

Inheritance of grain yield, its components and resistance to cereal cyst nematode in wheat (*Triticum aestivum* L.)

By

Niketa Yadav

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In

Genetics and Plant Breeding



**COLLEGE OF AGRICULTURE
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2016

CERTIFICATE – I

This is to certify that this thesis entitled, “**Inheritance of grain yield, its components and resistance to cereal cyst nematode in wheat (*Triticum aestivum* L.)**” submitted for the degree of **Doctor of Philosophy** in the subject of **Genetics and Plant Breeding** from Chaudhary Charan Singh Haryana Agricultural University, Hisar, is a bonafide research work carried out by **Niketa Yadav (Adm. No. 2012A38D)** under my supervision and that no part of this thesis has been submitted for any other degree.

The assistance and help received during the course of investigation have been duly acknowledged.

Dr. S.S. Dhanda
(Major Advisor)
Principal Scientist
Department of Genetics and Plant Breeding,
CCS Haryana Agricultural University,
Hisar (Haryana)

CERTIFICATE – II

This is to certify that this thesis entitled “**Inheritance of grain yield, its components and resistance to cereal cyst nematode in wheat (*Triticum aestivum* L.)**” submitted by **Niketa Yadav (Adm. No. 2012A38D)** to the Chaudhary Charan Singh Haryana Agricultural University, Hisar, in partial fulfillment of the requirements for the degree of **Doctor of Philosophy** in the subject of **Genetic and Plant Breeding** has been approved by the Student’s Advisory Committee after an oral examination on the same.

EXTERNAL EXAMINER

MAJOR ADVISOR

HEAD OF THE DEPARTMENT

DEAN, POSTGRADUATE STUDIES

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LIST OF SYMBOLS AND ABBREVIATIONS

%	:	Per cent
*	:	Significant at 0.05 level of probability
**	:	Significant at 0.01 level of probability
Approx	:	Approximately
B ₁	:	Backcross progeny with parent P ₁
B ₂	:	Backcross progeny with parent P ₂
CCN	:	Cereal Cyst Nematode
CCS HAU	:	Chaudhary Charan Singh Haryana Agricultural University
cm	:	Centimeter
<i>Cre</i>	:	Gene for cereal cyst nematode
d	:	Additive component of mean
D	:	Additive component of variance
df or DF	:	Degrees of freedom
E (MS)	:	Expected mean squares
E	:	Environmental component of variance
E _i	:	Expected mean of i th generation
<i>et al.</i>	:	And co-workers
etc	:	Et cetera / and other things / and so on
F ₁	:	First filial generation
F ₂	:	Second filial generation
g	:	Gram
GA	:	Genetic advance
GCV	:	Genotypic Coefficient of Variation
h	:	Dominance component of mean
H	:	Dominance component of variance
H ² or h ² (bs)	:	Heritability in broad sense
h ² or h ² (ns)	:	Heritability in narrow sense
HS	:	Highly Susceptible
i	:	Additive × additive epistasis
<i>i.e.</i>	:	That is
j	:	Additive × dominance epistasis
kg	:	Kilogram

I	:	Dominance $\times$ dominance epistasis
M ha	:	Million hectare
M t	:	Million tonnes
m	:	Mean
MR	:	Moderate Resistant
MS	:	Mean sum of square
n	:	Number of observations or sample size
O_i	:	Observed mean of i^{th} generation
P_1 and P_2	:	Parents
PCV	:	Phenotypic Coefficient of Variation
R	:	Resistant
Raj MR 1	:	Rajasthan <i>Molya Rodhak</i> 1
S	:	Susceptible
SD	:	Standard Deviation
SE	:	Standard Error
SS	:	Sum of square
t/ha	:	Tonnes <i>per</i> hectare
viz.	:	Namely
μm	:	Micrometer

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CHAPTER -I

INTRODUCTION

Wheat is an important and widely grown food grain crop all over the world providing ample calories and protein to the human population. It is the second most important cereal crop after rice grown under diverse agro-climatic conditions. India is the second largest wheat producer in the world after China. In the world, wheat was grown in 215 M ha area with the production of 704 M t and productivity of 3.74 t/ha during the year 2014-15 (Anonymous, 2015a). The corresponding figures in India were 30.37 M ha, 90.78 M t and 2.98 t/ha, respectively (Anonymous, 2015b). In Haryana, it was grown on 2.61 M ha area with grain production of 10.37 M t and productivity of 3.98 t/ha during the year 2014-15 (Anonymous, 2015c).

The knowledge of gene action controlling quantitative characters helps in selection of parents for use in the hybridization programme and also in the choice of appropriate breeding procedure for improvement various quantitative characters. Estimation of various genetic components of variances is used as a measure of gene action as well as it is essential for a plant breeder for starting judicious breeding programme. Choice of most efficient breeding procedure depends upon a large extent of knowledge of the genetic system controlling the characters to be selected. Grain yield is a complex trait and it is contributed through several polygenic component traits *i.e.* 1000-grain weight, tillers *per* plant, spike length, spikelets *per* spike and grains *per* spike *etc.* All types of gene actions (additive, dominance and epistatic) were reported for yield and its components (Shekhawat *et al.* 2000, Munir *et al.* 2009, Erkul *et al.* 2010, Ojaghi and Akhundova 2010).

A number of biometrical genetical methods of mating designs have been suggested from time to time for detecting and estimating the additive, dominance and epistatic components of genetic variances. The estimation of various genetic components depends on the assumption that the absence of epistasis, which is known to be wide occurrence in almost all crop plants and causes biasness in the estimates of additive and dominance component of genetic variance. The magnitude of the biasness depends upon the relative magnitude of epistatic effects influencing the additive (d) and dominance (h) type of gene effects. Haluvar and Miranda (1985) have presented extensive review on evaluating methods of genetic

components. All these methods, which are based on similarity between parents and the progeny of other relatives, provide the possibility of identifying genetic components of variances. As an example of these methods, diallel analysis is although effective and most widely used (Singh *et al.* 1987; Raghuvanshi *et al.* 1988; Mann *et al.* 1995; Patil *et al.* 1995) does not provide the estimates of non-allelic interactions (Sharma *et al.* 2003) and the evaluation of genetic variability is performed for one generation only.

Grain yield and its component traits are polygenic in nature which may involve epistatic gene interactions in their inheritance. The frequent occurrence of epistatic interactions in quantitative traits reveals their existence in the inheritance of quantitative characters like grain yield and its components (Vaezi *et al.* 2000; Haluvar and Miranda, 1985; Kearsey and Pooni, 1996). Generation mean analysis is a simple but useful technique for estimating gene effects for polygenic traits like grain yield and its components, its greatest merit lying in the ability to estimate epistatic gene interactions. Moreover, generation mean analysis belongs to the quantitative biometric methods based on performances of many generations *i.e.* parental, filial, backcross and segregating generations and give reliable information on genetic components in polygenic traits. Generation mean analysis also helps us in understanding the performance of the parents used in crosses and potential of crosses to be used both for heterosis exploitation or pedigree selection and for detection of epistasis using several generations from a cross between two inbred lines (Sharma and Sain, 2003). It provides information on the relative importance of gene effects in population created from two inbreds. It involves measuring the means of different generations derived from two inbreds and interpreting the means in terms of different genetic effects (Bernardo 2002).

There are several advantages of generation mean analysis. It is relatively simple and statistically reliable (Mather and Jink, 1971). In addition, the generation mean analysis working with the mean (first order statistics) rather than variances (second order statistics), the errors are inherently smaller as means are estimated with greater precision than variances. It can be extended to more complex models. It could be used to estimate the effects due to epistasis, environment, genotype by environment interactions and linkage (Mather and Jink, 1971). The individual performance within different generations could be used to estimate additive, dominance and environmental variance components.

In India, cyst nematode is considered to be the key pest causing an annual loss of Rs. 97.28 million *per year* (Pankaj *et al.* 2015). The cereal cyst nematode (*H. avenae*) was first

recorded in India from *Neem Ka Thana* village in Sikar district of Rajasthan state in 1958 (Vasudeva, 1958). It is now a problem in Rajasthan, Haryana, Punjab, western Uttar Pradesh, Himachal Pradesh and Jammu & Kashmir states of India. The symptoms of molya disease, *i.e.*, stunted growth, discoloration of leaves, low tillering, patches of stunted plants, knotted and bunched roots arise as a result of CCN developing giant/multinucleate cells in the roots of its hosts. Crop rotation and nematicides are effective for controlling this nematode (Nicol and Rivoal, 2007). However, nematicides may leave residual toxicity which causes health hazards and is very expensive if used on a large scale in wheat cultivation. Instead, breeding for resistance is an economical option for managing *H. avenae* (Cook, 2004). Study of inheritance pattern is a pre-requisite before undertaking a project on breeding for resistance to *H. avenae*. Genetics of this trait can greatly facilitate the breeders for development of nematode resistance wheat varieties.

Keeping the above points in view, the present investigation was carried out with the following objectives.

1. To estimate additive, dominance and epistatic parameters
2. To estimate variability, heritability and genetic advance for grain yield and its components
3. To develop the selection strategy for grain yield, its components and nematode resistance in wheat

CHAPTER - II

REVIEW OF LITERATURE

The review of literature pertinent to present investigation has been presented under the following headings.

2.1 Studies on the parameters of genetic variability, heritability and genetic advance

2.1.1 Grain yield and its component traits

Singh and Yunus (1988) observed that both genotypic and phenotypic coefficients of variations were high for grain yield *per plant*. High heritability (ns) was noticed for spikelets *per spike* and grain weight *per ear*. High values of heritability and expected genetic advance for grain weight *per ear*, were also observed in wheat. Ehdaie and Waines (1989) reported that heritability estimates ranged from 43 to 97% for grain yield and its components. Expected genetic advance, expressed as percent of the mean, was around 20% for number of earheads *per plant*, number of grains *per earhead* and 1000-grain weight. Pawar *et al.* (1990) reported that heritability values for 1000-grain weight were relatively higher as compared to those for grain yield, tiller number *per plant* and grain number *per spike* indicating that the latter three characters were influenced more by the environment.

Kaushik *et al.* (1997) observed less heritability for 1000-grain weight in both the crosses. F₂ generation was observed for tillers *per plant* and grain *per ear* under most of the selection criteria. F₄ progenies selected via grain yield exhibited more genetic advance than the control F₂ for grain yield and biological yield. Korkut *et al.* (2001) determined that the highest phenotypic coefficients of variation value were found for plant height, 1000-kernel weight and grain yield. For plant height, grain yield and test weight, the broad sense heritability was found high, while it was low for spike length, number of spikelets *per spike*. Begum *et al.* (2002) conducted genetic study on 1000-grain weight and reported that heritability estimates as well as genetic advances were high for 1000-grain weight.

Kamboj (2003) studied that high heritability with higher genetic advance for ear length suggested better scope for phenotypic selection for yield improvement. Shabana *et al.* (2007) revealed high heritability with high genetic advance for plant height, number of spikelets *per spike* and numbers of grains *per spike*. Erkul *et al.* (2010) reported that heritability estimates

and genetic advances were low for number of kernels *per* spike, thousand kernel weight and grain yield; medium for spike length, number of kernels *per* spikelet, high for number of spikelet *per* spike, spike yield and fertile tiller number. Zaazaa *et al.* (2012) observed moderate heritability for 1000-grain weight, tillers *per* plant and grains *per* ear.

2.1.2 Morphological traits

Singh and Yunus (1988) reported high heritability (ns) for plant height, while lowest heritability for harvest index. The predicted genetic advance ranged from 6.27% for plant height to 18.24% for biological yield. Kaushik *et al.* (1997) reported that randomly selected progenies exhibited more expected genetic advance than control F₂ population for harvest index and biological yield. Kashif and Khaliq (2004) observed moderate to high broad sense heritability for all morphological characters except fertile tillers *per* plant. Plant height exhibited the highest heritability value, while fertile tillers *per* plant showed minimum value.

2.1.3 Phenological traits

Munir *et al.* (2009) reported high heritability estimates for days to heading. Singh *et al.* (2013) reported high heritability coupled with high genetic advance for days to heading and days to maturity. Khan (2013) reported that there was not significance difference in material for days to maturity. Azam *et al.* (2013) revealed highly significant differences among genotypes for days to heading. They reported low broad sense heritability and low expected genetic advance for days to heading. Also they reported significant differences for days to maturity between parents and populations. Moderate heritability in broad-sense and low genetic advance for days to maturity were observed. Yaqoob (2016) showed low variability and heritability estimates for days to maturity.

2.2 Mean values of parents and their generations

Naidu *et al.* (1984) studied that F₁ mean value deviated significantly from mid-parent and F₂ means. Sharma and Sain (2004) reported that epistatic interaction involving dominance in the F₂ generations caused significant inbreeding depression for grains *per* spike. In such situations selective diallel mating and / or biparental mating could be used for amelioration of grains *per* spike in wheat. Akhtar and Chowdhary (2006) reported that the F₁ means for spike length and 1000-grain weight exhibited heterosis in both crosses. Mahamood *et al.* (2006) showed significant heterosis for grain yield, biomass, plant height, spike length, spikelets *per* spike and 1000-grain weight. Rabbani *et al.* (2009) reported that traits like tillers *per* plant,

1000-grain weight and grain yield *per* plant showed over-dominance while spike length exhibited over-dominance under irrigated conditions and additive effect under rainfed conditions. Azam *et al.* (2013) revealed that mean values for days to heading were greater for parents, indicating that progeny had segregation for this trait.

2.3 Inheritance studies on gene effects

2.3.1 Grain yield and its components

Ketata *et al.* (1976a) observed that epistasis was found to contribute significantly to heading date, plant height, tiller number, spikelets *per* spike and grain yield. They further reported that additive effects were the main source of genetic variation for kernel weight, indicating that early generation selection for higher kernel weight would be effective in their material. Naidu *et al.* (1984) studied that additive and dominance gene effects were important for several characters. The dominance effects were generally larger than the additive effects. Out of three epistatic effects, additive $\times$ additive type was the most important.

Chatrath *et al.* (1986) showed that the additive and additive $\times$ additive gene effects were more important in the genetic control of grain yield of wheat. Thus, study demonstrated that immediate improvement in wheat can be achieved through exploitation of additive genetic effects as the magnitude and nature of epistasis in the present material do not suggest heterosis breeding. Sharma *et al.* (1986) reported that additive as well as dominance gene effects governed the inheritance of grain weight *per* spike in both the crosses, but additive effects were of higher magnitude. Additive $\times$ additive component was important in the both crosses. Dominance gene effects with duplicate type of epistasis were observed for the inheritance of grain yield in both the crosses.

Bhatiya *et al.* (1987) revealed that, both additive as well as non-additive gene effects are important in the inheritance of grain yield and its component traits. They suggested biparental mating and / or mating between selected plants from early segregating generations could help in developing durum wheat populations, which upon selection will result into high yielding varieties. Singh and Rai (1987) reported additive $\times$ additive component for spike length and 1000-grain weight. The dominance component was positive and highly significant for all the traits in all the crosses except for spike length. The additive component was also present in sizable proportion. Additive $\times$ dominance component for number of productive tillers and grain yield *per* plant and dominance for grains *per* spike were major components

of genetic variance and complementary type of epistasis was more common for number of productive tillers, grains *per* spike and grain yield *per* plant.

Pawar *et al.* (1988) revealed that involvement of additive, dominance and epistatic gene effects in the inheritance of yield and its component traits. Among the interaction parameters, magnitude of additive $\times$ additive epistasis was higher than dominance $\times$ dominance epistasis. They further reported that complimentary epistasis for tiller number and 1000-grain weight, while for grain number *per* spike duplicate epistasis was observed. Bebyakin and Starichikova (1989) reported that additive gene effects predominated in the control of 1000-grain weight. Kapoor and Luthra (1990) reported that the digenic epistatic model (six parameter model), was failed for spike number and 1000-grain weight indicating the existence of high order interactions or linkages in the material under study.

Jitender Kumar *et al.* (1994) reported that significance of additive gene effects (d) for yield *per* plant, dominance effect (h) was significant for grain yield *per* plant, number of grains *per* spike and 1000-grain weight, epistatic effects, additive $\times$ additive (i) effects appeared to be significant for yield *per* plant. Additive $\times$ dominance (j) type of gene action was found significant for grain yield *per* plant, number of grains *per* spike and 1000-grain weight. Dominance $\times$ dominance (l) type of epistatic effects were observed significant for yield *per* plant, number of grains *per* spike and 1000-grain weight.

Pawar *et al.* (1998) showed epistasis for grain yield, tillers *per* plant, grains *per* spike and 1000-grain weight. All three kinds of gene effects (*i.e.* additive dominance and epistatic) were involved in the inheritance of the characters studied. The additive gene effects were relatively more important than dominance gene effects for grain weight but a reverse situation was observed for grain yield. Six out of eight cases indicated predominance of complementary epistasis. Relatively greater importance of additive and additive $\times$ additive gene effect in the control of component trait especially for 1000-grain weight was indicated. Hence, in case of wheat crop genetic improvement in grain yield *per* plant would be easier through indirect selection for component traits like 1000-grain weight and grain number *per* spike.

Satyavart *et al.* (1999) reported both additive and non-additive components were important for grain yield *per* plant and its three components viz., 1000-grain weight, number of grains *per* ear and ear length in bread wheat. Duplicate type of epistasis was observed for grain yield and 1000-grain weight and complementary type of epistasis for ear length. Yadav and Narsinghani (1999) observed that most of the yield components had predominant of additive gene effects, which would be useful in exploiting transgressive variation for those

traits among the progenies. Duplicate type of epistasis were also expressed in most of the characters in all crosses, while complementary type of epistasis were expressed in spike length and grain yield *per* plant. Shekhawat *et al.* (2000) reported that grain yield *per* plant and tillers *per* plant were mostly governed by dominance, dominance $\times$ dominance and dominance $\times$ dominance $\times$ dominance type of gene effects, with higher magnitude, but were unexploitable due to duplicate type of epistasis. 1000-grain weight was found to be under control of both additive and non-additive gene effects with inadequate trigenic epistasis. Simultaneous utilization of both additive and non-additive genetic effects can be achieved by intermating of segregants in early segregating generations.

