weltzien (2003), Pethani *et al.* (2004), Yadav (2006), Vetriventhan *et al.* (2008), Jethva *et al.* (2012), Vagadiya *et al.* (2010), Maryam (2015), Jog *et al.* (2016), Pucher *et al.* (2016), Karvar *et al.* (2017),

Kanfany *et al.* (2018), Ladumor *et al.* (2018) and Zakari *et al.* (2019). For inbreeding depression, Lal and Singh (1968), Khadr and El-Rouby (1978), Shinde *et al.* (1984), Rai *et al.* (1985), Shanmuganathan (2010) and Jog *et al.* (2016) reported results in agreement with these findings.

4.4.9 Harvest index (%)

The estimates of relative heterosis ranged from -0.88 per cent in cross 2 (02889 B $\times$ 16317 R) to 9.97 per cent in cross 1 (05888 B $\times$ 15001 R). The significant and positive relative heterosis were manifested in cross 1 (05888B $\times$ 15001 R), cross 3 (01555 B $\times$ 15990 R), 4 (98222 B $\times$ 15550 R) and cross 5 (1202 B $\times$ 16317 R) with 9.97 per cent, 6.75 per cent, 4.92 per cent and 5.59 per cent respectively.

Heterobeltiosis varied from -2.34 % (05888 B $\times$ 16066 R) to 6.75 % (05888 B $\times$ 15001 R). significant and positive Heterobeltiosis found in cross 1 (05888 B $\times$ 15001 R) (6.75 %) followed by cross 5 (1202 B $\times$ 16317 R) (5.32 %) and cross 3 (01555 B $\times$ 15990 R) (4.64 %). Inbreeding depression ranged from -3.78 per cent in cross 6 (05888 B $\times$ 16066 R) to 12.92 per cent in cross 3 (01555 B $\times$ 15990 R). Whereas Cross 3 (01555 B $\times$ 15990 R) (12.92 %), cross 4 (98222 B $\times$ 16317 R) (11.19 %), cross 1 (05888 B $\times$ 15001 R) (6.39 %) and cross 5 (1202 B $\times$ 16317 R) (6.09 %) differed significantly and positively from their respective F_1 's.

Yadav (2006), Jethva *et al.* (2012), Vagadiya *et al.* (2010) and Ladumor *et al.* (2018) observed similar results for heterosis. While for inbreeding depression Shanmuganathan (2010) and Jog *et al.* (2016) reported results in agreement with those findings for harvest index.

4.4.10 Carbohydrate (g/100 g)

Out of six crosses, only one cross 05888 B $\times$ 16066 R registered with significant positive relative heterosis with 6.97 per cent. The estimates of relative or mid-parent heterosis for this character ranged from -32.96 per cent in cross 1 (05888 B $\times$ 15001 R) to 6.97 per cent in cross 6 (05888 B $\times$ 16066 R). The maximum heterobeltiosis was manifested by cross 6 (05888 B $\times$ 16066 R) (0.31 %) whereas it was lowest in cross 1 (05888 B $\times$ 15001 R) (-41.19 %). The inbreeding depression for this character ranged from cross 1 (05888 B $\times$ 15001 R) (-46.30 %) to cross 2 (02889 B $\times$ 16317 R) (7.85 %). The maximum inbreeding depression was observed in cross 2 (02889 B $\times$ 16317 R) (7.85 %).

Table 4.4: Estimates of relative heterosis (RH %), heterobeltiosis (HB %) and inbreeding depression (ID %) in six crosses of pearl millet for grain yield and its contributing characters

Estimates (%)	Days to flowering	Plant height	Number of effective tiller per plant	Earhead length	Earhead girth	Days to maturity	Test weight	Grain yield per plant
Cross 1 (05888 B × 15001 R)								
RH %	-7.08**	23.83**	9.86	17.11**	-0.19	-0.83	1.83	35.06**
HB %	-5.05**	32.02**	8.33	5.54	-2.12	-0.74	-2.94	20.69**
ID %	-9.22**	0.39	-10.90	2.71	0.21	-0.10	0.10	28.47**
Cross 2 (02889 B × 16317 R)								
RH %	-2.38*	10.22**	-3.90	9.28*	12.38**	0.24	4.41	-6.73**
HB %	0.13	10.29**	-11.90	1.99	10.67**	0.28	2.10	-13.59**
ID %	-3.59**	-5.88**	-25.68*	2.06	3.96	0.61	2.35	-7.77*
Cross 3 (01555 B × 15990 R)								
RH %	3.81**	-7.83**	24.73*	6.18	0.16	-3.81**	1.98	22.76**
HB %	7.07**	5.65**	18.37	1.27	-3.46	-1.16	0.47	0.51
ID %	16.18**	-8.43**	-2.59	1.22	-10.30**	-0.61	0.93	-4.68
Cross 4 (98222 B × 15550 R)								
RH %	2.99*	16.76**	-8.70	2.34	12.49**	-0.22	-0.81	15.40**
HB %	4.81**	21.13**	-10.64	-4.86	9.63**	0.44	-1.57	7.18**
ID %	-2.60*	13.79**	-41.07**	6.69	12.29**	-6.17	4.27	-24.66**
Cross 5 (1202 B × 16317 R)								
RH %	-1.99	-0.03	-15.89	-13.03**	3.37	0.20	1.88	14.68**
HB %	-0.60	6.09**	-25.00	-20.39**	2.01	0.74	-1.17	9.26**
ID %	8.42**	-6.04**	-12.78	-19.69**	1.09	-1.48	4.17	-23.96**
Cross 6 (05888 B × 16066 R)								
RH %	1.96	-3.14*	1.15	-8.75*	2.54	-6.36**	3.86	16.08**
HB %	2.78*	0.28	-2.22	-10.40*	1.07	-6.07**	-1.38	12.08**
ID %	8.35**	-10.74**	-25.00*	-27.48**	1.11	-1.83	5.98	-30.54**

* and **, significant at 5% and 1% level of significance, respectively

4.4.11 Tannin (mg/100 g)

An examination of the data presented in Table 4.4 indicated that out of six crosses, relative heterosis for tannin content in cross 6 (05888 B $\times$ 16066 R) and cross 2 (02889 B $\times$ 16317 R) estimated highly significant negative with -47.81 per cent and -12.78 per cent, respectively while highly significant positive in cross 4 (98222 B $\times$ 15550 R). It was ranged from -47.81 per cent for cross 6 (05888 B $\times$ 16066 R) to 29.02 per cent for cross 4 (9822 B $\times$ 15550 R). In case of heterobeltiosis, the cross 4 (98222 B $\times$ 15550R) (81.22 %) followed by cross 5 (1202 B $\times$ 16317 R) (50.09 %), cross 3 (01555 B $\times$ 15990 R) (21.89 %) and cross 1 (05888 B $\times$ 15001 R) (3.79 %) differed significantly positive over the better parent.