Kawar *et al.* (2003) observed that presence of duplicate type of gene action for almost all the yield contributing traits. Population improvement approach in the form of biparental mating among potentially desirable plants in early segregating generations was advised. Fatehi *et al.* (2004) observed mean and additive components for plant height, length of the longest culm, 1000-grain weight were significant. Which indicated that selection in early generations was effective. For plant height, spike length of the longest culm, peduncle length of the longest culm and grain yield *per* plant the components of (d) and (l) have the opposition marks, showing the presence of digenic epistasis. In majority of traits additive $\times$ additive epistasis was significant indicating importance of this component. In respect of epistatic effects, additive $\times$ additive effects were more important than dominant $\times$ dominant effects and only complementary epistasis was observed.

Sharma and Sain (2004) showed that both digenic and trigenic interactions with duplicate epistasis involved in the inheritance of yield and its component traits. Inamullah *et al.* (2006) reported that the additive component was significant for all the yield components *i.e.* spike length, grains *per* spike, 1000-grain weight, harvest index except tillers *per* plant and yield *per* plant. The dominance component was significant for spike length, tillers *per* plant and yield *per* plant. Ahmad *et al.* (2007) reported that most of the genetic parameters including mean (m), additive (d), dominant (h), additive $\times$ additive (i), additive $\times$ dominant (j) and dominant $\times$ dominant (l) effects were significant for grains yield, plant height, tiller number, spike length, grains *per* spikes and 1000-grain weight. The dominant gene effect was the most contributor factor to inheritance of the majority of traits. Munir *et al.* (2009) revealed that additive dominance and epistatic effects were involved in the inheritance of yield and yield components. The traits, *viz.*, days to heading, spikelets *per* spike, grain weight *per* spike and harvest index were controlled by additive genes coupled with high heritability.

Erkul *et al.* (2010) showed that additive-dominance model was valid for spike length, number of spikelets *per* spike, thousand kernel weight, fertile tiller number, and grain yield. Ojaghi and Akhundova (2010) revealed additive type of gene action for number of grains *per* spike and plant height and over dominant type of gene effects for the rest of traits. They further reported that duplicate dominant epistasis only observed for number of spikelets *per* spike, number of tillers and grain yield *per* plant. Gauraha and Rao (2011) showed major contribution of dominance effects associated with dominance $\times$ dominance type of interaction effects for grain yield and its components. Duplicate type of epistasis played a major role in the expression of most of the characters studied in the crosses.

2.3.2 Morphological traits

Fatehi *et al.* (2004) observed additive components for plant height indicated that selection in early generations is effective. Higher value of (d) comparing with (h) is observed for biomass. For plant height, the components of (d) and (l) have the opposition marks, showing the presence of duplicate epistasis. In majority of traits additive $\times$ additive epistasis was significant indicating importance of this component. Shrikant *et al.* (2004) reported that both additive and dominance gene effects were prevalent for harvest index and epistatic interactions were also significant for harvest index. Akhtar and Chowdhary (2006) indicated that additive, dominance and epistatic genetic effects seemed to played a major role in the inheritance of plant height and biomass *per* plant. The additive or additive $\times$ additive gene effects were found to be more prevalent for plant height while dominance or dominance $\times$ dominance effects was noticed prevalent for biomass *per* plant.

Sood *et al.* (2007) observed preponderance of additive gene action for plant height, whereas non-additive gene action was preponderant for biomass yield *per* plant. Kumar and Sharma (2008) revealed that dominance gene effects were prevailed over additive gene effects for biological yield. Epistatic and duplicate type of interactions were also observed for this trait. Hybridization system such as biaparental mating and / or diallel selective matings could be useful for the improvement of this traits. Munir *et al.* (2009) showed that harvest index was controlled by additive gene effects.

2.3.3 Phenological traits

Ketata *et al.* (1976a) observed that epistasis was found to contribute significantly to days to heading. Also a duplicate interaction was detected for days to heading and grain yield,

suggesting difficulty would be encountered in selecting earlier maturity or higher yield. Kathiria *et al.* (1997) found that both additive as well as non additive gene effects were involved in the inheritance of days to heading and maturity with preponderance of additive gene effects. Biparental mating approach would be useful for enhancing genetic variability and creation of transgressive segregates. Sood (2004) observed preponderance of non-additive gene action and over dominance for days to maturity. Sood *et al.* (2009) observed that the additive dominance model was found to be adequate for days to maturity, and reported the presence of additive gene action for this trait. Munir *et al.* (2009) reported that days to heading was controlled by additive genes coupled with high heritability. The result suggested that it may be possible to obtain early maturing and high yielding lines with a relatively simple breeding procedure involving no progeny test.

2.4 Components of genetic variances

2.4.1 Grain yield and its components

Singh *et al.* (1986) reported additive genetic variance was higher than dominance genetic component of variance for grain yield *per* plant, number of grains *per* spike, spikelets *per* spike and 1000-grain weight. Rahman *et al.* (2003) reported additive genetic variance was higher than dominance genetic component of variance for number of grains *per* spike. Meena and Sastry (2003) reported that the magnitude of dominance genetic variances was higher than additive genetic variance for tillers *per* plant. They further observed that higher magnitude of dominance genetic variance than additive genetic variance for spike length. Dere and Yildirim (2006) reported dominance genetic variance was higher than additive genetic variance for grain yield *per* plant. Inamullah *et al.* (2006) revealed that additive genetic variance was higher than dominance genetic variance for tillers *per* plant, spike length, grains *per* spike, 1000-grains weight and grain yield *per* plant. They further reported that dominance genetic variance was higher than additive genetic variance for spike length, tillers *per* plant and grain yield *per* plant.

Akhtar and Chowdhary (2006) reported that the magnitude of additive genetic variance was lower than the dominance genetic variance in majority of the crosses for 1000-grain weight. But additive genetic variance was higher than dominance genetic variance for spikelets *per* spike. Hussain *et al.* (2008) revealed that the higher magnitude of dominance genetic variances than additive genetic variance for grain yield *per* plant, while, Ojaghi and

Akhundova (2010) reported that the magnitude of additive genetic variance was higher than the dominance genetic variance for number of grains *per* spike.

2.4.2 Morphological traits

Singh *et al.* (1986) observed that the magnitude of additive genetic variance was lower than the dominance genetic variance for harvest index. Also, Inamullah *et al.* (2006) reported that the magnitude of additive genetic variance was lower than the dominance genetic variance for harvest index. Meena and Sastry. (2003) reported that the magnitude of additive genetic variance was higher than the dominance genetic variance for plant height. They also reported dominance genetic variance was higher than additive genetic variance for biomass *per* plant and harvest index. Akhtar and Chowdhary (2006) observed that the magnitude of dominance genetic variance was higher than additive genetic variance for harvest index. Ojaghi and Akhundova (2010) reported that the magnitude of additive genetic variance was comparatively higher than dominance genetic variance for plant height.

4.3 Phenological traits

Tefera and Peat (1997) reported that the additive genetic variances was higher than the respective dominance genetic variance for days to heading and days to maturity and suggested that selection for these traits would be effective in early generations.. Moussa (2010) reported that the magnitude of dominance genetic variance was higher than the additive genetic variance for days to heading and days to maturity which indicates that improving these traits through selection in the early generations could not be effective. Abd El Rahman and Hammad (2009) reported that the magnitude of dominance genetic variance was higher than the additive genetic variance for days to heading and days to maturity and advised to delay selection for these traits to later generations with increased homozygosity. Khan (2009) showed that the magnitude of additive genetic variance was higher than dominance genetic variance for days to heading and days to maturity. Further, Abd El-Rahman (2013) also revealed that additive genetic variance was larger than dominance genetic variance for days to heading and days to maturity.

2.5 Inheritance of resistance to cereal cyst nematode

Cook (1974) reviewed the occurrence, nature, and inheritance of varietal resistance in cereals. Evaluation of the practical significance of nematode resistance in a particular host-nematode combination is discussed in relation to host efficiency, host sensitivity, genetic

control of resistance and presence of virulence in the nematode population. Yadav *et al.* (1987), Burrows (1992), Eastwood *et al.* (1994) and Cook (2004) made concerted efforts to study the genetics of resistance in wheat to cereal cyst nematode (*Heterodera avenae*). These studies characterized that the inheritance governed by a single dominant gene. Also, Pankaj *et al.* (1995) reported that resistance was dominant over susceptibility. In F₂ the plants segregated into 3 resistant: 1 susceptible ratio thus suggesting a monogenic dominant control of resistant over susceptibility.

Pankaj *et al.* (2008) found that resistance to cereal cyst nematode and the F₂ population segregated in a 3 resistant: 1 susceptible ratio. Thus, the resistance gene showed monogenic dominance over susceptibility. Rohatgi *et al.* (2009) studied biochemical basis of nematode disease resistance by analysis of the activity of three enzymes, peroxidase (PO), polyphenol oxidase (PPO), and phenylalanine ammonia lyase (PAL) in the shoot and root tissues of resistant and susceptible genotypes of wheat before and after inoculation with the cereal cyst nematode *H. avenae*. In addition, Crowder *et al.* (2003) reported additive gene action, while predominant role of dominance gene action was reported by Hayes *et al.* (1995) for tobacco cyst nematode.

Rivoal *et al.* (2001), Mokabli *et al.* (2002), Vanstone *et al.* (2008), Smiley and Nicol (2009) reported many single genes for resistance to cereal cyst nematode over places in different wheat species *i.e.* Cre 1 in AUS 10894/Loros of *Triticum aestivum*, Cre 2 in AP-1, H-93-8 of *Aegeolopas ventricosa*, Cre 3 in AUS 18913, Cre 4 in CPI 110813 of *Aegeolopas tauschii*, Cre 5 in VPM 1 of *Aegeolopas ventricosa*, Cre 6 in AP-1, H-93-8, H-93-35 of *Aegeolopas ventricosa*, Cre 7 in TR-353 of *Aegeolopas triuncclatis* and Cre 8 in *Triticum aestivum*. Imren *et al.* (2013) identified the Cre 1 gene in *T. aestivum* showed resistance against almost all pathotypes.

Table 2.1: A brief review of various studies on gene effects in bread wheat

Traits	Genetic components					References
	d	h	i	j	l	
Grain yield		√	√		√	Shekhawat <i>et al.</i> (2006)
per plant		√				Amaya <i>et al.</i> (1972), Chowdhry <i>et al.</i> (2001)
		√	√			Sharma and Ahmad (1980) , Erkul <i>et al.</i> (2010)
		√	√	√		Dhiman and Dawa (1999)

Traits	Genetic components					References
	d	h	i	j	l	
		√	√			Busch <i>et al.</i> (1971)
	√	√				Abedi <i>et al.</i> (2015)
Tillers per plant	√					Verma and Yunus (1986)
		√	√	√	√	Akhtar and Chowdhary (2006)
	√	√				Singh <i>et al.</i> (1986)
		√				Shekhawat <i>et al.</i> (2006), Abedi <i>et al.</i> (2015)
1000-grain weight		√			√	Fethi and Mohamed (2010)
	√	√				Rahman <i>et al.</i> (2003), Dhaduk and Shukla (1998)
	√	√				Erkul <i>et al.</i> (2010)
	√					Bhatt (1972), Ketata <i>et al.</i> (1976b), Awaad (1996)
	√					Abedi <i>et al.</i> (2015), Golparvar <i>et al.</i> (2004)
Spikelets per spike	√	√				Erkul <i>et al.</i> (2010)
	√	√				Abedi <i>et al.</i> (2015)
Grains per spike		√	√	√	√	Ketata <i>et al.</i> (1976b)
	√	√				Abedi <i>et al.</i> (2015)
Plant height		√				Bhatia <i>et al.</i> (1986)
	√		√			Haleem A.E. (2009)
	√	√	√		√	Tonk <i>et al.</i> (2011)
	√					Abedi <i>et al.</i> (2015)
	√	√	√	√	√	Khattab <i>et al.</i> (2010)
	√					Sharma and Ahmad (1980), Awaad (1996)
	√	√				Chowdhry <i>et al.</i> (1992)
			√			Amawate and Behl (1995)
Spike length	√	√				Erkul <i>et al.</i> (2010), Walia <i>et al.</i> (1995).
	√	√				Abedi <i>et al.</i> (2015)
Days to heading	√	√				Singh <i>et al.</i> (1987)

CHAPTER - III

MATERIALS AND METHODS

The present investigation was carried out during the period of *rabi* 2013-14 and *rabi* 2014-15 at Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana, India. The details of experiment materials and methods adopted are described under following heads.

3.1 Field Experiment

3.1.1 Plant material

The experimental materials for present study comprised three diverse parents for developing two cross combinations. The parental material has been selected on the basis of disease reaction against cereal cyst nematodes. The pedigree and nematode reaction of parents are given in Table 3.1. The study included of different generations viz., P₁, P₂, F₁, F₂, B₁ and B₂ of each cross combination.

Table 3.1: Parentage/source of genotypes used in crossing programme and their nematode reaction

Parents	Pedigree	Reaction to nematode resistance
P 12210	W462//UEE/KOEL/3/PEG/HRL/BUC	Susceptible
P 12231	WBLL1*2/K1RITATI	Susceptible
Raj MR 1	AUS 15854/J-24	Resistant

Using parents given in table 3.1 the experimental material was developed from the following two crosses:

F₁: P 12210/Raj MR 1 and P 12231/Raj MR 1

B₁: P 12210*2/Raj MR 1

P 12231*2/Raj MR 1

B₂: P 12210/2* Raj MR 1

P 12231/2* Raj MR 1

Experimental material of all six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) with respect to each cross combination for first season *rabi* 2013-14 were obtained from the Wheat and Barley section, Department of Genetics and Plant Breeding, CCS HAU, Hisar. Whereas, crosses were attempted during 2013-2014 (*rabi*) to generate the seeds for F_1 , F_2 , B_1 and B_2 for *rabi* 2014-15.

3.1.2 Layout

The experimental material consisted of different generations viz., P_1 , P_2 , F_1 , F_2 , B_1 and B_2 of two crosses were evaluated in Compact Family Block Design with three replications, during *rabi* 2013-2014 and 2014-2015 in the Department of Genetics and Plant Breeding, CCSHAU, Hisar.

Among the treatments, the non segregating generations, viz., parents P_1 , P_2 , and F_1 were grown in single row of 3m length. The segregating F_2 generation was grown in ten rows of 3m row length and backcrosses B_1 and B_2 were grown in four rows of 3m length. The row to row and plant to plant distance was maintained 23 cm and 10 cm, respectively.

3.1.3 Agronomic practices

All recommended package of practices were followed to raise the healthy crop. Details of the plants raised and selected randomly *per* generation is given below.

Table 3.2: Number of plants selected *per* generation for observations under field experiment

Generation	Number of plants raised/ replication	Number of plants selected/replication
P_1	30 (Single row)	5
P_2	30 (Single row)	5
F_1	30 (Single row)	5
F_2	300 (Ten rows)	50
B_1	120 (Four rows)	20
B_2	120 (Four rows)	20

3.1.4 Observations recorded

- i. Grain yield (g/plant):** Grains threshed from the harvested plants in each treatment in each replication were collected, weighted and values were worked out as grain yield *per plant* (g).
- ii. Number of tillers *per plant*:** The spikes which bear seed at the time of harvest and contributed to yield were considered for effective tillers and total number of such tillers *per plant* were counted and recorded.
- iii. 1000-grain weight (g):** A random sample of 100 grains of each entry from each replication was counted, weighed and multiplied by a factor of ten to derive 1000-grain weight.
- iv. Number of grains *per spike*:** Total number of grains obtained from the spike of main tiller were counted and recorded.
- v. Spike length (cm):** Spike length was measured from the base to the tip of the main tiller spike including awns at maturity of randomly selected plants.
- vi. Number of spikelets *per spike*:** Total number of spikelets of main tiller spike were counted and recorded at maturity.
- vii. Plant height (cm):** Plant height was measured in centimeters from stem base to the tip of spike including awns of main tiller of randomly selected plants in each plot at the time of harvest.
- viii. Biomass *per plant* (g):** Above ground biomass of randomly selected and sun dried plants were weighed in grams.
- ix. Harvest Index (%):** It was the ratio of seed yield *per plant* (g) to biological yield *per plant* (g) as given below.

$$HI (\%) = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

- x. Number of days to heading:** The date on which the 75% spikes emerged from flag leaf was recorded and the numbers of days were calculated from the date of sowing.
- xi. Number of days to maturity:** The date on which the 75% spikes matured was recorded and numbers of days were calculated from the date of sowing.

3.2 Pot Experiment

3.2.1 Plant Material

The plant material included all the three parents, and their six generations viz., P₁, P₂, F₁, F₂, B₁ and B₂ of each cross combinations. Detailed plant material used and cross combinations generated for pots studies were given in heading 3.1.1.

3.2.2 Layout

The pot experiment was carried out in the screen house of Department of Nematology, CCS HAU, Hisar. The experiment was conducted to study the development of *H. avenae* in the above-mentioned one resistant and two susceptible wheat lines and their six generations. For this purpose, five plants in each P₁, P₂, F₁ non segregating generations; twenty plants in each B₁, B₂ generations and forty plants in F₂ segregating generation (Table 3.3) has been raised *per* replication in pots using completely randomized block design in three replications.

Naturally infested field soil was collected from field of department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during the first week of November 2013. All the parental lines/varieties, filial and backcross generations were sown in pots of size 6 inches in diameter. Each Pot contains 1kg naturally infested soil (4 cysts/100 cm³ = 150 g, and each cyst contains averaging 120-210 eggs).

Two seeds *per* pot were sown and finally thinned to one seedling *per* pot after two weeks of germination pots were irrigated regularly with distilled water to avoid any infection.