Inbreeding depression ranged from -91.79 per cent in cross 2 (02889 B $\times$ 16317 R) to 37.68 per cent in cross 5 (1202 B $\times$ 16317 R). Estimates of significant inbreeding depression was observed in cross 2 (02889 B $\times$ 16317 R) with -91.79 per cent, while it was found positively and significant in cross 5 (1202 B $\times$ 16317 R) with 37.68 per cent.

4.4.12 Iron content (mg/kg)

Among the six crosses, none of the cross recorded significant and positive relative heterosis. It was ranged from -36.76 per cent in cross 5 (1202 B $\times$ 16317 R) to -10.05 per cent in cross 3 (01555 B $\times$ 15990 R). Heterobeltiosis ranged from -38.84 per cent for cross 5 (1202 B $\times$ 16317 R) to -15.86 per cent for cross 2 (02889 B $\times$ 16317 R). Out of six crosses, none of the cross showed positive and significant better parent heterosis for this trait. It was observed negative and significant heterobeltiosis for all crosses studied.

Govindaraj *et al.* (2013), Karvar *et al.* (2017), Ladumor *et al.* (2018) and Zakari *et al.* (2019) reported similar heterosis for iron content.

Inbreeding depression ranged from -12.13 per cent in cross 5 (1202 B $\times$ 16317 R) to 45.77 per cent in cross 1 (05888 B $\times$ 15001 R). Cross 1 (05888 B $\times$ 15001 R) (45.77 %) followed by cross 4 (98222 B $\times$ 15550 R) (32.78 %) and (01555 B $\times$ 15990 R) (27.68 %) exhibits higher inbreeding depression value.

4.4.13 Zinc content (mg/kg)

Relative heterosis was ranged from -11.34 per cent in cross 5 (1202 B $\times$ 16317 R) to 22.25 per cent in cross 4 (98222 B $\times$ 15550 R). An experimentation of the data presented in Table 4.4 indicated that among the six crosses highly significant and positive relative heterosis was estimated for cross 4 (98222 B $\times$ 15550 R) (22.25 %), followed by cross 3 (01555 B $\times$ 15990 R) (14.33 %) and cross 6 (05888 B $\times$ 16066 R) (5.02 %). Heterobeltiosis ranged from -1932 per cent in cross 2 (02889 B $\times$ 16317 R) to 21.97 per cent in cross 4 (98222 B $\times$ 15550 R). Out of six crosses only cross 4 (98222 B $\times$ 15550 R) (21.97 %) differed significantly positive over the better parent.

followed by cross 3 (01555 B $\times$ 15990 R) (8.41 %) and cross 6 (05888 B $\times$ 16066 R) (4.76 %) showed positively significant heterosis. Similar significant relative heterosis and heterobeltiosis for iron content was also reported Govindaraj *et al.* (2013), Karvar *et al.* (2017), Ladumor *et al.* (2018) and Zakari *et al.* (2019).

Inbreeding depression ranged from -14.54 per cent for cross 5 (1202 B $\times$ 16317 R) to 20.79 % for cross 3 (01555 B $\times$ 15990 R). Estimates of inbreeding depression were significant and positive in cross 3 (01555 B $\times$ 15990 R) (20.79 %) followed by cross 4 (98222 B $\times$ 15550 R) (7.50 %), cross 6 (05888 B $\times$ 16066 R) (4.26) and cross 1 (05888 B $\times$ 15001 R) (4.06 %) exhibits higher inbreeding depression.

4.4.14 Oil content (%)

The data given in Table 4.4 revealed that out of six crosses, cross 4 (98222 B $\times$ 15001 R) (11.23 %) and cross 6 (05888 B $\times$ 16066 R) (7.97 %) manifested positive and significant heterosis over mid- parent. The relative heterosis varied from -1.90 per cent in cross 1 (05888 B $\times$ 15001 R) to 11.23 per cent in cross 4 (98222 B $\times$ 15550 R). In case of heterobeltiosis out of six crosses only one cross, cross 1 (05888 B $\times$ 15001 R) (-2.43 %) was found with negative. Heterobeltiosis ranged from -2.43 per cent in cross 1 (05888 B $\times$ 15001 R) to 9.14 per cent in cross 4 (98222 B $\times$ 15550 R). None of the cross recorded significant and negative heterosis. Highest heterobeltiosis was recorded in cross 4 (98222 B $\times$ 15550 R) with 9.14.

Inbreeding depression was non-significantly differed for all crosses except cross 1 (05888 B $\times$ 15001 R) (-11.40). Cross 4 (98222 B $\times$ 15550 R) exhibit highest inbreeding depression (7.037 %) whereas inbreeding depression was lowest in cross 1 (05888 B $\times$ 15001 R) (-11.40 %).

4.4.15 Protein content (%)

The estimates of relative heterosis varied from -12.31 per cent in cross 6 (05888 B $\times$ 16066 R) to 20.30 per cent in cross 3 (01555 B $\times$ 15990 R). Among all six crosses, only cross 1 (05888 B $\times$ 15001 R) recorded significant positive highest heterosis over mid-parent with 14.53 per cent. In case of heterobeltiosis all six crosses registered with negative and significant effects. Jethva *et al.* (2012) and Patel *et al.* (2021) observed similar heterobeltiosis for protein content.

The range of inbreeding depression was recorded from cross 5 (1202 B $\times$ 16317 R) (-36.94 %) to cross 3 (01555 B $\times$ 15990 R) (9.56). Cross 3 (01555 B $\times$ 15990 R) (9.56 %) followed by cross 1 (05888 B $\times$ 15001 R) (7.47 %) exhibit highest inbreeding depression whereas it was lowest in cross 5 (1202 B $\times$ 16317 R) (-36.94 %).

Table 4.4 Continue....