Table 3.3: Number of plants raised *per* generation under pot experiment

Generation	Number of plants raised/ replication
P ₁	5
P ₂	5
F ₁	5
F ₂	40
B ₁	10
B ₂	10

3.2.3 Observations recorded:

The final cyst population was ascertained 90-94 days after sowing. For this, the soil with roots removed from each pot, suspended to extract all cysts in 5 liter water and sieved through nested 20 (840 µm) and 60 (250 µm) mesh sieves (Cobb, 1918). The residue collected on the 60 (250 µm) mesh sieve was examined under a binocular microscope to

count the number of cysts *per* plant. Based on the number of cysts formed, the plants were categorized as resistant (0-4 cysts/plant), moderately resistant (5-9 cysts/plant) and susceptible (10 and above cysts/plant) as per scale used in All India Coordinated Wheat and Barley Improvement Project (Pankaj *et al.* 2006).

Table 3.4 Categories of nematode reaction based on number of cyst nematode

No. of cyst nematode	Class
0-4	Resistant
4-9	Moderate resistant
9-20	Susceptible
>20	Highly susceptible

3.3 Statistical analysis

Standard statistical procedures used in this study are described under following subheads.

3.3.1 Mean

Mean value ($\bar{X}$) of each character was determined by dividing the sum of the observed values with the corresponding number of observations.

$$\bar{X} = \frac{\sum_{i=1}^N X_i}{N}$$

Where,

X_i - Observation of the i^{th} treatment

N - Total number of observations.

3.3.2 Standard error (SE)

The standard error was calculated by the formula given by Altman and Bland, 2005 of the precision of sample mean. To know how widely some scattered measurements are, standard deviation is used and to indicate the uncertainty around the estimate of mean measurement, the standard error of the mean is quoted.

$$SE = \frac{SD}{\sqrt{n}}$$

Where,

SE - Standard error,

SD - Standard deviation and

n - Number of observations or sample size.

3.3.3 Analysis of variance for various characters

The analysis of variance was performed to test the significance of difference between the years, progenies and interactions of year $\times$ progenies of each generation for all the characters. Analysis of variance was carried out as per method described by Little and Hill (1978). The analysis of variance was based on following assumptions.

- i) The error terms are randomly, independently and normally distributed
- ii) The variances of different samples are homogeneous
- iii) Variances and means of different samples are not correlated
- iv) The main effects are additive

Model of analysis of variance:

$$Y_{ijk} = u + a_i + b_j + ab_{ij} + R_{jk} + E_{ijk}$$

$$E_{ijk} \sim N(0, \sigma^2)$$

Where,

Y_{ijk} is the effect of i^{th} genotype in j^{th} environment in k^{th} replication

u is the overall grand mean

a_i is the main effect due to i^{th} genotypes

b_j is the main effect due to j^{th} environment (year)

ab_{ij} is the interaction effect of i^{th} genotype to j^{th} environment

R_{jk} is the effect due to k^{th} replication in j^{th} environment

E_{ijk} is the residual of i^{th} genotype in j^{th} environment in k^{th} replication

Table 3.5: Analysis of variance of various progenies evaluated over the years

Source of variation	d.f.	SS	MS	E (MS)	F
Year	(y-1)	SSy	SSy/ y-1	$\sigma^2_e + r.\sigma^2_{py} + r.p.\sigma^2_y$	MSy/ MSe
Replication	y(r-1)	SSr	SSr/ y(r-1)	$\sigma^2_e + p.y.\sigma^2_r$	MSr/ MSe
Progenies	p-1	SSp	SSp/ p-1	$\sigma^2_e + r.\sigma^2_{py} + r.y.\sigma^2_p$	MSp/ MSe
Progenies × year	(y-1)(p-1)	SSpy	SSpy/(y-1)(p-1)	$\sigma^2_e + r.\sigma^2_{py}$	MSp/ MSe
Residual	y(r-1)(p-1)	SSe	SSe/ y(r-1)(p-1)	σ^2_e	
Total	(yrp-1)	SSt	SSt/(yrp-1)		

Where,

y = year

r = Number of replications

p = Number of progenies

e = error/residual

df= Degrees of freedom

SS = Sum of square

MS = Mean sum of square

E (MS) = Expected mean squares

Genotypic variance (σ^2_g) = (MSp - MSe)/r.y

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

σ^2_e = MSe

3.3.4 Parameters of variability

The coefficients of genotypic and phenotypic variation were calculated by the formula given by Burton and Devane (1953) as follows-

$$\text{Genotypic coefficient of variation (GCV)} = \sqrt{\frac{\text{Genotypic variance}}{\text{Mean}}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \sqrt{\frac{\text{Phenotypic variance}}{\text{Mean}}} \times 100$$

3.3.5 Heritability in broad sense and genetic advance

Heritability percentage in broad sense and genetic advance as percent of mean was calculated for each character as per formula and standard procedure prescribed by Singh and Chaudhary (1985).

$$\text{Heritability in broad sense (H}^2\text{)} = [\sigma^2_g / \sigma^2_p] \times 100$$

3.3.6 Genetic advance

Genetic advance for each character was also calculated as per the formula.

$$Gs = k \cdot H^2 \cdot \sigma^2_p$$

Where,

k = selection differential constant (2.06 at 5% selection intensity)

H²= heritability in broad sense

σ^2_p = Phenotypic variance

Genetic advance expressed in terms, percentage of mean is given by

$$G.A(\%) = (GS / \bar{F}_2) \times 100$$

Where,

$\bar{F}_2$ = mean of F₂

3.3.7 Generation mean analysis

While estimating the parameters of gene effects from the generation mean analysis, the following assumptions were made.

- i) Diploid segregation
- ii) Homozygous parents
- iii) Absence of multiple alleles

- iv) Absence of linkage
- v) Absence of lethal genes
- vi) No differential viability and fertility of gametes in different segregating generations
- vii) Environmental effects are additive with the genotypic value.

3.3.7.1 Three parameter model of Joint scaling test

Joint scaling test outlined by Cavalli (1952) was applied to six generations P_1 , P_2 , F_1 , F_2 , B_1 and B_2 to fit three parameter model accordingly given in Dabholkar (1992). It consists of estimating the parameters m , d and h using weighted least squares method.

Table 3.6: Estimation of gene effects using three parameter model through weighted least square analysis

Generations	Weights	m	d	h	Observed $\times$ Weight
P_1	W_1	1	1	0	$O_1 \times W_1$
P_2	W_2	1	-1	0	$O_2 \times W_2$
F_1	W_3	1	0	1	$O_3 \times W_3$
F_2	W_4	1	0	$\frac{1}{2}$	$O_4 \times W_4$
B_1	W_5	1	$\frac{1}{2}$	$\frac{1}{2}$	$O_5 \times W_5$
B_2	W_6	1	$-\frac{1}{2}$	$\frac{1}{2}$	$O_6 \times W_6$
Total		b_{11}	b_{12}	b_{13}	S_1

Where,

$O_1, O_2, \dots, O_6$ are the observed means of respective generations.

$W_1, W_2, \dots, W_6$ are the weights calculated as reciprocals of variances.

Formulation of matrix of coefficients of parameters (J matrix):

$$J = \begin{bmatrix} b_{11} & b_{12} & b_{13} \\ b_{21} & b_{22} & b_{23} \\ b_{31} & b_{32} & b_{33} \end{bmatrix}$$

Formulation of C matrix (J^{-1}) and multiply by S matrix for the expectations as: $\hat{M} = J^{-1}.S$

$$C = \begin{bmatrix} c_{11} & c_{12} & c_{13} \\ c_{21} & c_{22} & c_{23} \\ c_{31} & c_{32} & c_{33} \end{bmatrix} \quad M = \begin{bmatrix} m \\ (d) \\ (h) \end{bmatrix} \quad S = \begin{bmatrix} S_1 \\ S_2 \\ S_3 \end{bmatrix}$$

Where,

S is the vector of observed generation means,

C is the matrix of inverse of coefficients of the parameters (J)

M is the vector of the parameters, m, (d) and (h).

Calculation of estimates for three parameter model:

$$\hat{m} = c_{11} \times S_1 + c_{12} \times S_2 + c_{13} \times S_3$$

$$\hat{d} = c_{21} \times S_1 + c_{22} \times S_2 + c_{23} \times S_3$$

$$\hat{h} = c_{31} \times S_1 + c_{32} \times S_2 + c_{33} \times S_3$$

Test of significance of the estimates:

$$t(m) = \frac{\hat{m} - o}{SE(m)}$$

Where, S.E. (m) = $\sqrt{c_{11}}$ compared with 't' value at 5% level of significance for n-1 d.f.

$$t(d) = \frac{\hat{d} - o}{SE(d)}$$

Where, S.E. (d) = $\sqrt{c_{22}}$ compared with 't' value at 5% level of significance for n-1 d.f.

$$t(h) = \frac{\hat{h} - o}{SE(h)}$$

Where, S.E. (h) = $\sqrt{c_{33}}$ compared with 't' value at 5% level of significance for n-1 d.f.

Chi-square test:

The test of goodness of fit was calculated the method as given below.

$$\chi^2 \text{ at } (n - p) \text{ d. f.} = \sum_{i=1}^n (O_i - \bar{E}_i)^2 W_i$$

Where,

O_i = observed mean of i^{th} generation

$\bar{E}_i$ = expected mean of i^{th} generation

W_i = weight of information of i^{th} generation

n = number of generations

p = number of parameters estimated

Table 3.7: Chi-square analysis to test of goodness of fit of three parameter model

Generations	Observed	Expected	$O_i - E_i$	$(O_i - E_i)^2 \times W_i$
P₁	O_1	$E_1 = m + d$	$O_1 - E_1$	$(O_1 - E_1)^2 \times W_1$
P₂	O_2	$E_2 = m - d$	$O_2 - E_2$	$(O_2 - E_2)^2 \times W_2$
F₁	O_3	$E_3 = m + h$	$O_3 - E_3$	$(O_3 - E_3)^2 \times W_3$
F₂	O_4	$E_4 = m + \frac{1}{2} h$	$O_4 - E_4$	$(O_4 - E_4)^2 \times W_4$
B₁	O_5	$E_5 = m + \frac{1}{2} d + \frac{1}{2} h$	$O_5 - E_5$	$(O_5 - E_5)^2 \times W_5$
B₂	O_6	$E_6 = m - \frac{1}{2} d + \frac{1}{2} h$	$O_6 - E_6$	$(O_6 - E_6)^2 \times W_6$

When the three parameter model was inadequate, the six parameter model was applied through weighted least square technique of Cavalli (1952).

3.3.7.2 Six parameter model of joint scaling test

Table 3.8: Estimation of gene effects using six parameter model through weighted least square analysis

Generations	Weights	m	d	h	i	J	l	Observed $\times$ Weight
P₁	W_1	1	1	0	1	0	0	$O_1 \times W_1$
P₂	W_2	1	-1	0	1	0	0	$O_2 \times W_2$
F₁	W_3	1	0	1	0	0	1	$O_3 \times W_3$
F₂	W_4	1	0	$\frac{1}{2}$	0	0	$\frac{1}{4}$	$O_4 \times W_4$

Generations	Weights	m	d	h	i	J	l	Observed × Weight
B₁	W ₅	1	½	½	¼	¼	¼	O ₅ × W ₅
B₂	W ₆	1	- ½	½	¼	- ¼	¼	O ₆ × W ₆
Total		b₁₁	b₁₂	b₁₃	b₁₄	b₁₅	b₁₆	S₁

Where,

O₁, O₂,.....O₆ are the observed means of respective generations.

W₁, W₂,.....W₆ are the weights calculated as reciprocals of variances.

Formulation of matrix of coefficients of parameters (J matrix):

$$J = \begin{bmatrix} b_{11} & b_{12} & b_{13} & b_{14} & b_{15} & b_{16} \\ b_{21} & b_{22} & b_{23} & b_{24} & b_{25} & b_{26} \\ b_{31} & b_{32} & b_{33} & b_{34} & b_{35} & b_{36} \\ b_{41} & b_{42} & b_{43} & b_{44} & b_{45} & b_{46} \\ b_{51} & b_{52} & b_{53} & b_{54} & b_{55} & b_{56} \\ b_{61} & b_{62} & b_{63} & b_{64} & b_{65} & b_{66} \end{bmatrix}$$

Formulation of C matrix (J⁻¹) and multiply by S matrix for the expectations as: $\hat{M} = J^{-1}.S$

$$C = \begin{bmatrix} c_{11} & c_{12} & c_{13} & c_{14} & c_{15} & c_{16} \\ c_{21} & c_{22} & c_{23} & c_{24} & c_{25} & c_{26} \\ c_{31} & c_{32} & c_{33} & c_{34} & c_{35} & c_{36} \\ c_{41} & c_{42} & c_{43} & c_{44} & c_{45} & c_{46} \\ c_{51} & c_{52} & c_{53} & c_{54} & c_{55} & c_{56} \\ c_{61} & c_{62} & c_{63} & c_{64} & c_{65} & c_{66} \end{bmatrix} \quad M = \begin{bmatrix} m \\ (d) \\ (h) \\ (i) \\ (j) \\ (l) \end{bmatrix} \quad S = \begin{bmatrix} S_1 \\ S_2 \\ S_3 \\ S_4 \\ S_5 \\ S_6 \end{bmatrix}$$

Where,

S is the vector of observed generation means,

C is the matrix of inverse of coefficients of the parameters (J)

M is the vector of the parameters, m, (d), (h), (i), (j) and (l).

Calculation of estimates for three parameter model:

$$\hat{m} = c_{11} \times S_1 + c_{12} \times S_2 + c_{13} \times S_3 + c_{14} \times S_4 + c_{15} \times S_5 + c_{16} \times S_6$$

$$\hat{d} = c_{21} \times S1 + c_{22} \times S2 + c_{33} \times S3 + c_{24} \times S4 + c_{25} \times S5 + c_{26} \times S6$$

$$\hat{h} = c_{31} \times S1 + c_{32} \times S2 + c_{33} \times S3 + c_{34} \times S4 + c_{35} \times S5 + c_{36} \times S6$$

$$\hat{i} = c_{41} \times S1 + c_{42} \times S2 + c_{43} \times S3 + c_{44} \times S4 + c_{45} \times S5 + c_{46} \times S6$$

$$\hat{j} = c_{51} \times S1 + c_{52} \times S2 + c_{53} \times S3 + c_{54} \times S4 + c_{55} \times S5 + c_{56} \times S6$$

$$\hat{l} = c_{61} \times S1 + c_{62} \times S2 + c_{63} \times S3 + c_{64} \times S4 + c_{65} \times S5 + c_{66} \times S6$$

Test of significance of the estimates:

$$t(m) = \frac{\hat{m} - o}{SE(m)}$$

Where, S.E. (m) = $\sqrt{c_{11}}$ compared with 't' value at 5% level of significance for n-1 d.f.

$$t(d) = \frac{\hat{d} - o}{SE(d)}$$

Where, S.E. (d) = $\sqrt{c_{22}}$ compared with 't' value at 5% level of significance for n-1 d.f.

$$t(h) = \frac{\hat{h} - o}{SE(h)}$$

Where, S.E. (h) = $\sqrt{c_{33}}$ compared with 't' value at 5% level of significance for n-1 d.f.

$$t(i) = \frac{\hat{i} - o}{SE(i)}$$

Where, S.E. (i) = $\sqrt{c_{44}}$ compared with 't' value at 5% level of significance for n-1 d.f.

$$t(j) = \frac{\hat{j} - o}{SE(j)}$$

Where, S.E. (j) = $\sqrt{c_{55}}$ compared with 't' value at 5% level of significance for n-1 d.f.

$$t(l) = \frac{\hat{l} - o}{SE(l)}$$

Where, S.E. (l) = $\sqrt{c66}$ compared with 't' value at 5% level of significance for n-1 d.f.

3.3.8 Estimates of Components of genetic variances and heritability in narrow sense

The components of genetic variances and heritability in narrow sense for generations were calculated by the formulae of Mather and Jinks (1982) as given below

$$D = 4V_{F2} - 2(V_{B1} - V_{B2})$$

$$H = 4(V_{B1} + V_{B2} - V_{F2} - V_E)$$

$$E = 1/4(V_{P1} + V_{P2} + 2V_{F1})$$

Heritability in narrow sense was worked out as follows –

$$\text{Heritability in narrow sense (h}^2\text{)} = \left[\frac{D/2}{D/2 + H/4 + E} \right] \times 100$$

Where:

D – additive genetic variance.

H – dominance genetic variance.

E – environmental component of variance.

3.3.9 Inheritance of resistance to cereal cyst nematode

A Chi-Square test was performed for genetic analysis of discrete categories to test whether the observed plants in different filial and backcross generations of the cross combinations in study followed the theoretical or the expected ratios based on the laws of inheritance. As per Yates correction rule (whenever d.f. =1) a value of 0.5 was subtracted from the absolute value of each calculated O-E term. The following formula was used for calculations:

$$\chi^2 = \sum_{i=1}^k \frac{(O_i - E_i)^2}{E_i}$$

Table 3.9: Chi-square analysis for nematode resistance

Categories	Observed	Expected	$O_i - E_i$	$[(O_i - E_i)^2 - 0.5]/E_i^*$
Resistant	O_1	$E_1 = r(R) \times \text{Total}$	$O_1 - E_1$	$[(O_1 - E_1)^2 - 0.5]/E_1$
Susceptible	O_2	$E_2 = r(S) \times \text{Total}$	$O_2 - E_2$	$[(O_2 - E_2)^2 - 0.5]/E_2$
Total	$O_1 + O_2$	$E_1 + E_2$		S_{1-k}

* Minus 0.5, Yates correction factor whenever tested only two categories

Where,

O_i = Observed frequency in i^{th} cell

E_i = Expected frequency in i^{th} cell

$r(R)$ = expected ratio of the resistant category

$r(S)$ = expected ratio of the susceptible category

D.F. = $K - 1$ (K is number of discrete categories)

S_{1-k} = Sum of chi-square values over the K categories

CHAPTER -IV

EXPERIMENTAL RESULTS

Wheat improvement programme deals with development of high yielding varieties. However, how best to choose the selection strategies and breeding methods is the main goal for breeders to focus. Most of the researchers focus on choice based on behavior of genetic components (additive, dominance and epistasis) of the traits. Therefore, in present investigation “Inheritance of grain yield, its components and resistance to cereal cyst nematode in wheat (*Triticum aestivum* L.)” an attempt has been made to estimate additive, dominance and epistatic parameters for grain yield and its components and to determine inheritance of cereal cyst nematode resistance in wheat. Results of various experiments conducted on these subjects are presented experiment-wise under the following headings:

4.1 Analysis of variance

Analyses of variances of different crosses are given below.