Estimates (%)	Harvest index	Carbohydrate	Tannin	Iron content	Zinc content	Oil content	Protein content
Cross 1 (05888 B × 15001 R)							
RH %	9.97**	-32.96**	-0.45	-11.82**	-7.28**	-1.90	14.53**
HB %	6.75**	-41.19**	3.79**	-22.74**	-7.95**	-2.43	-10.22**
ID %	6.36**	-46.30**	4.59**	45.77**	4.06**	-11.40*	7.47*
Cross 2 (02889 B × 16317 R)							
RH %	-0.88	-4.01**	-12.78**	-14.99**	-1.83*	4.47	-9.77*
HB %	-1.43	-10.19**	-12.59**	-15.86**	-19.32**	1.16	-23.51**
ID %	1.89	7.85**	-91.79**	-1.22	1.35	2.54	-28.18**
Cross 3 (01555 B × 15990 R)							
RH %	6.75**	-1.65	8.41**	-10.05**	14.33**	7.64	20.30**
HB %	4.64**	-2.51	21.89**	-19.97**	8.41**	1.67	-10.80*
ID %	12.92**	6.33**	-61.46**	27.68**	20.79**	4.70	-7.86
Cross 4 (98222 B × 15550 R)							
RH %	4.92**	-10.82**	29.02**	-27.06**	22.25**	11.23*	3.29*
HB %	-0.89	-16.48**	81.22**	-29.82**	21.97**	9.14	-3.41
ID %	11.76 **	-7.72**	6.99**	32.78**	7.50**	7.03	9.56**
Cross 5 (1202 B × 16317 R)							
RH %	5.59**	-12.65**	34.37**	-36.76**	-11.34**	3.69	4.63
HB %	5.32**	-16.79**	50.09**	-38.84**	-12.55**	3.07	-13.49**
ID %	6.09**	-9.45**	37.68**	-12.13**	-14.54**	-5.83	-36.94**
Cross 6 (05888 B × 16066 R)							
RH %	2.21	6.97**	-47.81**	-16.41**	5.02**	7.97*	-12.31**
HB %	-2.34	0.31	-46.31**	-18.17**	4.76**	5.16	-36.50**
ID %	-3.78*	-2.09	-14.21**	1.09	4.26**	1.63	-30.17**

* and **, significant at 5% and 1% level of significance, respectively

4.5 Heritability and genetic advance

Estimate of heritability serves as a useful guide to the plant breeder. The breeder is able to appreciate the proportion of variation that is due to genotypic (broad sense heritability) or additive (narrow sense heritability) effects, that is, the heritable portion of variation in the first case and the portion of genetic variation that is fixable in pure lines in the later case. If heritability of a character is very high, selection for the character should be fairly easy because there would be a close correspondence between the genotype and phenotype due to relatively smaller contribution of the environment to phenotype. But for a character with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects. Thus, estimates of heritability are useful in predicting the transmission of characters from the parents to their offspring.

Heritability is a measure of the efficiency of a selection system in separating genotypes. The quantitative traits are largely influenced by environments; therefore, those are not highly heritable. High, moderate and low heritability are not rigidly defined as it varies with character to character, but the following values are widely accepted (Robinson *et al.* 1949):

1. Low heritability : 0 - 30 %
2. Moderate heritability : 30 - 60 %
3. High heritability : > 60 %

The value of expected genetic advance for various characters is demarcated into three categories viz., low, moderate and high as follows (Johnson *et al.* 1955):

1. Low genetic advance : 0 - 10%
2. Moderate genetic advance : 10 - 20 %
3. High genetic advance : > 20 %

Narrow sense heritability estimates were calculated and presented in table 4.5. Heritability in narrow sense is more helpful in the selection of segregating populations and that is why the genetic advance was calculated on the basis of narrow sense heritability to ascertain more reliable results.

The results obtained on these aspects for different characters studied in six crosses of pearl millet viz., cross 1 (05888 B × 15001 R), cross 2 (02889 B × 16317 R), cross 3 (01555 B × 15990 R), cross 4 (98222 B × 15550 R), cross 5 (1202 B × 16317 R) and cross 6 (05888 B × 16066 R) here after referred to as cross 1, cross 2, cross 3, cross 4, cross 5 and cross 6 respectively are presented and discussed in the following paragraphs.

4.5.1 Days to flowering

High narrow sense heritability found in cross 5 (1202 B x 16317 R) and cross 6 (05888 B x 16066 R) with 64.05 per cent and 118.65 per cent.

The expected genetic advance low for cross 5 (1202 B x 16317 R) with 9.89 per cent. Highest expected genetic advance was observed for cross 6 (05888 B x 16066 R) with 20.59 per cent. High heritability coupled with low genetic advance was observed for cross 5 (1202 B x 16317 R) which indicative of non-additive gene action. High heritability coupled with high genetic advance was observed for cross 6 (05888 B x 16066 R) indicated that heritability of this trait was due to additive gene action and selection may be effective.

Similar results for high heritability and low expected genetic advance was also recorded by Sandhu and Phul (1984) and Govindaraj *et al.* (2011) as well as high heritability coupled with high expected genetic advance was also recorded by Singh and Singh (2016), Singh *et al.* (2017^b), Zakari *et al.* (2019) and Pujar *et al.* (2020).

4.5.2 Plant height (cm)

Cross 2 (1.38) and cross 3 (21.84) showed low narrow sense heritability with low genetic advance of cross 2 (0.45 %) and cross 3 (5.65 %) for this character was tabulated in Table 4.5. Low heritability coupled with low genetic advance was observed for cross 2 and 3 which suggested that the trait was under the control of non-additive gene action. Vagadiya *et al.* (2013) recorded low heritability with low genetic advance.

4.5.3 Number of effective tiller per plant

The lowest narrow sense heritability was observed for cross 2 (15.19 %), cross 4 (6.62 %) and cross 5 (7.41 %), whereas highest narrow sense heritability was observed for cross 3 showed 73.99 per cent.

Highest genetic advance was recorded for cross 3 with 115.80 per cent followed by moderate value of cross 2 (19.86 %) and low value for cross 4 (9.48 %) and cross 5 (8.15 %). High heritability coupled with high genetic advance was observed for cross 3 indicated that heritability was due to additive gene action and selection may be effective. Low heritability coupled with low genetic advance was observed for cross 4 and cross 5 which suggested that the trait was governed by non-additive gene action.

Lakshmana *et al.* (2009), Govindaraj *et al.* (2011), Manga (2013), Dapke *et al.* (2014), Sathya *et al.* (2014), Singh and Singh (2016), Nehra *et al.* (2017), Ramya *et al.* (2017), Singh *et al.* (2017^a), Singh *et al.* (2017^b), Kumar *et al.* (2019), Kumawat *et al.* (2019) and Priyanka *et al.* (2019) reported high heritability coupled with high genetic advance, whereas Kumar *et al.*

al. (2014^a) and Basavaraj *et al.* (2017) suggested low heritability with moderate genetic advance for number of tiller per plant.