4.1.1 Cross P 12210/Raj MR 1

Analysis of variance showed that variation due to years was significant at 0.01 level of probability for grain yield *per* plant, tillers *per* plant, biomass *per* plant, days to heading and days to maturity (Table 4.1). For plant height, variation due to years was significant at 0.05 level of probability. Significance of variation due to year indicated that there were differences for the environmental conditions during these years for above characters. Variation due to replications showed that differences for replication effects for all the traits were nonsignificant. Variation due to progenies indicated that grain yield *per* plant, tillers *per* plant, 1000-grain weight, grains *per* spike, spike length, spikelets *per* spike, plant height, biomass *per* plant, days to heading and days to maturity were significant at 0.01 level of probability, while harvest index was significant at 0.05 level of probability. This indicated the presence of sufficient magnitude of variation for all characters undertaken. Variation due to progenies $\times$ year showed that tillers *per* plant, spikelet *per* spike and harvest index were significant at 0.05 level of probability, while plant height, biomass *per* plant were significant at 0.01 level of probability. This revealed that different progenies behaved differently over the different years, for these traits.

Table 4.1: Analysis of variance for various traits of cross P 12210/Raj MR 1 in bread wheat during the years 2013-14 and 2014-15

Source of variation	DF	Grain yield per plant	Tillers per plant	1000-grain weight	Grains per spike	Spike length	Spikelets per spike	Plant height	Biomass per plant	Harvest index	Days to heading	Days to maturity
Year	1	124.3**	13.1**	0.7	8.9	1.4	1.4	57.2*	251.5**	48.6	225.0**	36.0**
Replications	4	2.8	2.1	0.6	3.5	0.2	0.2	8.4	1.2	35.4	0.2	0.1
Progenies	5	13.6**	7.7**	133.2**	124.9**	5.7**	3.9**	89.9**	75.6**	55.4*	13.0**	62.6**
Progenies × year	5	2.9	6.6**	2.5	35.5	1.1	2.6**	29.5*	24.5*	128.0**	0.1	0.1
Residual	20	1.7	1.1	1.9	19.4	0.5	0.6	9.9	7.6	18.2	0.2	0.4
Total	35	145.3	30.6	138.9	192.2	8.9	8.7	194.9	360.4	285.6	238.5	99.2

*, **: Significant at 5% and 1% level of probability, respectively

Table 4.2: Analysis of variance for various traits of cross P 12231/Raj MR 1 in bread wheat during the years 2013-14 and 2014-15

Source of variation	DF	Grain yield per plant	Tillers per plant	1000- grain weight	Grains per spike	Spike length	Spikelets per spike	Plant height	Biomass per plant	Harvest index	Days to heading	Days to maturity
Year	1	72.3**	0.6**	0.4	5.8	8.2	0.1	37.1*	155.3**	153.1	225.0**	36.0**
Replications	4	3.5	1.3	4.1	5.7	0.6	0.1	1.1	5.7	40.7	0.1	0.1
Progenies	5	24.0**	5.3**	147.7**	166.2**	2.9**	2.1**	83.5**	55.0**	99.6*	15.4**	36.3**
Progenies × year	5	6.9	2.3**	7.4	17.1	0.9	1.2**	42.7*	71.9*	50.5**	0.1	0.1
Residual	20	0.9	0.7	1.7	12.4	0.3	0.2	12.2	3.9	18.5	0.2	0.1
Total	35	107.6	10.2	161.3	207.2	12.9	3.7	176.6	291.8	362.4	240.8	72.6

*, **: Significant at 5% and 1% level of probability, respectively

4.1.2 Cross P 12231/Raj MR 1

Analysis of variance showed that variation due to years was significant at 0.01 level of probability for grain yield *per plant*, tillers *per plant*, biomass *per plant*, days to heading and days to maturity, (Table 4.2). For plant height variation due to years was significant at 0.05 level of probability. Significance of variation due to year indicated that there were differences for the environmental conditions during these years for above characters. Variation due to replications showed that differences for replication effects for all the traits were nonsignificant. Variation due to progenies indicated that grain yield *per plant*, tillers *per plant*, 1000-grain weight, grains *per spike*, spike length, spikelets *per spike*, plant height, biomass *per plant*, days to heading and days to maturity were significant at 0.01 level of probability, while harvest index was significant at 0.05 level of probability. This indicated the presence of sufficient magnitude of variation for all characters undertaken except days to heading and days to maturity. Variation due to progenies $\times$ year showed that tillers *per plant*, spikelet *per spike* and harvest index were significant at 0.05 level of probability, while plant height, biomass *per plant* were significant at 0.01 level of probability. This revealed that different progenies behaved differently over the different years, for these traits.

4.2 Mean performance

The mean performance of each generation with their respective families in different years and crosses are given in Table 4.3.

4.2.1 Grain yield *per plant*

Cross P 12210/Raj MR 1

During the year 2013-14, data for grain yield *per plant* revealed that both parents P 12210 (16.9 ± 0.64) and Raj MR 1 (16.9 ± 0.59) had similar grain yield *per plant*. However, the grain yield *per plant* was higher in F_1 ($18.7 \pm 1.04g$) than parents indicating the dominance effect. F_2 ($21.5 \pm 0.76g$) was also had higher grain yield *per plant* than both the parents indicating heterosis. The B_1 (17.4 ± 1.38) and B_2 (16.0 ± 1.01) were at par for grain yield *per plant* to their recurrent parents.

During the year 2014-15, the parent P 12210 (13.6 ± 0.87) was at par to Raj MR 1 (12.5 ± 0.68) in grain yield *per plant*. The grain yield *per plant* of F_1 (14.3 ± 0.29) was similar to its better parent P12210 which showed dominance. F_2 (15.8 ± 0.44) generation was higher than its better parent P12210 which showed heterosis. The B_1 (15.5 ± 0.38) also had higher grain

yield *per* plant than its recurrent parent which indicated epistasis effects for grain yield *per* plant.

Cross P 12231/Raj MR 1

During the year 2013-14, the data revealed the parent Raj MR 1 (18.3 ± 0.59) was at par to the parent P 12231 (17.7 ± 1.09). The F_1 (19.3 ± 0.96) also at par to the parents showed dominance. The F_2 (23.1 ± 0.30 g) had given higher grain yield *per* plant than its better parent indicated heterosis. The B_1 (17.8 ± 1.12) was at par to its recurrent parent while, B_2 (15.3 ± 0.31) had given less grain yield *per* plant than its recurrent parent.

During the year 2014-15, the parent P 12231 (13.7 ± 0.73) and Raj MR 1 (13.7 ± 0.29) had given similar grain yield *per* plant. The F_1 (16.0 ± 0.23) and F_2 (18.3 ± 0.73) had given higher grain yield *per* plant than their better parent which showed heterosis. The B_1 (17.4 ± 0.42) and B_2 (15.4 ± 0.25) generations also had higher grain yield *per* plant than their respective recurrent parent which indicated epistasis for grain yield *per* plant.

Overall the grain yield *per* plant showed over dominance effect in the expression of F_1 and F_2 generations. The mean performance of B_1 and B_2 were higher than their respective recurrent parents in majority of the crosses which showed presence of epistatic interactions.

4.2.2 Tillers *per* plant

Cross P 12210/Raj MR 1

During the year 2013-14, the data pertaining to tillers *per* plant showed that parent Raj MR 1 (7.1 ± 0.41) had higher tillers than parent P 12210 (5.1 ± 0.18). The mean tillers *per* plant in F_1 (8.9 ± 0.98) was higher than their better parent Raj MR 1 which showed heterosis. The mean tillers *per* plant in F_2 (8.1 ± 1.17) was at par to the better parent Raj MR 1 which showed dominance. The B_1 (10.9 ± 1.16) and B_2 (10.0 ± 0.96) had higher tillers *per* plant than their respective recurrent parents indicating epistasis.

During the year 2014-15, mean tillers *per* plant for parent Raj MR 1 (8.1 ± 0.29) was higher than P 12210 (6.1 ± 0.18) in year 2014-15. But the F_1 (6.9 ± 0.07) was intermediate to the parents. The mean tillers *per* plant in F_2 (7.8 ± 0.06) was also intermediate to the parents indicated lack of dominance. The B_1 (7.2 ± 0.48) was at par with recurrent parent while B_2 (6.7 ± 0.23) had lesser tillers than its recurrent parent Raj MR 1.

Cross P 12231/Raj MR 1

During the year 2013-14, the parent Raj MR 1 (7.1 ± 0.18) and P 12231 (6.3 ± 0.64) had produced similar tillers *per plant*. The F_1 (5.9 ± 0.47) was at par to P 12231 showed dominance. The mean tillers *per plant* F_2 (8.8 ± 0.84) generation was higher than its better parent Raj MR 1 which showed heterosis. The B_1 (8.3 ± 0.35) had higher tillers than the recurrent parent P 12231 showed epistasis. While B_2 (6.6 ± 0.36) was at par to its recurrent parent.

During the year 2014-15, mean tillers *per plant* for parent Raj MR 1 (8.7 ± 0.37) was higher than P 12231 (6.3 ± 1.11). The F_1 (5.7 ± 0.58) was at par to P 12231 showed dominance. The F_2 (7.6 ± 0.18) was intermediate to the parents showed lack of dominance. The B_1 (6.4 ± 0.48) was at par to its recurrent parent while B_2 (6.9 ± 0.12) generation had low tillers than its recurrent parent Raj MR 1.

The parent Raj MR 1 had high tillers than P 12210 and P 12231 and in majority of the crosses the F_1 and F_2 generations showed dominance effect. The average performance of B_1 was higher than its recurrent parent in majority of the crosses showed presence of epistatic interactions.

4.2.3 1000-grain weight

Cross P 12210/Raj MR 1

During the year 2013-14 the data showed that parent P 12210 (40.9 ± 0.59) had higher 1000-grain weight than Raj MR 1 (28.9 ± 0.59). The F_1 (39.1 ± 0.58) and F_2 (40.5 ± 0.33) had intermediate 1000-grain weight to parents showed lack of dominance. The B_1 (40.0 ± 0.58) was at par with recurrent parent while B_2 (31.9 ± 0.47) had high 1000-grain weight than its recurrent parent showed presence of epistasis.

During the year 2014-15, similarly to previous year, parent P 12210 (39.9 ± 0.47) had higher 1000-grain weight than Raj MR 1 (30.9 ± 0.59) during year 2014-15. The F_1 (39.4 ± 1.14) and F_2 (38.8 ± 1.44) had intermediate 1000-grain weight to parents showed lack of dominance. The B_1 (39.3 ± 0.33) and B_2 (31.2 ± 0.99) were at par to their respective recurrent parent.

Cross P 12231/Raj MR 1

During the year 2013-14, the Parent P 12231 (44.3 ± 0.33) had higher 1000-grain weight than Raj MR 1 (28.9 ± 0.59). The F_1 (41.7 ± 0.33) and F_2 (35.4 ± 0.87) were intermediate to the

parents showed lack of dominance. The B_1 (40.8 ± 0.39) had less 1000-grain weight than its recurrent parent. While, B_2 (33.9 ± 0.59) generation had more 1000-grain weight than its recurrent parent Raj MR 1 showed epistasis.

During the year 2014-15, parent P 12231 (40.7 ± 0.88) had higher 1000-grain weight than Raj MR 1 (30.5 ± 1.25). The F_1 (42.3 ± 0.33) generation had higher 1000-grain weight than its better parent P 12231 this indicated heterosis. The F_2 (37.8 ± 1.97) was intermediate to its parent. The B_1 (39.8 ± 0.39) was at par to its recurrent parent while B_2 (35.2 ± 0.39) had more 1000-grain weight than its recurrent parent, indicated epistasis.

The parent P12231 had higher 1000-grain weight than P 12210 and Raj MR 1. In majority of the crosses the F_1 and F_2 generations had intermediate 1000-grain weight to their parents indicated lack of dominance. Backcross generations showed presence of epistatic interactions in majority of the crosses and years.

4.2.4 Grains *per* spike

Cross P 12210/Raj MR 1

During the year 2013-14, data revealed that parent P 12210 had more number (64.9 ± 2.12) of grains *per* spike than Raj MR 1 (46.4 ± 1.22). The F_1 (56.6 ± 4.36) and F_2 (59.6 ± 1.37) had intermediate grains *per* spike to their parents showed lack of dominance. The B_1 (60.4 ± 2.39) and B_2 (51.4 ± 5.32) were at par to their respective recurrent parents.

During the year 2014-15, similarly to previous year, parent P 12210 had more number (60.8 ± 0.64) of grains *per* spike than Raj MR 1 (56.5 ± 0.68). The F_1 (55.3 ± 1.45) was at par to its parent Raj MR 1 showed dominance. The F_2 (59 ± 0.92) was intermediate to its parents showed lack of dominance. The B_1 (60.4 ± 0.91) was at par to its recurrent parent while, B_2 (53.4 ± 1.29) beard less grains *per* spike than its parents.

Cross P 12231/Raj MR 1

During the year 2013-14 data revealed that, parent P 12231 had produced more number (67.1 ± 1.77) of grains *per* spike than Raj MR 1 (48.1 ± 0.94). The F_1 (59.3 ± 0.44) and F_2 (62.0 ± 3.01) were intermediate to the parents showed lack of dominance. The B_1 (60.9 ± 2.88) had produced less grains *per* spike than its recurrent parent while, B_2 (55.7 ± 1.04) had produced more grains *per* spike than its recurrent parent indicated epistasis.

During the year 2014-15, parent P 12231 had more number (67.8 ± 2.95) of grains *per* spike than Raj MR 1 (55.3 ± 3.10). The F_1 (58.5 ± 0.77) was at par to the parent Raj MR 1 showed dominance. The F_2 (61.0 ± 1.49) had produced intermediate grains *per* spike showed lack of dominance. The B_1 (58.6 ± 1.08) had produced less grains *per* spike than its recurrent parent while B_2 (56.8 ± 0.55) was at par its recurrent parent.

The parent P12231 had higher grains *per* spike than P 12210 and Raj MR 1. In majority of the crosses F_1 and F_2 generations were intermediate to their parents showed lack of dominance. The backcross generations were either low or equal to their recurrent parents which showed lack of epistasis for grains *per* spike.

4.2.5 Spike length

Cross P 12210/Raj MR 1

During the year 2013-14, the data showed that spike length of parent P 12210 (13.9 ± 0.27) was higher than Raj MR 1 (12.5 ± 0.48). The spike length in F_1 (13.9 ± 0.44) was at par to its better parent showed dominance while in F_2 (12.7 ± 0.43) spike length was intermediate to the parents. Both B_1 (14.5 ± 0.12) and B_2 (13.4 ± 0.29) had higher spike length than their respective recurrent parent which indicated epistasis for spike length.

During the year 2014-15, spike length in parent P 12210 (15.7 ± 0.29) was higher than Raj MR 1 (12.5 ± 0.66). The F_1 (14.7 ± 0.41) was intermediate to the parents. The F_2 (13.0 ± 0.12) was at par to the parent Raj MR 1 which indicated dominance. The B_1 (14.7 ± 0.33) had lesser spike length than its recurrent parent P 12210 while B_2 (12.8 ± 0.15) was at par to its recurrent parent showed epistasis.

Cross P 12231/Raj MR 1

During the year 2013-14 the data showed that spike length of parent P 12231 (13.1 ± 0.24) was higher than Raj MR 1 (12.5 ± 0.35). The F_1 (12.3 ± 0.24) and F_2 (12.0 ± 0.23) were at par to the parent Raj MR 1 showed dominance. The backcross generations B_1 (12.2 ± 0.37) and B_2 (11.3 ± 0.27) had less spike length than their respective recurrent parent.

During the year 2014-15, the spike length of parent P 12231 (14.6 ± 0.53) was higher than Raj MR 1 (12.1 ± 0.48). The F_1 (12.9 ± 0.58) was at par to the parent Raj MR 1 showed dominance. The F_2 (13.0 ± 0.18) was intermediate to the parents. The B_1 (14.0 ± 0.20) and B_2 (12.4 ± 0.07) were at par to their respective recurrent parent.

Table 4.3: Mean values of the progenies for various traits in bread wheat during the years 2013-14 and 2014-15

Generations	Crosses/Years	Grain yield <i>per</i> plant (g)	Tillers <i>per</i> plant	1000-grain weight (g)	Grains <i>per</i> spike
P1	P 12210/Raj MR 1 (2013-14)	16.9±0.64	5.1±0.18	40.9±0.59	64.9±2.12
	P 12210/Raj MR 1 (2014-15)	13.6±0.87	6.1±0.18	39.9±0.47	60.8±0.64
	P 12231/Raj MR 1 (2013-14)	17.7±1.09	6.3±0.64	44.3±0.33	67.1±1.77
	P 12231/Raj MR 1 (2014-15)	13.7±0.73	6.3±1.11	40.7±0.88	67.8±2.95
P2	P 12210/Raj MR 1 (2013-14)	16.9±0.59	7.1±0.41	28.9±0.59	46.4±1.22
	P 12210/Raj MR 1 (2014-15)	12.5±0.68	8.1±0.29	30.9±0.59	56.5±0.68
	P 12231/Raj MR 1 (2013-14)	18.3±0.59	7.1±0.18	28.9±0.59	48.1±0.94
	P 12231/Raj MR 1 (2014-15)	13.7±0.29	8.7±0.37	30.5±1.25	55.3±3.10
F1	P 12210/Raj MR 1 (2013-14)	18.7±1.04	8.9±0.98	39.1±0.58	56.6±4.36
	P 12210/Raj MR 1 (2014-15)	14.3±0.29	6.9±0.07	39.4±1.14	55.3±1.45
	P 12231/Raj MR 1 (2013-14)	19.3±0.96	5.9±0.47	41.7±0.33	59.3±0.44
	P 12231/Raj MR 1 (2014-15)	16.0±0.23	5.7±0.58	42.3±0.33	58.5±0.77
F2	P 12210/Raj MR 1 (2013-14)	21.5±0.76	8.1±1.17	40.5±0.33	59.6±1.37
	P 12210/Raj MR 1 (2014-15)	15.8±0.44	7.8±0.06	38.8±1.44	59.0±0.92
	P 12231/Raj MR 1 (2013-14)	23.1±0.30	8.8±0.84	35.4±0.87	62.0±3.01
	P 12231/Raj MR 1 (2014-15)	18.3±0.73	7.6±0.18	37.8±1.97	61.0±1.49
B1	P 12210/Raj MR 1 (2013-14)	17.4±1.38	10.9±1.16	40.0±0.58	60.4±2.39
	P 12210/Raj MR 1 (2014-15)	15.5±0.38	7.2±0.48	39.3±0.33	60.4±0.91
	P 12231/Raj MR 1 (2013-14)	17.8±1.12	8.3±0.35	40.8±0.39	60.9±2.88
	P 12231/Raj MR 1 (2014-15)	17.4±0.42	6.4±0.48	39.8±0.39	58.6±1.08
B2	P 12210/Raj MR 1 (2013-14)	16.0±1.01	10.0±0.96	31.9±0.47	51.4±5.32
	P 12210/Raj MR 1 (2014-15)	13.5±0.75	6.7±0.23	31.2±0.99	53.4±1.29
	P 12231/Raj MR 1 (2013-14)	15.3±0.31	6.6±0.36	33.9±0.59	55.7±1.04
	P 12231/Raj MR 1 (2014-15)	15.4±0.25	6.9±0.12	35.2±0.39	56.8±0.55
Mean	P 12210/Raj MR 1 (2013-14)	16.5±0.65	7.5±0.50	37.5±0.65	58.2±1.80

Table 4.3: Contd.....

Generations	Crosses/Years	Spike length (cm)	Spikelets per spike	Plant height (cm)	Biomass per plant (g)
P1	P 12210/Raj MR 1 (2013-14)	13.9±0.27	21.7±0.52	94.0±3.69	39.3±1.45
	P 12210/Raj MR 1 (2014-15)	15.7±0.29	20.9±0.33	98.5±2.03	35.6±1.75
	P 12231/Raj MR 1 (2013-14)	13.1±0.24	22.3±0.07	99.9±1.07	41.7±1.33
	P 12231/Raj MR 1 (2014-15)	14.6±0.53	22.3±0.37	96.7±1.43	34.4±0.42
P2	P 12210/Raj MR 1 (2013-14)	12.5±0.48	22.8±0.42	94.3±2.25	36.3±1.2
	P 12210/Raj MR 1 (2014-15)	12.5±0.66	21.0±0.31	88.7±1.39	34.3±1.3
	P 12231/Raj MR 1 (2013-14)	12.5±0.35	22.7±0.18	94.6±0.87	39.3±0.88
	P 12231/Raj MR 1 (2014-15)	12.1±0.48	21.3±0.07	88.7±0.41	31.0±0.95
F1	P 12210/Raj MR 1 (2013-14)	13.9±0.44	22.7±0.47	101.8±1.60	40±0.58
	P 12210/Raj MR 1 (2014-15)	14.7±0.41	21.8±0.58	97.5±2.19	32.9±0.79
	P 12231/Raj MR 1 (2013-14)	12.3±0.24	21.5±0.29	93.5±2.52	39.0±1.16
	P 12231/Raj MR 1 (2014-15)	12.9±0.58	22.4±0.31	97.8±2.08	36.5±1.92
F2	P 12210/Raj MR 1 (2013-14)	12.7±0.43	23.1±0.06	95.7±0.70	48.2±1.96
	P 12210/Raj MR 1 (2014-15)	13.0±0.12	22.9±0.53	94.2±0.41	42.4±0.43
	P 12231/Raj MR 1 (2013-14)	12.0±0.23	21.4±0.15	87.3±0.15	48.2±1.34
	P 12231/Raj MR 1 (2014-15)	13.0±0.18	20.6±0.13	90.9±0.88	39.1±1.36
B1	P 12210/Raj MR 1 (2013-14)	14.5±0.12	20.0±0.55	103.7±3.76	40.4±2.53
	P 12210/Raj MR 1 (2014-15)	14.7±0.33	22.1±0.12	95.7±3.03	39.6±1.19
	P 12231/Raj MR 1 (2013-14)	12.2±0.37	20.5±0.24	89.5±0.67	44.3±1.17
	P 12231/Raj MR 1 (2014-15)	14.0±0.20	21.3±0.20	94.9±2.73	37.5±0.59
B2	P 12210/Raj MR 1 (2013-14)	13.4±0.29	23.3±0.42	90.9±3.64	45.3±1.88
	P 12210/Raj MR 1 (2014-15)	12.8±0.15	22.5±0.36	90.6±4.16	33.2±1.19
	P 12231/Raj MR 1 (2013-14)	11.3±0.27	21.8±0.20	84.9±3.78	32.3±1.42
	P 12231/Raj MR 1 (2014-15)	12.4±0.07	21.9±0.20	92.8±1.93	41.6±0.95
Mean	P 12210/Raj MR 1 (2013-14)	13.2±0.35	21.8±0.30	94.1±1.97	38.2±1.22

Table 4.3: Contd.....

Genera tions	Crosses/Years	Harvest index (%)	Days to heading	Days to maturity
P1	P 12210/Raj MR 1 (2013-14)	43.1±0.03	90.0±0.01	130.0±0.01
	P 12210/Raj MR 1 (2014-15)	43.7±0.04	95.0±0.01	132.0±0.01
	P 12231/Raj MR 1 (2013-14)	38.3±0.04	94.7±0.33	131.0±0.01
	P 12231/Raj MR 1 (2014-15)	40.3±0.06	99.7±0.33	133.0±0.01
P2	P 12210/Raj MR 1 (2013-14)	47.4±0.05	92.0±0.01	129.0±0.01
	P 12210/Raj MR 1 (2014-15)	46.5±0.04	97.0±0.01	131.0±0.01
	P 12231/Raj MR 1 (2013-14)	38.3±0.06	92.0±0.01	129.0±0.01
	P 12231/Raj MR 1 (2014-15)	48.4±0.09	97.0±0.01	131.0±0.01
F1	P 12210/Raj MR 1 (2013-14)	46.9±0.06	95.0±0.01	136.0±0.01
	P 12210/Raj MR 1 (2014-15)	50.1±0.06	100.0±0.01	138.0±0.01
	P 12231/Raj MR 1 (2013-14)	44.1±0.06	92.0±0.01	133.0±0.01
	P 12231/Raj MR 1 (2014-15)	50.5±0.10	97.0±0.01	135.0±0.01
F2	P 12210/Raj MR 1 (2013-14)	47.1±0.03	91.0±0.58	129.7±0.67
	P 12210/Raj MR 1 (2014-15)	51.5±0.04	96.0±0.58	131.7±0.67
	P 12231/Raj MR 1 (2013-14)	48.3±0.05	90.3±0.33	132.7±0.33
	P 12231/Raj MR 1 (2014-15)	59.5±0.06	95.3±0.33	134.7±0.33
B1	P 12210/Raj MR 1 (2013-14)	45.3±0.04	94.0±0.01	135.7±0.33
	P 12210/Raj MR 1 (2014-15)	44.6±0.05	99.0±0.01	137.7±0.33
	P 12231/Raj MR 1 (2013-14)	54.7±0.08	91.7±0.33	136.0±0.01
	P 12231/Raj MR 1 (2014-15)	51.7±0.06	96.7±0.33	138.0±0.01
B2	P 12210/Raj MR 1 (2013-14)	37.7±0.03	92.7±0.33	134.3±0.33
	P 12210/Raj MR 1 (2014-15)	49.5±0.07	97.7±0.33	136.3±0.33
	P 12231/Raj MR 1 (2013-14)	50.0±0.07	94.0±0.01	134.3±0.33
	P 12231/Raj MR 1 (2014-15)	48.6±0.10	99.0±0.01	136.3±0.33
Mean	P 12210/Raj MR 1 (2013-14)	46.9±0.06	95.1±0.20	133.0±0.15

The parent P 12231 had higher spike length than P 12210 and Raj MR 1. Predominantly the spike length in F_1 and F_2 generations was equal to their better parent showed dominance effect. Also the lower F_2 mean than F_1 showed inbreeding depression for spike length. While in backcross generations, spike length was either lower or equal to their recurrent parents showed lack of epistasis

4.2.6 Spikelets *per* spike

Cross P 12210/Raj MR 1

During the year 2013-14, the data showed that the spikelets *per* spike was higher in Raj MR 1 (22.8 ± 0.42) than P 12210 (21.7 ± 0.52). The F_1 (22.7 ± 0.47) and F_2 (23.1 ± 0.06) were at par to their better parent Raj MR 1 exhibited dominance. The B_1 (20.0 ± 0.55) generations showed lower spikelets *per* spike than its recurrent parent while the B_2 (23.3 ± 0.42) was at par to donor parent Raj MR 1 which indicates epistasis for this trait.

During the year 2014-15, both parents P 12210 (20.9 ± 0.33) and Raj MR 1 (21.0 ± 0.31) had similar spikelets *per* spike. The F_1 (21.8 ± 0.58) was also at par to its parents. The F_2 (22.9 ± 0.53) spikelets *per* spike was higher than the parents showed heterosis. Also the higher spikelets *per* spike in B_1 (22.1 ± 0.12) and B_2 (22.5 ± 0.36) generations then their respective recurrent parents showed epistasis.

Cross P 12231/Raj MR 1

During the year 2013-14, the numbers of spikelets *per* spike were higher in Raj MR 1 (22.7 ± 0.18) than P 12231 (22.3 ± 0.07). But spikelets *per* spike were low in F_1 (21.5 ± 0.29) and F_2 (21.4 ± 0.15) than their parents showed heterosis in opposite direction. Also, B_1 (20.5 ± 0.24) and B_2 (21.8 ± 0.20) showed lower spikelets *per* spike than their respective recurrent parents.

During the year 2014-15, the parent P 12231 (22.3 ± 0.37) had beard higher spikelets *per* spike than Raj MR 1 (21.3 ± 0.07). The F_1 (22.4 ± 0.31) was at par to its better parent showed dominance. While the F_2 (20.6 ± 0.13) had beard low spikelets *per* spike than its parents which showed inbreeding depression. The B_1 (21.3 ± 0.20) had less spikelets *per* spike than its recurrent parent while B_2 (21.9 ± 0.20) had more spikelets *per* spike than recurrent parent showed epistasis.

The parent Raj MR 1 had beard more spikelets *per* spike than P 12210 and P 12231. The expression of F_1 and F_2 generations showed over dominance effects in majority of the cases.

Furthermore, the mean performance of B₁ and B₂ were higher than their recurrent parents in majority of the crosses showed presence of epistatic interactions.

4.2.7 Plant height (cm)

Cross P 12210/Raj MR 1

During the year 2013-14, the data showed that, the parent P 12210 (94.0±3.69) was at par to the parent Raj MR 1 (94.3±2.25). The F₁ (101.8±1.60) was taller than both the parents showed heterosis while the F₂ (95.7±0.70) was at par to the parents. The B₁ (103.7±3.76) was taller than its recurrent parent indicated epistasis while B₂ (90.9±3.64) was at par to its parents.

During the year 2014-15, parent P 12210 (98.5±2.03) was taller than Raj MR 1 (88.7±1.39). The F₁ (97.5±2.19) was at par to the taller parent P12210 showed dominance. The F₂ (94.2±0.41) was intermediate to the parents. The B₁ (95.7±3.03) and B₂ (90.6±4.16) were at par to their respective recurrent parents.

Cross P 12231/Raj MR 1

During the year 2013-14, the Parent P 12231(99.9±1.07) was taller than Raj MR 1 (94.6±0.87). The F₁ (93.5±2.52) was at par to the parent Raj MR 1 showed dominance. The F₂ (87.3±0.15) had lower plant height than its parents, indicated inbreeding depression for plant height. Also the B₁ (89.5±0.67) and B₂ (84.9±3.78) had less height than their respective recurrent parent.

During the year 2014-15, parent P 12231(96.7±1.43) was taller than Raj MR 1 (88.7±0.41). The F₁ (97.8±2.08) was at par to its taller parent P12231 showed dominance. The F₂ (90.9±0.88) was intermediate to its parents. The B₁ (94.9±2.73) was at par to its recurrent parent while, B₂ (92.8±1.93) was taller than its recurrent parent, which indicated epistasis.

The expression of F₁ and F₂ generations showed both dominance and over dominance effects. Also the lower F₂ mean than F₁ showed inbreeding depression for plant height. Furthermore, the mean performance of B₁ and B₂ were higher than their recurrent parents in majority of the crosses showed presence of epistatic interactions.

4.2.8 Biomass *per plant*

Cross P 12210/Raj MR 1

During the year 2013-14, data revealed that parent P 12210 (39.3 ± 1.45) had higher biomass production than Raj MR 1 (36.3 ± 1.2). The F_1 (40 ± 0.58) was at par to its better parent P 12210 showed dominance. The F_2 (48.2 ± 1.96) had produced higher biomass than its better parent P 12210 showed heterosis. The B_1 (40.4 ± 2.53) was at par to its recurrent parent while B_2 (45.3 ± 1.88) had produced higher biomass *per plant* than its recurrent parent which indicated epistasis.

During the year 2014-15, the parent P 12210 (35.6 ± 1.75) was at par to the parent Raj MR 1 (34.3 ± 1.3). The F_1 (32.9 ± 0.79) was at par to the parent Raj MR 1 showed dominance. Furthermore, the biomass *per plant* of F_2 (42.4 ± 0.43) generation was higher than its better parent P12210 which showed heterosis. The B_1 (39.6 ± 1.19) had produced higher biomass production than its recurrent parent which indicated epistasis while the B_2 (33.2 ± 1.19) was at par to its recurrent parent.

Cross P 12231/Raj MR 1

During the year 2013-14, the data recorded for biomass *per plant* revealed that parent P 12231 (41.7 ± 1.33) had higher biomass production than Raj MR 1 (39.3 ± 0.88). The F_1 (39.0 ± 1.16) was at par to the parent Raj MR 1 showed dominance. The F_2 (48.2 ± 1.34) produced higher biomass than its better parent P 12231 showed heterosis. The B_1 (44.3 ± 1.17) had higher biomass than its recurrent parent indicated epistasis while, the B_2 (32.3 ± 1.42) had lower biomass *per plant* than its recurrent parent for this trait.

During the year 2014-15, parent P 12231 (34.4 ± 0.42) had higher biomass production than Raj MR 1 (31.0 ± 0.95). The F_1 (36.5 ± 1.92) was at par to its better parent showed dominance. The biomass *per plant* in F_2 (39.1 ± 1.36) was higher than the better parent which showed heterosis. The B_1 (37.5 ± 0.59) and B_2 (41.6 ± 0.95) generations also had higher biomass production than their respective recurrent parent which indicating epistasis.

The parent P 12231 had higher biomass production than P 12210 and Raj MR 1. The biomass *per plant* in F_1 and F_2 generations showed both dominance and over dominance effects. Also the lower F_2 mean than F_1 showed inbreeding depression for biomass *per plant*. Furthermore, the average performance of B_1 and B_2 were higher than their recurrent parents in majority of the crosses showed presence of epistatic interactions.

4.2.9 Harvest index

Cross P 12210/Raj MR 1

During the year 2013-14, the parent Raj MR 1 (47.4 ± 0.05) had higher harvest index than P 12210 (43.1 ± 0.03). The F_1 (46.9 ± 0.06) and F_2 (47.1 ± 0.03) were intermediate to the parents showed lack of dominance. The B_1 (45.3 ± 0.04) generation had higher harvest index than the recurrent parent which indicated epistasis while the B_2 (37.7 ± 0.03) generation had lower harvest index than its recurrent parent.

During the year 2014-15, Raj MR 1 (46.5 ± 0.04) had higher harvest index than P 12210 (43.7 ± 0.04). The F_1 (50.1 ± 0.06) generation had higher harvest index than the better parent P 12210 showed heterosis. Also F_2 (51.5 ± 0.04) generation had higher harvest index than the better parent P 12210 indicated heterosis. Furthermore, B_1 (44.6 ± 0.05) and B_2 (49.5 ± 0.07) generations had higher harvest index than their respective recurrent parent indicated epistasis.

Cross P 12231/Raj MR 1

During the year 2013-14, the harvest index by P 12231 and Raj MR 1 were similar ($38.3 \pm 0.04\%$ and $38.3 \pm 0.06\%$, respectively). The F_1 (44.1 ± 0.06) and F_2 (48.3 ± 0.05) had given higher harvest index than their better parent, this indicated heterosis. Also in B_1 (54.7 ± 0.08) and B_2 (50.0 ± 0.07) the harvest index was higher than their respective recurrent parent indicating epistasis.

During the year 2014-15, Raj MR 1 (48.4 ± 0.09) had higher harvest index than P 12231 (40.3 ± 0.06). The F_1 (50.5 ± 0.10) and F_2 (59.5 ± 0.06) had higher harvest index than their better parent Raj MR 1 indicated heterosis. The B_1 (51.7 ± 0.06) and B_2 (48.6 ± 0.10) also had high harvest index than their respective recurrent parent indicated epistasis.

The parent Raj MR 1 had higher harvest index than P 12210 and P 12231. The harvest index of F_1 and F_2 generations were higher than their better parent showed over dominance effect. Also the lower F_2 mean than F_1 showed inbreeding depression for harvest index. The mean performance of B_1 and B_2 were higher than their recurrent parents in majority of the crosses showed presence of epistatic interactions.

4.2.10 Days to heading

Cross P 12210/Raj MR 1

During the year 2013-14, the data showed that, parents P 12210 required 90.0 ± 0.01 days to heading and Raj MR 1 required 92.0 ± 0.01 days to heading, while F_1 got comparatively more time (95.0 ± 0.01 days) for heading than both parents and showed heterosis. On the other hand, F_2 generation headed in 91.0 ± 0.58 days which indicating inbreeding depression. Both B_1 and B_2 generations required higher days to heading (94.0 ± 0.01 and 92.7 ± 0.33 days, respectively) than recurrent and donor parent respectively which indicated epistatic effect.