4.5.4 Earhead length (cm)

For earhead length, cross 2 (02889 B x 16317 R) shows low narrow sense heritability with 25.72 per cent. Highest narrow sense heritability was recorded for cross 4 (98222 B x 15550 R) with 76.69 per cent.

Highest genetic advance was recorded for cross 4 with 47.60 per cent followed by moderate value of cross 2 (11.68 %). High heritability coupled with high genetic advance was observed for cross 4 indicated that heritability was due to additive gene action and selection may be effective.

Shekhawat *et al.* (1993), Tomar *et al.* (2008), Lakshmana *et al.* (2009), Manga (2013), Vagadiya *et al.* (2013), Dapke *et al.* (2014), Kumar *et al.* (2014^a), Manga (2014), Ezeaku *et al.* (2015), Singh and Singh (2016), Nehra *et al.* (2017), Ramya *et al.* (2017), Shanthi *et al.* (2017), Singh *et al.* (2017^b), Subbulakshmi *et al.* (2018), Priyanka *et al.* (2019), Sattler *et al.* (2019) and Zakari *et al.* (2019) recorded high heritability with high genetic advance.

4.5.5 Earhead girth (mm)

Moderate narrow sense heritability was recorded for cross 4 (49.19 %), cross 3 (48.83 %) and cross 1 (34.70 %) whereas highest narrow sense heritability was recorded for cross 5 (69.27 %). Highest genetic advance was recorded for cross 3 with 26.81 per cent, cross 5 with 24.65 per cent and cross 4 with 20.41 per cent. Moderate genetic advance was recorded for cross 1 with 12.10 per cent.

High heritability coupled with high genetic advance was observed for cross 5 indicated that heritability was due to additive gene action and selection may be effective. Moderate heritability coupled with moderate genetic advance was observed for the cross 1, which indicate heritability was due to non-additive gene action. Moderate heritability coupled with high genetic advance was observed for cross 3 and cross 4 indicated that heritability of this trait was due to additive gene action and selection may be effective.

Ghorpade and Metta (1993), Tomar *et al.* (2008), Lakshmana *et al.* (2009), Manga (2013), Vagadiya *et al.* (2013), Kumar *et al.* (2014^a), Singh and Singh (2016), Basavaraj *et al.* (2017), Nehra *et al.* (2017), Ramya *et al.* (2017), Singh *et al.* (2017^b) and Priyanka *et al.* (2019) found high heritability with high genetic advance for this trait. Shanthi *et al.* (2017) recorded moderate heritability with high genetic advance while Solanki *et al.* (2017), Subbulakshmi *et al.* (2018) and Kumar *et al.* (2020^a) found moderate heritability with moderate genetic advance.

4.5.6 Days to maturity

Highest narrow sense heritability was recorded for cross 6 with 78.43 per cent followed by cross 3 (71.81 %). Moderate narrow sense heritability was manifested in cross 2 (52.54) and cross 5 (44.23).

The values of expected genetic advance were low for cross 2 (5.68 %), cross 3 (9.18 %) and cross 5 (6.51 %). Moderate genetic advance was manifested in cross 6 (12.42). High to moderate heritability coupled with low to moderate genetic advance was observed for the crosses cross 2, cross 3, cross 5 and cross 6, which indicate heritability of this trait was due to non-additive gene action.

Sathya *et al.* (2014) and Dhedhi *et al.* (2016) reported high heritability coupled with moderate genetic advance while Tomar *et al.* (2008), Vagadiya *et al.* (2013), Kumar *et al.* (2014^b), Singh and Singh (2016) and Kumar *et al.* (2020^b) found high heritability but low genetic advance. Lakshmana *et al.* (2009) found moderate heritability and low genetic advance.

4.5.7 Test weight (g)

Highest narrow sense heritability was observed for cross 1 with 72.18 per cent followed by cross 6 (11.87 %) and cross 2 (4.78 %). Cross 6 and cross 2 expressed low narrow sense heritability. The value of expected genetic advance was low for cross 2 (1.47 %) and cross 6 (5.00 %). Highest values of genetic advance were observed in cross 1 (28.50 %).

High heritability coupled with high genetic advance was observed for cross 1 indicated that heritability of this trait was due to additive gene action and selection may be effective. Cross 2 and cross 6 possess Low heritability accompanied with low genetic advance indicates that character is highly influenced by environmental effects and selection would be ineffective.

Manga (2014) supported the results showed low heritability and low genetic advance. Lal and Singh (1970), Tomar *et al.* (2008), Lakshmana *et al.* (2009), Manga (2013), Vagadiya *et al.* (2013), Kumar *et al.* (2014^b), Sathya *et al.* (2014), Singh and Singh (2016), Basavaraj *et al.* (2017), Nehra *et al.* (2017), Ramya *et al.* (2017), Shanthi *et al.* (2017), Singh *et al.* (2017^b), Solanki *et al.* (2017), Subbulakshmi *et al.* (2018), Priyanka *et al.* (2019), Kumar *et al.* (2020^b) and Pujar *et al.* (2020) recorded high heritability coupled high genetic advance.

4.5.8 Grain yield per plant (g)

Narrow sense heritability estimates were high for cross 4 and cross 6, it was ranged from 63.35 per cent in cross 4 to 60.45 per cent in cross 6.

The highest estimated genetic advance was manifested by cross 4 (37.74 %) followed by cross 6 (33.43 %). High heritability coupled with high genetic advance was observed for cross 4 and cross 6 indicated that heritability of this trait was due to additive gene action and selection may be effective.

Tomar *et al.* (2008), Lakshmana *et al.* (2009), Bhadalia *et al.* (2012), Manga (2013), Vagadiya *et al.* (2013), Dapke *et al.* (2014), Kumar *et al.* (2014^a), Kumar *et al.* (2014^b), Manga (2014), Sathya *et al.* (2014), Dhedhi *et al.* (2016), Basavaraj *et al.* (2017), Nehra *et al.* (2017), Solanki *et al.* (2017), Subbulakshmi *et al.* (2018), Priyanka *et al.* (2019), Kumar *et al.* (2020^a), Kumar *et al.* (2020^b), Pujar *et al.* (2020) and Sharma *et al.* (2020) reported high heritability with high genetic advance.

4.5.9 Harvest index (%)

Crosses 2 (16.62 %), 3 (18.39 %) and 6 (1.01 %) expressed low narrow sense heritability; cross 5 (35.54 %) expressed moderate and cross 1 (95.82 %) showed maximum narrow sense heritability.

The value of expected genetic advance was low for Crosses 2 (4.16 %), 3 (5.94 %) and 6 (0.31 %). The highest genetic advance was observed for cross 1 showing 28.53 per cent followed by moderate genetic advance was observed for cross 5 (11.42 %). Low narrow sense heritability coupled with low genetic advance suggests that harvest index is highly influenced by environmental effects and selection would be ineffective. Moderate heritability coupled with moderate genetic advance was observed for the cross 5, which indicate heritability was due to non-additive gene action. High heritability coupled with high genetic advance was observed for cross 1 indicated that heritability of this trait was due to additive gene action and selection may be effective.

Bhadalia *et al.* (2012), Manga (2013), Dapke *et al.* (2014), Manga (2014), Singh and Singh (2016) and Priyanka *et al.* (2019) recorded high heritability coupled with high genetic advance for harvest index.

4.5.10 Carbohydrate (g/100 g)

Maximum narrow sense heritability was observed in cross 1 with 120.53 per cent, cross 2 (99.61 %) and cross 4 (67.07 %). While maximum genetic advance was observed in cross 1 with 33.83 per cent followed by cross 2 (23.84 %) and moderate value of cross 4 (18.54 %).

Table 4.5: Estimates of heritability and genetic advance per cent of mean in six crosses of pearl millet for grain yield and its contributing characters

Estimates (%)	Days to flowering	Plant height	Number of effective tiller per plant	Earhead length	Earhead girth	Days to maturity	Test weight	Grain yield per plant
Cross 1 (05888 B × 15001 R)								
Heritability (NS) %	-	-	-	-	34.70	-	71.27	-
Genetic Advance % mean (Narrow sense)	-	-	-	-	12.10	-	27.98	-
Cross 2 (02889 B × 16317 R)								
Heritability (NS) %	-	1.38	15.19	25.72	-	52.54	4.79	-
Genetic Advance % mean (Narrow sense)	-	0.45	19.85	11.67	-	5.68	1.46	-
Cross 3 (01555 B × 15990 R)								
Heritability (NS) %	-	21.84	73.99	-	48.83	71.81	-	-
Genetic Advance % mean (Narrow sense)	-	5.65	115.80	-	26.81	9.18	-	-
Cross 4 (98222 B × 15550 R)								
Heritability (NS) %	-	-	6.62	76.69	49.19	-	-	63.35
Genetic Advance % mean (Narrow sense)	-	-	9.48	47.60	20.41	-	-	37.74
Cross 5 (1202 B × 16317 R)								
Heritability (NS) %	64.04	-	7.41	-	69.27	44.22	-	-
Genetic Advance % mean (Narrow sense)	9.88	-	8.15	-	24.65	6.50	-	-
Cross 6 (05888 B × 16066 R)								
Heritability (NS) %	118.65	-	-	-	-	78.42	8.21	60.45
Genetic Advance % mean (Narrow sense)	20.59	-	-	-	-	12.42	3.46	33.43

High heritability coupled with high genetic advance was observed for cross 1 and cross 2 indicated that heritability of this trait was due to additive gene action and selection may be effective. High heritability with moderate genetic advance suggested that non-additive gene action is predominant and the high heritability is being exhibited due to favorable influence of environment rather than genotype.

4.5.11 Tannin (mg/100 g)

The value of narrow sense heritability was high for cross 2 (129.83 %) and cross 4 (169.16 %), moderate for cross 3 (34.03 %). The expected genetic advance expressed high in cross 2 (26.28 %) and cross 4 (58.87 %) whereas it was estimated low for cross 3 (6.06 %).

High to moderate heritability coupled with high genetic advance in cross 2 and cross 4 suggested that the trait was under control of additive gene action while in cross 3, moderate heritability with low genetic advance indicate that the trait was influenced by non-additive gene action. Sharma *et al.* (2020) reported high heritability coupled with high genetic advance for tannin content.

4.5.12 Iron content (mg/kg)

The highest narrow sense heritability was recorded for cross 4 with 145.27 per cent followed by cross 3 (81.98 %) and cross 6 (41.20 %). Genetic advance was highest for cross 4 (52.53 %) followed by cross 3 (21.36 %). It was low in cross 6 (4.10 %). High heritability coupled with high genetic advance in cross 4 and 3 suggested that the trait was under control of additive gene action.

Govindaraj *et al.* (2011), Mahendrakar *et al.* (2019), Priyanka *et al.* (2019), Kumar *et al.* (2020^a) and Pujar *et al.* (2020) recorded high heritability with high genetic advance.

4.5.13 Zinc content (mg/kg)

The value of narrow sense heritability was moderate for cross 3 (57.17 %), cross 6 (45.07 %) and cross 4 (32.20 %).

The expected genetic advance was expressed low in cross 3 (8.81 %), cross 6 (8.29 %) and cross 4 (6.33 %). Moderate heritability coupled with low genetic advance observed in cross 3, cross 6 and cross 4 which suggest the trait was under control of non-additive gene action. Zakari *et al.* (2019) found moderate heritability for zinc content.

4.5.14 Oil content (%)

The value of narrow sense heritability was moderate for cross 2 (51.57 %) and cross 4 (32.07 %). Highest expected genetic advance observed in cross 2 with 31.52 per cent followed by cross 4 (16.53 %).

Table 4.5 Continue....

Estimates (%)	Harvest index	Carbohydrate	Tannin	Iron content	Zinc content	Oil content	Protein content
Cross 1 (05888 B × 15001 R)							
Heritability (NS) %	95.82	120.53	-	-	-	-	-
Genetic Advance % mean (Narrow sense)	28.53	33.83	-	-	-	-	-
Cross 2 (02889 B × 16317 R)							
Heritability (NS) %	16.62	99.61	129.83	-	-	51.56	-
Genetic Advance % mean (Narrow sense)	4.16	23.83	26.28	-	-	31.51	-
Cross 3 (01555 B × 15990 R)							
Heritability (NS) %	18.39	-	34.03	81.98	57.17	-	72.86
Genetic Advance % mean (Narrow sense)	5.94	-	6.06	21.36	8.81	-	51.51
Cross 4 (98222 B × 15550 R)							
Heritability (NS) %	-	67.07	169.16	145.27	32.20	32.07	-
Genetic Advance % mean (Narrow sense)	-	18.54	58.87	52.53	6.33	16.53	-
Cross 5 (1202 B × 16317 R)							
Heritability (NS) %	35.54	-	-	-	-	-	-
Genetic Advance % mean (Narrow sense)	11.42	-	-	-	-	-	-
Cross 6 (05888 B × 16066 R)							
Heritability (NS) %	1.01	-	-	41.20	45.07	-	-
Genetic Advance % mean (Narrow sense)	0.31	-	-	4.10	8.28	-	-

Moderate heritability with high genetic advance for cross 2 suggested that oil content was under control of additive gene action. Moderate heritability with moderate genetic advance for cross 4 suggested that oil content was under control of non-additive gene action the high heritability is being exhibited due to favorable influence of environment rather than genotype.