During the year 2014-15, parent P 12210 required 95.0 ± 0.01 days to heading and Raj MR 1 required 95.0 ± 0.01 days to heading. F_1 plants required more number of days to heading (100.0 ± 0.01 days) than both the parents showed heterosis. The F_2 (96.0 ± 0.58 days) headed earlier comparatively to the parents. Both B_1 and B_2 generations took more days to heading (99.0 ± 0.01 days and 97.7 ± 0.33 days, respectively) than parents which indicated epistatic effect.

Cross P 12231/Raj MR 1

During the year 2013-14, the Parent P 12231 was significant later in heading (94.7 ± 0.33) than Raj MR 1 (92.0 ± 0.01). The F_1 was at par with Raj MR 1 (92.0 ± 0.01) and showed dominance. The F_2 (90.3 ± 0.33) generation required less days to heading than parents. The B_1 took less days to heading (91.7 ± 0.33) than its recurrent parent, while, B_2 had required more days was later in heading (94.0 ± 0.01) than its recurrent parent which showed epistatic effect.

During the year 2014-15, parent P 12231 was later in heading (99.7 ± 0.33 days) than Raj MR 1 (97.0 ± 0.01). Similar to the last year, F_1 was equal to the Raj MR 1 for days to heading (97.0 ± 0.01). The F_2 took lesser days to heading (95.3 ± 0.33) than both the parents. The B_1 was earlier in heading (96.7 ± 0.33) than its recurrent parent, while B_2 was later in heading (99.0 ± 0.01) than its recurrent parent Raj MR 1.

The parent P12231 required more days to heading than P 12210 and Raj MR 1. The days to heading, in general, showed over dominance effect. The lower F_2 mean than their respective F_1 s showed inbreeding depression. The average performance of B_1 and B_2 were higher than their recurrent parents in majority of the crosses which showed presence of epistatic effect.

4.2.11 Days to maturity

Cross P 12210/Raj MR 1

During the year 2013-14, the parents P 12210 (130.0 ± 0.01) took significantly more days to maturity than Raj MR 1 (129.0 ± 0.01). The F_1 was also significantly later in its maturity (136.0 ± 0.01) than its better parent. The F_2 (129.7 ± 0.67) was at par to its better parent indicating dominance. B_1 (135.7 ± 0.33) and B_2 (134.3 ± 0.33) generations were took higher days to maturity than their respective recurrent parents which indicating epistatic effect.

Similarly, during the year 2014-15, parent P 12210 took more days to mature (132.0 ± 0.01) than Raj MR 1 (131.0 ± 0.01). F_1 plants required more number of days for maturity (138.0 ± 0.01 days) than its better parent P 12210. The F_2 (131.7 ± 0.67 days) was at par to the parent P 12210 showed dominance. Both B_1 and B_2 generations were later in maturity (137.7 ± 0.33 days and 136.3 ± 0.33 days, respectively) than their respective recurrent parents which indicating epistatic effect.

Cross P 12231/Raj MR 1

During the year 2013-14, the parent P 12231 was later in maturity (131.0 ± 0.01) than Raj MR 1 (129.0 ± 0.01). The F_1 (133.0 ± 0.01) and F_2 (132.7 ± 0.33) were also later in maturity than their respective better parent P12231. The B_1 and B_2 generations required higher days (136.0 ± 0.01 and 134.3 ± 0.33 , respectively) for maturity than their respective recurrent parents which indicated epistasis.

Similarly, during the year 2014-15, parent P 12231 required more days to maturity (133.0 ± 0.01) than Raj MR 1 (131.0 ± 0.01). The F_1 (135.0 ± 0.01) and F_2 (134.7 ± 0.33) took more time than better parent P 12231 for maturity this showed heterosis. The B_1 and B_2 were later in maturity (138.0 ± 0.01 and 136.3 ± 0.33 , respectively) than their respective recurrent parents which indicated epistasis.

The parent P12231 required more days to maturity than P 12210 and Raj MR 1. The days to maturity showed over dominance effect and the average performance of B_1 and B_2 were higher than their respective recurrent parents in majority of the crosses indicating presence of epistatic interactions.

4.3 Genetic variability parameters

The estimates of genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability in broad sense (H) and genetic advance as per cent of mean (GA) are given in Table 4.4 and 4.5 for cross P 12210/Raj MR 1 and P 12231/Raj MR 1, respectively.

4.3.1 Parameters of variability in cross P 12210/Raj MR 1

High GCV (39.5) and PCV (44.0) values were recorded for grain yield *per plant*. Grain yield *per plant* had high heritability in broad sense (89.3%) coupled with high genetic advance (73.1%). Tillers *per plant* had high GCV (36.3) and high PCV (40.2) values. Further, tillers *per plant* had high heritability in broad sense (82.9%) coupled with high genetic advance (67.9%). 1000-grain weight had moderate GCV (12.1) and low PCV (14.3) values, high heritability in broad sense (87.4%) and low genetic advance (20.9%).

Table 4.4: Parameters of genetic variability, heritability and genetic advance for various traits of bread wheat for cross P 12210/Raj MR 1 during the years 2013-14 and 2014-15

Characters	Cross P 12210/Raj MR 1			
	Genotypic Coefficient of Variance	Phenotypic Coefficient of Variance	Heritability in broad sense	Genetic Advance (as percent of mean)
Grain yield <i>per plant</i>	39.5	44.4	89.3	73.1
Tillers <i>per plant</i>	36.3	40.2	82.9	67.9
1000-grain weight	12.1	14.3	87.4	20.9
Grains <i>per spike</i>	14.1	20.2	42.9	20.4
Spike length	9.8	15.3	71.4	13.1
Spikelets <i>per spike</i>	5.8	8.6	63.8	8.3
Plant height	17.3	18.5	93.7	33.6
Biomass <i>per plant</i>	35.3	36.9	84.9	64.8
Harvest index	55.6	59.6	90.2	74.2
Days to heading	27.3	28.5	83.7	23.6
Days to maturity	30.1	32.6	79.8	38.2

Grains *per* spike had moderate values for GCV (14.0) and PCV (20.2), heritability in broad sense (42.9%) was low and genetic advance (20.4%) was also moderate. For spike length GCV (9.8) and PCV (15.3) values were low and heritability in broad sense (71.4%) was moderate and genetic advance (13.1%) was low. Similarly, spikelets *per* spike had low GCV (5.8) and low PCV (8.6) values. The heritability in broad sense was moderate (63.8%) for this trait but low genetic advance (8.3%) indicating low scope of selection for this trait.

Plant height had moderate GCV (17.3) and low PCV (18.5) values. The heritability in broad sense was high (93.7%) with high genetic advance (33.6 %) for plant height. Biomass *per* plant had high GCV (35.3) and high PCV (36.9) estimates. High heritability in broad sense (84.9%) with high genetic advance (64.8%) was recorded for biomass *per* plant. Likewise, harvest index had high GCV (55.6), high PCV (59.6), high heritability in broad sense (90.2%) and high genetic advance (74.2%) indicating better chances of improvement for this trait. High GCV (27.3) and moderate PCV (28.5) values were recorded for days to heading. Days to heading had high heritability in broad sense (83.7%) and moderate genetic advance (23.6%). Days to maturity had high values for GCV (30.1) and high PCV (32.6), heritability in broad sense (80.8%) was high with high genetic advance (38.2%) indicating better chances of improvement.

Thus grain yield *per* plant, tillers *per* plant, harvest index, biomass *per* plant, days to heading and days to maturity had high estimates for majority of variability parameters, heritability and genetic advance indicating better scope of selection in these traits. Plant height, 1000-grain weight and grains *per* spike had low to moderate values, while spike length and spikelets *per* spike had low estimates for majority of the parameters indicating moderate to low scope of selection for these traits.

4.3.2 Parameters of variability in cross P 12231/Raj MR 1

Grain yield *per* plant had high GCV (36.6) and high PCV (41.0) values along with high heritability in broad sense (88.9%) and high genetic advance (67.5 %). Tillers *per* plant had high GCV (35.6) and high PCV (42.9) values, high heritability in broad sense (90.3%) and high genetic advance (61.7%). One thousand grain weight had moderate GCV (13.9) and low PCV (15.9) values, and high heritability in broad sense (84.6%) and moderate genetic advance (25.1 %).

Grains *per* spike had low GCV (7.8) and PCV (18.2). The heritability in broad sense (69.8%) was moderate and genetic advance (8.4%) was low for this trait. For spike length GCV (11.0) value was moderate and PCV (15.4) value was low and heritability in broad sense (64.1%) was moderate and genetic advance (16.4%) was also low. Spikelets *per* spike had low GCV (4.4), low PCV (6.9) and moderate values (67.4) for heritability in broad sense. Genetic advance (6.1%) was also low indicating low scope of selection for this trait.

Table 4.5: Parameters of genetic variability, heritability and genetic advance for various traits of bread wheat for cross P 12231/Raj MR 1 during the years 2013-14 and 2014-15

Characters	Cross P 12231/Raj MR 1			
	Genotypic Coefficient of Variance	Phenotypic Coefficient of Variance	Heritability in broad sense	Genetic Advance (as percent of mean)
Grain yield <i>per</i> plant	36.6	41.0	88.9	67.5
Tillers <i>per</i> plant	35.6	42.9	90.3	61.7
1000-grain weight	13.9	15.9	84.6	25.1
Grains <i>per</i> spike	7.8	18.2	69.8	8.4
Spike length	11.0	15.4	64.1	16.4
Spikelets <i>per</i> spike	4.4	6.9	67.4	6.1
Plant height	14.9	15.9	93.5	28.9
Biomass <i>per</i> plant	31.7	37.3	95.7	55.7
Harvest index	56.0	62.1	93.3	76.4
Days to heading	29.3	30.5	85.7	25.6
Days to maturity	32.1	34.6	82.8	40.2

Plant height had moderate GCV (14.9) and low PCV (15.9) values. Heritability in broad sense (93.5%) was high with moderate genetic advance (28.9 %) for this trait. Biomass *per* plant had high GCV (31.7) and high PCV (37.3) estimates. High heritability in broad sense (95.7%) with high genetic advance (55.7%) was recorded for biomass *per* plant. Harvest index had high GCV (56.0), high PCV (62.1), high heritability in broad sense (93.3%) and high genetic advance (76.4%) indicating better chances of selection for this trait. High GCV (29.3) and moderate PCV (30.5) values were recorded for days to heading. Days

to heading had high heritability in broad sense (85.7%) and moderate genetic advance (25.6%). Days to maturity had high values for GCV (32.1) and high PCV (34.6), heritability in broad sense (82.8%) was high with high genetic advance (40.2%) indicating better chances of improvement.

Thus, grain yield *per* plant, tillers *per* plant, harvest index, biomass, days to heading and days to maturity had high estimates for majority of variability parameters, heritability and genetic advance indicating better scope of selection in these traits. Plant height, 1000-grain weight and spike length had low to moderate values, while grains *per* spike, spikelets *per* spike had low estimates for majority of the parameters indicating moderate to low scope of selection for these traits.

4.4 Inheritance of various traits in bread wheat

All the characters were analyzed as per Joint Scaling Test (Cavalli, 1952) using three parameter model (Table 4.6). The characters with significant chi-square values were further analysed by using six parameter model. The estimates of additive (d), dominance (h) gene effects along with their interactions, *i.e.*, additive $\times$ additive (i), additive $\times$ dominance (j) and dominance $\times$ dominance (l) were estimated. The parameter 'm' was significant for all the characters in both years and crosses. This indicated that there were significant differences in all the progenies for all the traits over the years and crosses. Detailed results are given below.

4.4.1 Grain yield *per* plant

Cross P 12210/Raj MR 1

During year 2013-14 the data revealed that additive gene effect (1.33) was nonsignificant, but dominance gene effect (-17.39**) was significant and negative. This indicated predominant role of negative dominance gene action for inheritance of this trait. With regards to interactions the additive $\times$ additive (19.23**) and dominance $\times$ dominance (23.69**) type of interaction were significant, while additive $\times$ dominance interaction (2.60) was nonsignificant. The negative significant dominance gene effect and significant positive dominance $\times$ dominance gene interaction indicated duplicate type of interactions. During year 2014-15 the data revealed that additive gene effect (1.97*) was significant, but dominance gene effect (-4.07) was nonsignificant. This indicated predominant role of additive gene action. With regards to interactions the additive $\times$ additive (5.33*) interaction was significant,

while additive $\times$ dominance (2.87) and dominance $\times$ dominance (1.87) interactions were nonsignificant.

Cross P 12231/Raj MR 1

During year 2013-14 the data observed that additive gene effect (2.52) was nonsignificant, but dominance gene effect (-25.09**) was significant and negative. This indicated predominant role of negative dominance gene action in controlling the inheritance of this trait. With regards to interactions the additive $\times$ additive (26.35**) and dominance $\times$ dominance (34.65**) interactions were significant, while additive $\times$ dominance (5.57) interaction was nonsignificant. The negative significant dominance gene effect and significant positive dominance $\times$ dominance gene interaction indicated duplicate type of interaction. During year 2014-15 the data revealed that additive gene effect (2.03*) was significant, but dominance gene effect (5.41) was nonsignificant. This indicated predominant role of additive gene action. With regards to interactions the additive $\times$ additive (7.71*) interaction was significant, while additive $\times$ dominance (4.13) and dominance $\times$ dominance (1.51) interactions were nonsignificant.

Thus, for grain yield *per plant* both additive and dominance gene effects were prevalent, but the negative dominance component was more prevalent over the crosses and years. With regards to interactions additive $\times$ additive and duplicate type of interactions were prevalent. This suggested that the selection for grain yield *per plant* should be performed after a few generations of selfing.

4.4.2 Tillers *per plant*

Cross P 12210/Raj MR 1

During year 2013-14 the data revealed that additive gene effect (0.89) was nonsignificant but dominance gene effect (11.90**) was significant. This indicated predominant role of dominance gene action for inheritance of this trait. With regards to interactions the additive $\times$ additive (9.14**), additive $\times$ dominance (3.72**) and dominance $\times$ dominance (-20.82**) interactions were significant. The positive and significant dominance gene effect and significant negative dominance $\times$ dominance gene interaction indicated duplicate type of interaction. During year 2014-15, additive gene effect (0.52) was nonsignificant but dominance gene effect (-3.83*) was significant. This indicated predominant role of negative dominance gene action. The additive $\times$ additive (3.57*) and

additive $\times$ dominance (3.03*) type of interactions were significant, while dominance $\times$ dominance (3.93) type of interaction was nonsignificant.

Cross P 12231/Raj MR 1

During year 2013-14 the data revealed that additive gene effect (1.67**) was significant and dominance gene effect (-6.58**) was also significant but in negative direction. The additive $\times$ additive (5.81**) and additive $\times$ dominance (4.20**) interactions were significant, while dominance $\times$ dominance (1.48) interaction was nonsignificant. During year 2014-15, additive gene effect (0.47) was nonsignificant, but dominance gene effect (-5.83**) was significant and negative. This indicated predominant role of negative dominance gene action for inheritance of tillers *per* plant. The additive $\times$ additive (3.96**) interaction was significant, while additive $\times$ dominance (1.47) and dominance $\times$ dominance (4.03) interactions were nonsignificant.

Thus, for tillers *per* plant negative dominance effect and additive $\times$ additive and additive $\times$ dominance interactions were prevalent over the crosses for both years. With regards to interactions duplicate type of interaction was observed in the cross P 12210/Raj MR 1 during the year 2013-14. The predominance of duplicate type of interaction and dominance gene effect suggested that selection should be performed after a few generations of selfing.

4.4.3 1000-grain weight

Cross P 12210/Raj MR 1

During year 2013-14 additive gene effect (8.12**) was significant, but dominance gene effect (-1.43) was nonsignificant. This indicated predominant role of additive gene action for inheritance of this trait. Additive $\times$ additive (18.51**) and dominance $\times$ dominance (22.68**) type of interactions were significant, while additive $\times$ dominance (4.23) interaction was nonsignificant. During year 2014-15, the additive gene effect (1.90**) and dominance gene effect (3.26*) were significant. Additive $\times$ additive (2.63*) interaction was significant while additive $\times$ dominance (0.67) and dominance $\times$ dominance (0.24) interactions were nonsignificant.

Cross P 12231/Raj MR 1

During year 2013-14, additive gene effect (0.98**) was significant, but dominance gene effect (-1.45) was nonsignificant. This indicated predominant role of additive gene action for inheritance of this trait. With regards to interactions the additive $\times$ additive (0.91) interaction was nonsignificant, while additive $\times$ dominance (1.43*) and dominance $\times$ dominance (4.08**) type of interactions were nonsignificant. During year 2014-15, the chi-square value (5.92) was nonsignificant this indicated that the three parameter model was adequate, and only additive (4.92**) and dominance (6.57**) gene effects were responsible for inheritance.

Thus, for 1000-grain weight additive gene effect was more prevalent over the crosses and years. With regards to interactions there was presence of both 'i' type and 'I' type of interactions. Thus, the presence of additive gene effects and additive $\times$ additive type of interaction indicated that direct selection may effective for this trait.

4.4.4 Grains per spike

Cross P 12210/Raj MR 1

During year 2013-14 and 2014-15 the chi-square values 6.23 and 7.19, respectively were nonsignificant indicating that the three parameter model was adequate. The additive gene effect (9.07**) was significant, but dominance gene effect (3.66) was nonsignificant indicating predominant role of additive gene action for inheritance of this trait.

Cross P 12231/Raj MR 1

During year 2013-14, both additive gene effect (5.20*) and dominance gene effect (-13.14*) were significant. The additive component was positive and dominance component was in negative direction. Additive $\times$ additive (14.17**) interaction was significant, while additive $\times$ dominance (-8.60) and dominance $\times$ dominance (15.37) interactions were nonsignificant. During year 2014-15, additive gene effect (1.77) was nonsignificant, but dominance gene effect (-16.42**) was significant and negative. This indicated the predominant role of dominance gene action in controlling inheritance of this trait. With regards to interactions the additive $\times$ additive (13.32**) and dominance $\times$ dominance (22.65*) type of interactions were significant, while additive $\times$ dominance (-8.93) interaction was nonsignificant. The negative significant dominance gene effect and significant positive dominance $\times$ dominance gene interaction indicated duplicate type of interactions.