4.5.15 Protein content (%)

The value of narrow sense heritability was high for cross 3 (72.86 %). Highest expected genetic advance observed in cross 3 with 51.51 per cent.

High heritability coupled with high genetic advance in cross 3 suggested that the trait was under control of additive gene action. Govindaraj *et al.* (2011), Thomas *et al.* (2018), Priyanka *et al.* (2019), Pujar *et al.* (2020) and Sharma *et al.* (2020) reported high heritability with high genetic advance.

V. SUMMARY AND CONCLUSIONS

The objectives of present investigation were to study genetic basis of grain yield and its component characters as well as to investigate the extent of heterosis and inbreeding depression, heritability and genetic advance and underlying genetic causes for different characters in pearl millet. Therefore, the present investigation entitled, “**Generation mean analysis in pearl millet [*Pennisetum glaucum* (L.) R. Br.]**” was laid out in Compact Family Block Design (CFBD) with three replications. Each replication was divided in six compact blocks. Each six crosses consisting of six generations were randomly allotted to each plot within a block. Each plot consisted of one row of each parent and F_1 s, two rows of the backcrosses and four rows of the F_2 generations of each cross. Inter and intra row spacing was 45 cm and 10 cm, respectively with row length of three meter. The experiment was surrounded by four guard rows to avoid damage and border effects. Six generations, namely P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of six crosses of pearl millet viz., cross 1 (05888 B $\times$ 15001 R), cross 2 (02889 B $\times$ 16317 R), cross 3 (01555 B $\times$ 15990 R), cross 4 (98222 B $\times$ 15550 R), cross 5 (1202 B $\times$ 16317 R) and cross 6 (05888 B $\times$ 16066 R) were grown at Center for Crop Improvement (CCI), Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar, Gujarat during *kharif* 2020 and subsequently F_1 hybrids alongwith their both the respective parents were sown in *Summer* 2021 to produce seed for F_2 , BC_1 and BC_2 generations. All six populations were evaluated at Center for Crop Improvement (CCI), Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar, Gujarat during *kharif* 2021.

The observation were recorded on randomly selected ten plants in respect of non-segregating generation (P_1 , P_2 and F_1); twenty plants from backcrosses (BC_1 and BC_2) and forty plants from F_2 generation at different growth stages of the crop leaving the border plants on both ends of the row in each replication. The observations recorded for fifteen different characters viz., days to flowering, days to maturity, plant height (cm), number of effective tillers per plant, earhead length (cm), earhead girth (mm), test weight (g), grain yield per plant (g),

harvest Index (%), carbohydrate (g/100 g), tannin (mg/100 g), iron content (mg/kg), Zinc content (mg/kg), oil content (%) and protein content (g/100 g).

The findings of present investigation are summarized as under:

- (1) The analysis of variance between generations revealed that the mean squares due to generations (crosses) were significant for all the characters under study except days to maturity for cross 1 and 2, plant height for cross 5, ear head length for cross 2, ear head girth for cross 1, 5 and 6, test weight for cross 5 and 6 and oil content for all six crosses were recorded with non-significant differences. Significant differences suggested presence of sufficient variation for generation mean values of all the crosses for different traits, there by revealing existence of sufficient variation to analyze and interpret the results in terms of objectives under investigation.
- (2) The highest average value of F_1 was observed in cross 1 (40.33 g) followed by cross 3 (27.15 g), cross 4 (25.15 g) and cross 2 (25.13 g) for grain yield per plant. Cross 1 and cross 3 was also observed superior in mean performance for contributing traits viz., number of effective tillers per plant, ear head length (cm), test weight (g), harvest index (%) and days to maturity. While for days to flowering cross 1 found early than other crosses, cross 4 performed well for ear head girth (mm). For quality parameters, cross 6 for carbohydrate content (g/100 g); cross 2 and cross 6 for tannin content (mg/100 g), cross 1 and 3 for iron content (mg/ kg) and cross 3, 4 and 6 for zinc content (mg/ kg); cross 3 and 4 for oil content (%) and cross 1 for protein content (%) were superior in respect to *per se* performance.
- (3) The F_1 of all the crosses recorded significantly higher mean value except for cross 2 than both the parents indicating over dominance for higher grain yield per plant, while in cross 2 indicated partial dominance. Over dominance was observed in most of the crosses in most of the characters. Partial dominance was observed in cross 2 and 6 for number of effective tiller per plant; for cross 1, 2 and 4 in ear head length (cm); for cross 1 and 3 in ear head girth (mm), for cross 5 and 6 of test weight, for cross 1 and 3 of iron content (mg/ kg); for cross 2 in zinc content (mg/ kg) and for all six crosses in protein content (%).
- (4) Average of F_2 was recorded significantly higher than their respective F_1 mean in all the crosses indicated the presence of inbreeding depression for number of effective tiller per plant, cross 5 and 6 of ear head length (cm), grain yield per

plant except cross 1, iron content (mg/ kg) for crosses 2 and 5, zinc content (mg/ kg) for cross 3, oil content (%) in except cross 1 and 5, protein content (g/100 g) for cross 1 and 4. While mean of F_2 was recorded lower than their respective F_1 mean in days to flowering except cross 1 and 2; plant height for cross 4; test weight (g); harvest Index (%) in except cross 6; carbohydrate (g/ 100 g) in all crosses; tannin content (mg/ 100 g) in crosses 1, 4 and 5. The backcross progenies tended to resemble their recurrent female parent in most of the cases. Average value of backcross generation of most of the crosses significantly higher than their respective recurrent parent as like BC_1 of cross 1 and 4 for number of effective tiller per plant, BC_2 of cross 3 in ear head length, BC_2 of cross 5 in ear head girth, except for BC_2 of cross 1 for grain yield per plant. Back cross generations mean values were also found to be either closer or lower than their respective parents or/and/in between F_1 mean value.