Thus, for grains *per* spike both additive and dominance effects and additive $\times$ additive interaction were more prevalent in majority of the crosses. However, the dominance component was in negative direction. Therefore under such situations containment of dominance type of gene effect and its interaction will be essential to start the selection for grains *per* spike.

4.4.5 Spike length

Cross P 12210/Raj MR 1

During year 2013-14, both additive gene effect (1.12**) and dominance gene effect (5.49**) were significant. Additive $\times$ additive (4.79**) and dominance $\times$ dominance (-6.23**) type of interactions were significant while additive $\times$ dominance (0.83) interaction was nonsignificant. The positive and significant dominance gene effect and significant negative dominance $\times$ dominance gene interaction indicated duplicate type of interaction. During year 2014-15, both additive gene effect (1.90**) and dominance gene effect (3.26*) were significant and positive. Additive $\times$ additive (2.63*) interaction was significant, while additive $\times$ dominance (0.67) and dominance $\times$ dominance (0.24) interactions were nonsignificant.

Cross P 12231/Raj MR 1

During year 2013-14, the data observed that additive gene effect (0.98**) was significant, but dominance gene effect (-1.45) was nonsignificant. This indicated predominant role of additive gene action. Additive $\times$ additive (0.91) interaction was nonsignificant, while additive $\times$ dominance (1.43*) and dominance $\times$ dominance (4.08**) interactions were significant. During year 2014-15, the chi-square value (1.02) was nonsignificant indicating that the three parameter model was adequate. The additive gene effect (1.38**) was significant but dominance effect (-0.50) was nonsignificant. This indicated predominant role of additive gene action for inheritance of this trait.

For spike length both additive and dominance effects were prevalent. Additive $\times$ additive and dominance $\times$ dominance type of interactions were also significant in majority of the crosses over the years. Therefore, for improvement of spike length the dominance component need to be reduced.

4.4.6 Spikelets *per* spike

Cross P 12210/Raj MR 1

During year 2013-14, the data indicated that both additive gene effect (3.27**) and dominance gene effect (-5.37**) were significant, but dominance component was in negative direction. Additive $\times$ additive (5.77**), additive $\times$ dominance (-5.47**) and dominance $\times$ dominance (9.04**) type of interactions were significant. The negative significant dominance gene effect and significant positive dominance $\times$ dominance gene interaction indicated duplicate type of interaction. During year 2014-15, additive gene effect (0.10) was nonsignificant, but dominance gene effect (-2.83*) was significant. This indicated role of dominance gene action for controlling the inheritance of this trait. With regards to interactions the additive $\times$ additive (3.16**) interaction was significant, while additive $\times$ dominance (-0.47) and dominance $\times$ dominance (1.23) interactions were nonsignificant.

Cross P 12231/Raj MR 1

During year 2013-14, both additive gene effect (1.37**) and dominance gene effect (-2.21**) were significant, but the dominance component was in negative direction. Additive $\times$ additive (1.17) type of interaction was nonsignificant, while additive $\times$ dominance (-2.40**) and dominance $\times$ dominance (4.57**) type of interactions were significant. The negative and significant dominance gene effect and significant positive dominance $\times$ dominance gene interaction indicated duplicate type of interaction. During year 2014-15, additive gene effect (0.68) was nonsignificant, but dominance gene effect (4.41*) was significant, indicating the importance of dominance gene action for controlling this trait. Additive $\times$ additive (3.18*) interaction was significant, while additive $\times$ dominance (-2.43) and dominance $\times$ dominance (1.77) type of interactions were nonsignificant.

Both additive and dominance gene effects were prevalent for spikelets *per* spike, however, the dominance component was in negative direction in majority of the cases. Additive $\times$ additive and dominance $\times$ dominance interactions were more important as these were significant in majority of the cases. Predominantly, the negative significant dominance gene effect and significant positive dominance $\times$ dominance gene interaction indicated duplicate type of interactions for spikelets *per* spike. Therefore, the dominance component of gene effect needs to be reduced considerably before initiation of selection for spikelets *per* spike.

Table 4.6: Gene effects for various traits in bread wheat for two crosses during years 2013-14 and 2014-15

Characters	Crosses/Years	m	d	h	i	j	l	Chi-square value	Type of interaction
Grain yield per plant	P 12210/Raj MR 1 (2013-14)	21.51**	1.33	-17.39**	19.23**	2.60	23.69**	29.93**	Duplicate
	P 12210/Raj MR 1 (2014-15)	15.83**	1.97*	-4.07	5.33*	2.87	1.87	10.74*	-
	P 12231/Raj MR 1 (2013-14)	23.15**	2.52	-25.09**	26.35**	5.57	34.65**	37.24**	Duplicate
	P 12231/Raj MR 1 (2014-15)	18.33**	2.03*	5.41	7.71*	4.13	1.51	20.43**	-
Tillers per plant	P 12210/Raj MR 1 (2013-14)	8.12**	0.89	11.90**	9.14**	3.72**	-20.82**	83.85**	Duplicate
	P 12210/Raj MR 1 (2014-15)	7.80**	0.52	-3.83*	3.57*	3.03**	3.93	16.89**	-
	P 12231/Raj MR 1 (2013-14)	8.85**	1.67**	-6.58**	5.81**	4.20**	1.48	47.40**	-
	P 12231/Raj MR 1 (2014-15)	7.57**	0.47	-5.83**	3.96**	1.47	4.03	13.98**	-
1000- grain weight	P 12210/Raj MR 1 (2013-14)	40.55**	8.12**	-1.43	18.51**	4.23	22.68**	67.87**	-
	P 12210/Raj MR 1 (2014-15)	13.04**	1.90**	3.26*	2.63*	0.67	0.24	37.81**	-
	P 12231/Raj MR 1 (2013-14)	11.97**	0.98**	-1.45	0.91	1.43*	4.08**	39.04**	-
	P 12231/Raj MR 1 (2014-15)	34.81**	4.92**	6.57**	-	-	-	5.92	-
Grains per spike	P 12210/Raj MR 1 (2013-14)	55.91**	9.07**	3.66	-	-	-	6.23	-
	P 12210/Raj MR 1 (2014-15)	59.38**	4.15**	-3.24	-	-	-	7.19	-
	P 12231/Raj MR 1 (2013-14)	61.99**	5.20*	-13.14*	14.77**	-8.60	15.37	9.56*	-
	P 12231/Raj MR 1 (2014-15)	61.01**	1.77	-16.42**	13.32**	-8.93	22.65*	9.39*	Duplicate

Contd.....

Table 4.6: Contd.....

Characters	Crosses/Years	m	d	h	i	j	l	Chi-square value	Type of interaction
Spike length	P 12210/Raj MR 1 (2013-14)	12.74**	1.12**	5.49**	4.79**	0.83	-6.23**	53.12**	Duplicate
	P 12210/Raj MR 1 (2014-15)	13.04**	1.90**	3.26*	2.63*	0.67	0.24	16.36**	-
	P 12231/Raj MR 1 (2013-14)	11.97**	0.98**	-1.45	0.91	1.43*	4.08**	21.14**	-
	P 12231/Raj MR 1 (2014-15)	13.36**	1.38**	-0.50	-	-	-	1.02	-
Spikelets per spike	P 12210/Raj MR 1 (2013-14)	23.09**	3.27**	-5.37**	5.77**	-5.47**	9.04**	138.87**	Duplicate
	P 12210/Raj MR 1 (2014-15)	22.91**	0.10	-2.83*	3.16**	-0.47	1.23	17.91**	-
	P 12231/Raj MR 1 (2013-14)	21.43**	1.37**	-2.21**	1.17	-2.40**	4.57**	49.83**	Duplicate
	P 12231/Raj MR 1 (2014-15)	20.64**	0.68	4.41*	3.18*	-2.43	-1.77	65.57**	-
Plant height	P 12210/Raj MR 1 (2013-14)	95.72**	12.83**	14.05	6.39	25.93**	-3.79	22.93**	-
	P 12210/Raj MR 1 (2014-15)	92.88**	4.99**	3.48	-	-	-	2.24	-
	P 12231/Raj MR 1 (2013-14)	87.29**	4.63*	-4.11	0.41	4.00	33.21**	58.21**	-
	P 12231/Raj MR 1 (2014-15)	90.89**	2.18	16.93*	11.86*	-3.63	-6.23	10.34*	-
Biomass per plant	P 12210/Raj MR 1 (2013-14)	48.22**	4.85*	-19.48**	21.65**	-12.70**	6.08	68.30**	-
	P 12210/Raj MR 1 (2014-15)	42.33**	6.33	-25.80**	23.80*	11.33	14.00	24.85**	-
	P 12231/Raj MR 1 (2013-14)	48.18**	11.95**	-40.99**	39.49**	21.57**	45.25**	109.72**	Duplicate
	P 12231/Raj MR 1 (2014-15)	33.90**	0.48	8.06**	-	-	-	6.49	-

Contd.....

Table 4.6: Contd.....

Characters	Crosses/Years	m	d	h	i	j	l	Chi-square value	Type of interaction
Harvest index	P 12210/Raj MR 1 (2013-14)	47.01**	80.01*	-0.21	-0.23	1.90**	4.10*	15.22**	-
	P 12210/Raj MR 1 (2014-15)	48.21**	5.01	22.20*	0.16	0.09	6.10*	10.18*	-
	P 12231/Raj MR 1 (2013-14)	45.0**	20.00*	6.00	-	-	-	3.04	-
	P 12231/Raj MR 1 (2014-15)	56.01**	3.24	-32.02*	-0.38	1.41	2.70*	8.18*	Duplicate
Days to heading	P 12210/Raj MR 1 (2013-14)	94.72**	16.63**	4.25	6.39*	15.23**	-6.79	12.93**	-
	P 12210/Raj MR 1 (2014-15)	92.88**	6.85**	2.18	12.2**	2.13	3.61	32.24**	-
	P 12231/Raj MR 1 (2013-14)	96.29**	5.88*	3.11	2.41	5.01	13.21**	28.21**	-
	P 12231/Raj MR 1 (2014-15)	97.89**	12.18**	6.93*	10.56*	-4.63	-2.23	11.24*	-
Days to maturity	P 12210/Raj MR 1 (2013-14)	126.51**	10.12**	1.49	8.79**	0.63	-6.23	53.12**	-
	P 12210/Raj MR 1 (2014-15)	129.83**	11.90**	4.26*	2.01	6.69**	2.24	9.36*	-
	P 12231/Raj MR 1 (2013-14)	130.15**	9.98**	-2.45	4.91*	2.03	5.28*	21.14**	-
	P 12231/Raj MR 1 (2014-15)	135.33**	8.38**	-3.50	6.63**	1.02	-2.00	11.02*	-

*, **: Significant at 5% and 1% level of probability, respectively.

4.4.7 Plant height

Cross P 12210/Raj MR 1

During year 2013-14, the data revealed that additive gene effect (12.83**) was significant, but dominance gene effect (14.05) was nonsignificant, indicating a role of additive gene action for controlling inheritance of this trait. With regards to interactions the additive $\times$ additive (6.39) and dominance $\times$ dominance (-3.79) interactions were nonsignificant, while additive $\times$ dominance (25.93**) interaction was significant. During year 2014-15, the chi-square value (2.24) was nonsignificant which indicated that the three parameter model was adequate. The additive gene effect (4.99**) was significant, but dominance gene effect (3.48) was nonsignificant. This indicated predominant role of additive gene action for inheritance of this trait.

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that additive gene effect (4.63**) was significant, but dominance gene effect (-4.11) was nonsignificant indicating predominant role of additive gene action in the inheritance of this trait. Additive $\times$ additive (0.41) and additive $\times$ dominance (4.00) type of interactions were nonsignificant, while dominance $\times$ dominance (33.21**) type of interaction was significant. During year 2014-15 the additive gene effect (4.18) was nonsignificant, but dominance gene effect (16.93*) was significant. Additive $\times$ additive (11.86*) interaction was significant, while additive $\times$ dominance (-3.63) and dominance $\times$ dominance (-6.23) type of interactions were nonsignificant. Thus for plant height additive effect appeared to responsible for inheritance in majority of the cases.

Additive component of gene effect was in preponderance over the years and crosses for this trait. Therefore, selection in early segregating generations will be more effective for this trait.

4.4.8 Biomass *per* plant

Cross P 12210/Raj MR 1

During year 2013-14, the data revealed that both additive gene effect (4.85*) and dominance gene effect (-19.48**) were significant however the dominance effect was in negative direction. Additive $\times$ additive (21.65**) and additive $\times$ dominance (-12.70**) interactions were significant, while dominance $\times$ dominance (6.08) interaction was

nonsignificant. During year 2014-15, the additive gene effect (6.33) was nonsignificant, but dominance gene effect (-25.80**) was significant. This indicated the importance of negative dominance gene effect for controlling the inheritance of this trait. Additive $\times$ additive (23.80*) interaction was significant, while additive $\times$ dominance (11.33) and dominance $\times$ dominance (14.00) type of interaction were nonsignificant indicating role of additive gene action.

Cross P 12231/Raj MR 1

During year 2013-14, it was observed that both additive gene effect (11.95**) and dominance gene effects (-40.99**) were significant, but dominance component was in negative direction. With regards to interactions the additive $\times$ additive (39.49**), additive $\times$ dominance (21.57**) and dominance $\times$ dominance (45.25**) type of interactions were significant. The negative significant dominance gene effect and significant positive dominance $\times$ dominance gene interaction indicated duplicate type of interaction. During year 2014-15, the chi-square value (6.49) was nonsignificant indicating the adequacy of three parameter model. The additive gene effect (0.48) was nonsignificant, but dominance gene effect (8.06**) was significant, indicating the role of dominance gene action for controlling inheritance of this trait.

Thus, for biomass *per plant* both additive and dominance gene effects were prevalent, however the dominance component was in negative direction in majority of the crosses. With regard to interactions, additive $\times$ additive and additive $\times$ dominance type of interactions were more important as these were significant in majority of the cases. In this situation, the dominance component of gene effect need to be reduced before initiating the process of selection.

4.4.9 Harvest index

Cross P 12210/Raj MR 1

During year 2013-14, the data revealed that additive gene effect (80.01*) was significant but dominance gene effect (-0.21) was nonsignificant indicating the predominant role of additive effect for controlling inheritance of this trait. Additive $\times$ additive (-0.23) interaction was nonsignificant, while additive $\times$ dominance (1.90**) and dominance $\times$ dominance (4.10*) type of interactions were significant. During year 2014-15 the additive gene effect (5.01) was nonsignificant, but dominance gene effect (22.20*) was significant.

This indicated the importance of dominance effect. With regards to interactions the additive $\times$ additive (0.16) and additive $\times$ dominance (0.09) interactions were nonsignificant, while dominance $\times$ dominance (6.10*) interaction was significant.

Cross P 12231/Raj MR 1

During year 2013-14, the chi-square value (3.04) was nonsignificant this indicated that the three parameter model was adequate. The additive gene effect (20.00*) was significant, but dominance gene effect (6.00) was nonsignificant. This indicated predominant role of additive gene action for inheritance of this trait. During year 2014-15, the additive gene effect (3.24) was nonsignificant, but dominance gene effect (-32.02*) was negative and significant. This indicated the importance of negative dominance gene effect for controlling inheritance of this trait. Additive $\times$ additive (-0.38) and additive $\times$ dominance (1.41) type of interactions were nonsignificant, while dominance $\times$ dominance (2.70*) type of interaction was significant. The negative significant dominance gene effect and significant positive dominance $\times$ dominance gene interaction indicated duplicate type of interaction.

Thus, for harvest index both additive and dominance gene effects were prevalent. With regards to interaction dominance $\times$ dominance type of interaction was more important as it was significant in majority of the crosses. Therefore, under this type of situation selection will be more effective if it is started after a few generations of selfing.

Additive gene effect, in general, was predominant for 1000-grain weight and plant height. Thus the presence of additive gene effects and additive $\times$ additive type of interaction indicated that direct selection may effective for these traits.

Moreover, grain yield *per* plant and spikelets *per* spike had both additive and dominance gene effects. Also additive $\times$ additive and duplicate type of interactions were prevalent. Whereas, grains *per* spike, spike length, biomass *per* plant and harvest index had both additive and dominance gene effects; and additive $\times$ additive type and dominance $\times$ dominance type of interaction were prevalent in majority of the cases. Therefore, under this type of situation selection should be started after a few generations of selfing.

For tillers *per* plant, negative dominance effect and additive $\times$ additive, additive $\times$ dominance and duplicate type interactions were prevalent. The predominance of duplicate type of interaction and dominance gene effect suggested that selection should be performed after a few generations of selfing.

4.4.10 Days to heading

Cross P 12210/Raj MR 1

During year 2013-14, the data revealed that additive gene effect (16.63**) was significant, but dominance gene effect (4.25) was nonsignificant, indicating a role of additive gene action for controlling inheritance of this trait. With regards to interactions the additive $\times$ additive (6.39*) and additive $\times$ dominance (15.23**) interactions were significant, while dominance $\times$ dominance (-6.79**) interaction was nonsignificant. During year 2014-15, the additive gene effect (6.85**) was significant, but dominance gene effect (2.18) was nonsignificant. With regards to interactions the additive $\times$ additive (12.2**) interaction was significant, while additive $\times$ dominance (2.13) and dominance $\times$ dominance (3.61) interaction were nonsignificant. This indicated predominant role of additive gene action for inheritance of this trait.