- (5) On the basis of individual scaling test A, B, C and D the additive-dominance model was found adequate for description of variation in generation mean for cross 2 of days to maturity; cross 2, 3 and 5 of number of effective tillers per plant; cross 2 and 3 of ear head length (cm); cross 5 and 6 of ear head girth (mm); cross 3 and 5 of test weight (g); cross 1 and 4 of harvest index (%) and cross 2, 3, 4 and 6 of oil content (%). While 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 of digenic interaction as well as χ^2 value of joint scaling test was found significant in majority of traits and crosses, indicated the presence of appreciable amount of epistasis and inadequacy of additive-dominance model to calculate various non-allelic gene effects whereas in some cases there is some negligible amount of gene interaction was present so six parameter model (Hayman, 1958) was found adequate for some crosses of different characters.
- (6) Grain yield per plant and most of its component characters with quality parameters, additive (d) gene effects were found to be significant in almost all crosses except for cross 6 of days to flowering, cross 2 and 6 of plant height, test weight for cross 4, harvest index for cross 1, 3 and 4, tannin content for cross 2, zinc content for cross 4, 5 and 6. Whereas additive (d) gene effects were found non significant for all crosses in number of effective tiller per plant

except for cross 2, ear head length, ear head girth, days to maturity and oil content.

- (7) Dominant (h) gene effects were found to be significant in all crosses of days to flowering; number of effective tiller per plant except for cross 3 and 5; test weight; tannin content; iron content; zinc content; carbohydrate except for cross 5; protein content except for cross 1 and 3; plant height except for cross 6, ear head length except for cross 4; days to maturity except for cross 6; grain yield per plant except for cross 6 harvest index for cross 1 and 6; as well as dominant (h) gene effects found to be significant in only cross 2 and 3 of ear head girth and cross 1 and 5 of oil content.
- (8) Epistasis, additive $\times$ additive (i) gene interaction was found to be significant in all crosses of days to flowering; days to maturity; cross 1 of number of effective tiller per plant, test weight, ear head length except for cross 4; cross 5 and 6 of grain yield per plant; cross 4 and 6 of carbohydrate content; cross 1, 3 and 5 of tannin content; iron content except for cross 2; zinc content except for cross 2 and 3 and significant in cross 4 and 5 of protein content.
- (9) Epistasis, additive $\times$ dominant (j) gene interaction was significant in all crosses of days to flowering; plant height; cross 4 and 6 of days to maturity; cross 2 of ear head girth; cross 6 of test weight; cross 1 and 2 of grain yield per plant; cross 2 and 3 of harvest index; cross 2 of carbohydrate content; cross 2, 4 and 6 of tannin content and zinc content; cross 4 and 6 of iron content and cross 4 and 5 of protein content.
- (10) Epistasis, dominant $\times$ dominant (l) gene interaction was significant in all crosses of days to flowering; plant height except for cross 6; number of effective tiller per plant except for cross 3 and 5; days to maturity for crosses 3, 5 and 6; ear head length except for cross 4; cross 3 of ear head girth; all crosses for test weight and grain yield per plant; harvest index except for cross 6; carbohydrate content except for cross 5; all crosses for tannin content and iron content; zinc content except for cross 1 and 5; significant in cross 1 and 5 of oil content and all crosses of protein content except cross 1 and 3.
- (11) The sign of dominance (h) and dominance $\times$ dominance (l) parameter being opposite indicated involvement of duplicate type of epistasis in the inheritance of a trait. Duplicate type of gene interaction had been detected for most of the crosses where non allelic gene action was present, it could diminish the effect

of dominant genes and selection would be restricted in such cases and should look for crossing different parental lines that would lead to complementary epistasis and would increase the expression of the trait under study whereas sign of dominance (h) and dominance $\times$ dominance (l) parameter being similar indicated involvement of complementary type of epistasis in the inheritance of a trait. Complementary type of epistasis was found in cross 3 and 5 of days to flowering; cross 1 of plant height and cross 4 of iron content.

- (12) Chi-square value was found significant for best fit model in various crosses for many traits such as days to flowering (cross 3 and 5), plant height (cross 4), days to maturity (cross 3 and 5), grain yield per plant (cross 2 and 3), carbohydrate (cross 1 and 3), tannin content (crosses 1, 2, 3 and 5), iron content (crosses 1, 2 and 5), zinc content (crosses 2, 3 and 5) and protein content (cross 5) indicated that the digenic model was inadequate to explain inheritance of these traits indicating presence of higher order gene interaction.
- (13) Highly significant and positive value for relative heterosis, heterobeltiosis and inbreeding depression were found in many crosses. Significant heterosis over mid-parent and better parent along with positive and negative inbreeding depression may be attributed to major contribution from dominance (h) and additive $\times$ additive (i) gene effects, where selection will be effective only in later generations. For grain yield per plant, best heterotic crosses were cross 1, 4, 5 and cross 6. Cross 1 was also observed best heterosis for days to flowering, ear head length, harvest index and protein content, cross 4 was best for ear head length, harvest index, zinc content, oil content and protein content. While cross 5 for harvest index as well as cross 6 for days to maturity, plant height, carbohydrate, zinc content and oil content. Significant inbreeding depression was recorded only for crosses 1, 2 and 4 of days to flowering and for crosses 2, 3, 5 and 6 of days to maturity, for cross 4 of ear head girth, cross 1 of grain yield per plant, cross 1, 3, 4 and 5 of harvest index, cross 2 and 3 of carbohydrate, cross 2, 3 and 6 of tannin content, cross 1, 3 and 4 of iron content, cross 1, 3, 4 and 6 of zinc and cross 1 and 4 of protein content. Whereas for other traits in remaining crosses showed non-significant inbreeding depression.
- (14) High to moderate heritability with high to moderate genetic advance was observed for days to flowering (cross 6), days to maturity (cross 6), number of

effective tillers per plant (cross 3), ear head length (cross 4), ear head girth (cross 1, 3, 4 and 5), test weight (cross 1), grain yield per plant (cross 6), harvest index (cross 1 and 5), carbohydrate (cross 1, 2 and 4), tannin content (cross 2 and 4), iron content (cross 3, 4 and 6), oil content (cross 2 and 4) and protein content (cross 3) suggested presence of sufficient additive component may be rewarding for selection of such traits in future breeding programme of pearl millet improvement.

- (15) Crosses showed duplicate type of gene action indicated digenic interaction under such circumstances; it would be difficult for the breeder to get promising segregants better than the parents, so it was suggested to make simple crosses and their exploitation through heterosis breeding. Suitable breeding procedure which involves multiple crosses, biparental crosses would help in restoring desirable genes to get desirable segregants to develop good inbred lines having superiority of different characters.
- (16) The system of breeding that can be employed for exploiting any character depends upon the type of gene action involved for its expression. The type and magnitude of gene effects differed for different characters in the same cross and for the same character in different crosses, which necessitates specific handling of individual cross in segregating generations. In the present investigation, non-allelic (epistasis) interaction played pertinent role in determination of various characters in pearl millet. The breeding methods involving high volume crossing like biparental, recurrent and diallel selective mating systems for utilization of both additive and non-additive gene action seemed more promising for the improvement of various characters studied in the present investigation.

On the basis of *per se* performance, generation mean analysis, narrow sense heritability, genetic advance and inbreeding depression for different crosses showed different gene action of respective traits under study. Additive gene action and additive $\times$ additive type of gene interaction was found superior for days to flowering in all crosses except cross 2; grain yield per plant in cross 5 and 6; carbohydrate in cross 4 and 6; tannin content in cross 1, 3 and 5 and iron content in crosses 1, 3, 4 and 5. So these crosses may be used for exploitation heterosis for yield and its contributing with quality traits as well as in future breeding programme by utilizing biparental mating design and recurrent

selection method for development of superior pearl millet lines for these characters.

Whereas, non additive gene action viz., dominant (h) gene action, additive $\times$ dominance (j) gene interaction and dominance $\times$ dominance (l) gene interaction was found superior for days to flowering in cross 4 and 6; plant height in cross 1 and 2; number of effective tiller per plant for cross 1; ear head length in cross 6; ear head girth for cross 2 and 3; days to maturity for cross 3, 5 and 6; test weight for cross 1, 4 and 6; grain yield per plant in cross 1 and 2; harvest index in cross 2 and 3; carbohydrate in cross 2; tannin in cross 2, 4 and 6; iron content in cross 4; zinc content in cross 2, 4 and 6; oil content in cross 1 and 5 as well as protein content in cross 4 and 6. So these crosses or parents may be used for heterosis breeding to utilize high SCA effect for development of superior pearl millet hybrids for grain yield and its contributing characters.

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*Original does not seen.

APPENDIX

Appendix-A: Weekly meteorological data recorded during the crop growth period of June - 2020 to March - 2021

Standard week	Temperature (°C)		Relative humidity (%)		Sunshine hours	Rain fall (mm)	Wind velocity (km/hr)	Evapo-ration (mm)
	Max.	Min.	Morn.	Even.				
June -2020 :								
23	40.0	24.9	71	50	10.1	2.0	7.1	7.8
24	38.8	24.5	75	56	9.8	73.0	7.4	6.9
25	39.6	26.6	73	62	8.9	0.0	10.1	7.6
26	38.6	27.9	68	64	8.0	7.0	8.0	7.1
July-2020 :								
27	38.5	27.4	74	67	5.1	0.0	8.5	6.9
28	37.4	26.1	81	69	2.7	51.0	10.7	6.6
29	36.7	24.7	80	72	1.5	56.0	4.6	6.5
30	36.6	25.5	77	68	8.2	26.0	9.8	6.7
31	36.4	26.0	72	71	9.7	55.0	5.8	7.3
August-2020 :								
32	33.5	25.0	90	93	0.0	364.0	7.1	3.4
33	32.1	25.3	89	91	0.0	220.0	4.9	3.1
34	32.6	25.2	88	91	0.0	127.0	5.5	3.3
35	33.0	25.1	89	91	0.1	114.0	6.7	4.5
September-2020 :								
36	34.5	25.0	82	82	7.2	9.0	3.2	6.1
37	34.5	25.0	87	85	3.0	96.0	3.9	6.7
38	35.1	25.4	82	76	7.5	3.5	3.8	7.0
39	35.2	23.6	78	67	8.3	17.0	5.2	7.1
February-2021 :								
06	35.2	9.8	60	29	9.8	0.0	3.3	5.4
07	36.8	12.0	63	27	9.9	0.0	5.5	5.6
08	38.2	14.0	64	30	10.0	0.0	2.0	6.7
09	36.5	14.4	67	24	9.9	0.0	2.4	6.1
10	36.8	15.5	68	25	9.6	0.0	3.9	5.8
March-2021 :								
11	36.9	16.1	69	24	9.4	0.0	3.2	5.6
12	38.2	18.3	69	25	8.4	0.0	4.0	6.4
13	38.9	18.7	70	27	9.5	0.0	3.9	6.6
14	39.4	20.9	73	27	9.8	0.0	4.3	7.1

Appendix-B: Weekly meteorological data recorded during the crop growth period of April - 2021 to September - 2021

Standard week	Temperature (°C)		Relative humidity (%)		Sunshine Hours	Rain fall (mm)	Wind velocity (km/hr)	Evapo-ration (mm)
	Max.	Min.	Morn.	Even.				
April- 2021 :								
7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5
6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9
7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3
7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8
May-2021 :								
19	43.0	24.4	76	37	11.1	0.0	5.7	8.1
20	38.0	23.8	81	56	6.7	10.5	9.8	5.7
21	40.2	26.4	77	48	10.7	0.0	7.2	7.3
22	41.3	25.7	76	49	10.8	17.0	10.0	7.3
June-2021 :								
23	40.1	26.1	76	51	10.2	0.0	7.1	6.8
24	40.9	26.8	77	52	9.8	0.0	11.5	7.4
25	37.1	24.7	84	61	4.6	23.5	6.7	5.0
26	37.2	25.6	79	65	6.0	9.0	7.9	6.0
27	38.0	26.8	76	65	8.4	0.0	11.1	7.3
July-2021 :								
28	39.1	26.0	81	63	5.7	47.0	6.7	7.1
29	36.1	26.2	82	75	3.8	8.0	7.4	7.0
30	31.6	24.8	85	90	0.7	65.5	10.2	4.6
31	29.0	24.3	84	85	0.0	17.5	8.6	3.5
August-2021 :								
32	33.5	25.9	80	74	6.8	0.0	5.4	6.1
33	36.5	25.7	73	68	9.5	0.0	5.9	7.5
34	36.9	26.0	76	67	7.6	2.0	4.9	7.3
35	35.6	24.7	82	66	6.6	36.5	5.3	6.0
36	34.4	24.9	88	83	4.1	41.0	5.7	5.5
September-2021 :								
37	32.9	24.2	85	83	3.6	109.5	3.3	4.4
38	33.5	23.6	80	77	5.2	6.0	4.7	5.6
39	33.1	24.9	81	77	4.4	87.5	5.1	5.8
40	34.7	25.0	78	70	7.7	0.0	3.9	7.0

Source: Department of Agricultural Meteorology, C. P. College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar.

CERTIFICATE

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(PATEL HIREN S.)

Place : Sardarkrushinagar

Date : 11th January, 2023