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that additive gene effect (5.88**) was significant, but dominance gene effect (3.11) was nonsignificant indicating predominant role of additive gene action in the inheritance of this trait. Additive $\times$ additive (2.41) and additive $\times$ dominance (5.01) type of interactions were nonsignificant, while dominance $\times$ dominance (13.21**) type of interaction was significant. During year 2014-15 both additive gene effect (12.18**) and dominance gene effect (6.93*) were significant. Additive $\times$ additive (10.56*) interaction was significant, while additive $\times$ dominance (-4.63) and dominance $\times$ dominance (-2.23) type of interactions were nonsignificant. Thus for days to heading additive effect appeared to responsible for inheritance in majority of the cases.

Additive component of gene effect was in preponderance over the years and crosses for this trait. Therefore, selection in early segregating generations will be more effective for this trait.

4.4.11 Days to maturity

Cross P 12210/Raj MR 1

During year 2013-14 the additive gene effect (10.12**) was significant but dominance gene effect (1.49) was nonsignificant. Additive $\times$ additive (8.79**) type of interaction was significant while additive $\times$ dominance (0.63) and dominance $\times$ dominance (-6.23) types of

interactions were nonsignificant. During year 2014-15, both additive gene effect (11.90**) and dominance gene effect (4.26*) were significant. Additive $\times$ additive (2.01) and dominance $\times$ dominance (2.24) interaction were nonsignificant, while additive $\times$ dominance (6.69**) interaction was significant.

Cross P 12231/Raj MR 1

During year 2013-14, the data observed that additive gene effect (9.98**) was significant, but dominance gene effect (-2.45) was nonsignificant. This indicated predominant role of additive gene action. Additive $\times$ additive (4.91*) and dominance $\times$ dominance (5.28*) interactions were significant, while additive $\times$ dominance (2.03) interaction was nonsignificant. During year 2014-15, the additive gene effect (8.38**) was significant but dominance effect (-3.50) was nonsignificant. This indicated predominant role of additive gene action for inheritance of this trait. Additive $\times$ additive (6.63**) interaction was significant, while additive $\times$ dominance (1.02) and dominance $\times$ dominance (-2.00) interactions were nonsignificant. This indicated that additive effect appeared to responsible for inheritance in majority of the cases for days to maturity.

For days to maturity, additive effect was prevalent. Additive $\times$ additive type of interaction was significant in majority of the crosses over the years. Therefore, selection in early segregating generations will be more effective for this trait.

4.5 Components of variances

The results regarding components of variances additive (D), dominance (H) environment (E) and heritability in narrow sense (h^2) based on different generations are given in Table 4.7.

4.5.1 Grain yield *per plant*

Cross P 12210/Raj MR 1

During year 2013-14 the data showed that, the magnitude of additive genetic variance (224.49) was higher than the dominance genetic variance (173.52). Heritability in narrow sense was also high (88.00%). During year 2014-15, the magnitude of additive genetic variance (100.70) was higher than the dominance genetic variance (37.64). Heritability in narrow sense was also high (91.90%).

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that, the magnitude of additive genetic variance (143.44) was higher than the dominance genetic variance (75.84). Heritability in narrow sense was also high (69.70%). During year 2014-15, the magnitude of additive genetic variance (17.47) was lower than the dominance genetic variance (172.74). Heritability in narrow sense was also low (13.10%).

Thus the magnitude of additive genetic variance was in general higher than the dominance in over the crosses and years for grain yield *per* plant. Heritability estimates in narrow sense were also high in majority of the cases. This revealed the ample scope of selection for improvement of grain yield *per* plant.

4.5.2 Tillers *per* plant

Cross P 12210/Raj MR 1

During year 2013-14, the data showed that, the magnitude of additive genetic variance (18.85) was lower than the dominance genetic variance (62.55). Heritability in narrow sense was also low (34.60%). During year 2014-15, the magnitude of additive genetic variance (24.28) was higher than the dominance genetic variance (5.64). Heritability in narrow sense was also high (90.60%).

Cross P 12231/Raj MR 1

During year 2013-14 it was observed that, the magnitude of additive genetic variance (52.62) was higher than the dominance genetic variance (33.15). Heritability in narrow sense was also high (90.8%). During year 2014-15, the magnitude of additive genetic variance (4.46) was lower than the dominance genetic variance (21.27). Heritability in narrow sense was also low (21.00%).

Thus, for tillers *per* plant both additive and dominance genetic variances were prevalent in over the crosses and years. Heritability estimates in narrow sense were from low to high in different crosses and years. Therefore, selection for this trait may be deferred for a few generations to reduce the dominance gene action.

4.5.3 1000-grain weight

Cross P 12210/Raj MR 1

During year 2013-14, the data showed that, the magnitude of additive genetic variance (10.93) was lower than the dominance genetic variance (62.16). Heritability in narrow sense was also low (18.60%). During year 2014-15, the magnitude of additive genetic variance (16.01) was lower than the dominance genetic variance (66.16). Heritability in narrow sense was also low (22.90%).

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that, the magnitude of additive genetic variance (22.68) was lower than the dominance genetic variance (49.40). Heritability in narrow sense was also low (5.87%). During year 2014-15, the magnitude of additive genetic variance (44.28) was higher than the dominance genetic variance (25.09). Heritability in narrow sense was moderate (57.30%).

Thus, the magnitude of additive genetic variance was in general lower than the dominance in over the crosses and years for 1000-grain weight. Heritability estimates in narrow sense were also low to moderate in majority of the cases. This revealed that selection for this trait should be carried out after a few generations of selfing.

4.5.4 Grains *per* spike

Cross P 12210/Raj MR 1

During year 2013-14, the data revealed that, the magnitude of additive genetic variance (22.86) was lower than the dominance genetic variance (417.52). Heritability in narrow sense was also low (6.20%). During year 2014-15, the magnitude of additive genetic variance (64.24) was lower than the dominance genetic variance (72.08). Heritability in narrow sense was also low (25.60%).

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that the magnitude of additive genetic variance (13.08) was lower than the dominance genetic variance (241.24). Heritability in narrow sense was also low (4.30%). During year 2014-15, the magnitude of additive genetic variance (1.12) was lower than the dominance genetic variance (19.03). Heritability in narrow sense was also low (0.50%).

Thus the magnitude of additive genetic variance was lower than the dominance in over the crosses and years for grains *per* spike. Heritability estimates in narrow sense were also low in all of the cases. This revealed that selection for this trait should be carried out after a few generations of selfing.

4.5.5 Spike length

Cross P 12210/Raj MR 1

During year 2013-14, the data revealed that magnitude of additive genetic variance (0.87) was lower than the dominance genetic variance (5.57). Heritability in narrow sense was also low (14.90%). During year 2014-15, the magnitude of additive genetic variance (6.99) was higher than the dominance genetic variance (4.25). Heritability in narrow sense was moderate (54.80%).

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that, the magnitude of additive genetic variance (1.29) was lower than the dominance genetic variance (4.47). Heritability in narrow sense was also low (25.70%). During year 2014-15, the magnitude of additive genetic variance (1.12) was lower than the dominance genetic variance (5.66). Heritability in narrow sense was also low (10.70%).

Thus, the magnitude of additive genetic variance was in general lower than the dominance in over the crosses and years for spike length. Heritability estimates in narrow sense were also low to moderate in majority of the cases. This revealed that selection for this trait should be carried out after a few generations of selfing.

4.5.6 spikelets *per* spike

Cross P 12210/Raj MR 1

During year 2013-14, the data revealed that the magnitude of additive genetic variance (4.39) was higher than the dominance genetic variance (3.02). Heritability in narrow sense was high (82.80%). During year 2014-15, the magnitude of additive genetic variance (7.20) was higher than the dominance genetic variance (5.48). Heritability in narrow sense was high (67.20%).

Table 4.7: Components of variance for various traits in bread wheat for two crosses during year 2013-14 and 2014-15

Characters	Crosses/Years	Additive genetic variance (D)	Dominance genetic variance (H)	Environ- Mental variance (E)	Heritability (%) in narrow sense
Grain yield per plant	P 12210/Raj MR 1 (2013-14)	224.49	173.52	18.85	88.00
	P 12210/Raj MR 1 (2014-15)	100.70	37.64	8.49	91.90
	P 12231/Raj MR 1 (2013-14)	143.44	75.84	12.21	69.70
	P 12231/Raj MR 1 (2014-15)	17.47	172.74	14.63	13.10
Tiller per plant	P 12210/Raj MR 1 (2013-14)	18.85	62.55	2.15	34.60
	P 12210/Raj MR 1 (2014-15)	24.28	5.64	1.46	90.60
	P 12231/Raj MR 1 (2013-14)	52.62	33.15	3.94	90.80
	P 12231/Raj MR 1 (2014-15)	4.46	21.27	3.09	21.00
1000-grain weight	P 12210/Raj MR 1 (2013-14)	10.93	62.16	6.44	18.60
	P 12210/Raj MR 1 (2014-15)	16.01	66.16	8.36	22.90
	P 12231/Raj MR 1 (2013-14)	22.68	49.40	38.40	5.87
	P 12231/Raj MR 1 (2014-15)	44.28	25.09	10.25	57.30
Grains per spike	P 12210/Raj MR 1 (2013-14)	22.86	417.52	69.78	6.20
	P 12210/Raj MR 1 (2014-15)	64.24	72.08	15.37	25.60
	P 12231/Raj MR 1 (2013-14)	13.08	241.24	26.06	4.30
	P 12231/Raj MR 1 (2014-15)	1.12	19.03	1.61	0.50
Spike length	P 12210/Raj MR 1 (2013-14)	0.87	5.57	1.09	14.90
	P 12210/Raj MR 1 (2014-15)	6.99	4.25	0.95	54.80
	P 12231/Raj MR 1 (2013-14)	1.29	4.47	0.75	25.70
	P 12231/Raj MR 1 (2014-15)	1.12	5.66	1.26	10.70
Spikelets per spike	P 12210/Raj MR 1 (2013-14)	4.39	3.02	1.21	82.80
	P 12210/Raj MR 1 (2014-15)	7.20	5.48	1.13	67.20
	P 12231/Raj MR 1 (2013-14)	0.92	2.59	0.63	26.50
	P 12231/Raj MR 1 (2014-15)	1.98	1.34	0.90	38.80

Contd.....

Table 4.7: Contd.....

Characters	Crosses/Years	Additive genetic variance (D)	Dominance genetic variance (H)	Environ- Mental variance (E)	Heritability (%) in narrow sense
Plant height	P 12210/Raj MR 1 (2013-14)	514.92	161.27	35.03	77.40
	P 12210/Raj MR 1 (2014-15)	280.35	412.68	39.64	49.50
	P 12231/Raj MR 1 (2013-14)	163.65	366.07	41.50	23.79
	P 12231/Raj MR 1 (2014-15)	259.53	206.19	24.77	63.00
Biomass per plant	P 12210/Raj MR 1 (2013-14)	134.56	223.97	20.97	46.60
	P 12210/Raj MR 1 (2014-15)	329.71	964.44	20.03	38.70
	P 12231/Raj MR 1 (2013-14)	187.25	150.91	30.54	57.80
	P 12231/Raj MR 1 (2014-15)	340.30	276.95	113.84	48.20
Harvest index	P 12210/Raj MR 1 (2013-14)	90.00	20.00	10.10	90.00
	P 12210/Raj MR 1 (2014-15)	20.00	48.00	10.10	70.10
	P 12231/Raj MR 1 (2013-14)	100.10	20.90	10.00	50.70
	P 12231/Raj MR 1 (2014-15)	90.20	30.04	10.30	30.30
Days to heading	P 12210/Raj MR 1 (2013-14)	318.12	175.20	48.30	58.73
	P 12210/Raj MR 1 (2014-15)	410.13	156.21	39.66	67.68
	P 12231/Raj MR 1 (2013-14)	363.65	98.22	46.25	71.57
	P 12231/Raj MR 1 (2014-15)	388.54	201.01	36.44	62.07
Days to maturity	P 12210/Raj MR 1 (2013-14)	236.31	277.23	49.01	42.01
	P 12210/Raj MR 1 (2014-15)	310.21	88.23	36.54	71.32
	P 12231/Raj MR 1 (2013-14)	255.14	23.25	11.01	88.16
	P 12231/Raj MR 1 (2014-15)	326.25	136.12	38.02	65.20

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that, the magnitude of additive genetic variance (0.92) was lower than the dominance genetic variance (2.59). Heritability in narrow sense was also low (26.50%). During year 2014-15, the magnitude of additive genetic variance (1.98) was higher than the dominance genetic variance (1.34). Heritability in narrow sense was low (38.80%).

Thus, the magnitude of additive genetic variance was higher than the dominance genetic variance only for two out of four crosses over the years for spikelets *per* spike. Heritability estimates in narrow sense were also from low to high. This indicated a poor scope of direct selection. Therefore, the selection should be carried out after a few generations of selfing.

4.5.7 Plant height

Cross P 12210/Raj MR 1

During year 2013-14, it was observed that magnitude of additive genetic variance (514.92) was higher than the dominance genetic variance (161.27). Heritability in narrow sense was also high (77.40%). During year 2014-15, the magnitude of additive genetic variance (280.35) was lower than the dominance genetic variance (412.68). Heritability in narrow sense was moderate (49.50%).

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that the magnitude of additive genetic variance (163.65) was lower than the dominance genetic variance (366.07). Heritability in narrow sense was also low (23.79%). During year 2014-15, the magnitude of additive genetic variance (259.53) was higher than the dominance genetic variance (206.19). Heritability in narrow sense was also high (63.00%).

Thus, for plant height both additive and dominance genetic variances were prevalent in over the crosses and years and there was no clear trend. Heritability estimates in narrow sense were from low to high in different crosses and years. Therefore, selection for this trait may be deferred for a few generations to reduce the dominance gene action.

4.5.8 Biomass *per* plant

Cross P 12210/Raj MR 1

During year 2013-14, it was showed that the magnitude of additive genetic variance (134.56) was lower than the dominance genetic variance (223.97). Heritability in narrow sense was moderate (46.60%). During year 2014-15, the magnitude of additive genetic variance (329.71) was lower than the dominance genetic variance (964.44). Heritability in narrow sense was also low (38.70%).

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that, the magnitude of additive genetic variance (187.25) was higher than the dominance genetic variance (150.91). Heritability in narrow sense was moderate (57.80%). During year 2014-15, the magnitude of additive genetic variance (340.30) was higher than the dominance genetic variance (276.95). Heritability in narrow sense was moderate (48.20%).

Thus, for biomass *per* plant both additive and dominance genetic variances were prevalent in over the crosses and years and there was no clear trend. Heritability estimates in narrow sense were from low to moderate in different crosses and years. Therefore, selection for this trait may be differed for a few generations to reduce the dominance gene action.

4.5.9 Harvest index

Cross P 12210/Raj MR 1

During year 2013-14, it was observed that magnitude of additive genetic variance (90.00) was higher than the dominance genetic variance (20.00). Heritability in narrow sense was high (90.00%). During year 2014-15, the magnitude of additive genetic variance (20.00) was lower than the dominance genetic variance (48.00). Heritability in narrow sense was high (70.10%).

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that, the magnitude of additive genetic variance (100.10) was higher than the dominance genetic variance (20.90). Heritability in narrow sense was moderate (50.70%). During year 2014-15, the magnitude of additive genetic variance (90.20) was higher than the dominance genetic variance (30.04). Heritability in narrow sense was low (30.30%).

Thus the magnitude of additive genetic variance was in general higher than the dominance genetic variance in over the crosses and years for harvest index. Heritability estimates in narrow sense were also high to moderate in majority of the cases. This revealed the ample scope of selection for this trait.

For grain yield *per* plant, spikelets *per* spike and harvest index the magnitude of additive genetic variance was higher than the dominance variance followed by high narrow

sense heritability in majority of the crosses and years. This revealed the ample scope of selection for improvement of these traits.

For tillers *per* plant, plant height, biomass *per* plant, both additive and dominance genetic variances were prevalent. Heritability estimates in narrow sense were from low to high in different crosses and years. Therefore, selection for these traits may be deferred for a few generations to reduce the dominance gene action.

The magnitude of additive genetic variance was lower than the dominance for 1000-grain weight, grains *per* spike and spike length in majority of the crosses. Heritability estimates in narrow sense were also low to moderate in majority of the cases. This revealed that selection for this trait should be carried out after a few generations of selfing.

4.5.10 Days to heading

Cross P 12210/Raj MR 1

During year 2013-14, the data showed that, the magnitude of additive genetic variance (318.12) was higher than the component of dominance genetic variance (175.20). Heritability in narrow sense was moderate (58.73%). During year 2014-15, the magnitude of additive genetic variance (410.13) was higher than the dominance genetic variance (156.21). Heritability in narrow sense was also high (67.68%).

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that, the magnitude of additive genetic variance (363.65) was higher than the component of dominance genetic variance (98.22). Heritability in narrow sense was also high (71.57%). During year 2014-15, the magnitude of additive genetic variance (388.54) was higher than the dominance genetic variance (201.01). Heritability in narrow sense was also high (62.07%).

Thus, the magnitude of additive genetic variance was, in general, higher than the dominance component of genetic variance in over the crosses and years for days to heading. Heritability estimates in narrow sense were also high in majority of the cases. This revealed the ample scope of selection for improvement of days to heading.

4.5.11 Days to maturity

Cross P 12210/Raj MR 1

During year 2013-14, the data showed that the magnitude of additive genetic variance (236.31) was higher than the component of dominance genetic variance (277.23). Heritability in narrow sense was moderate (42.01%). Likewise, during year 2014-15, the magnitude of additive genetic variance (310.21) was higher than the dominance genetic variance (88.23). Heritability in narrow sense was also high (71.32%).

Cross P 12231/Raj MR 1

During year 2013-14, the data revealed that, the magnitude of additive genetic variance (255.14) was higher than the component of dominance genetic variance (23.25). Heritability in narrow sense was also high (88.16%). Similarly, during year 2014-15, the magnitude of additive genetic variance (326.25) was higher than the dominance genetic variance (136.12). Heritability in narrow sense was also high (65.20%).

Thus, the magnitude of additive genetic variance was in general higher than the dominance component of genetic variance in over the crosses and years for days to maturity. Heritability estimates in narrow sense were also high in majority of the cases. This revealed the ample scope of selection for improvement of days to maturity.

4.6 Inheritance of resistance to cereal cyst nematode

Detailed results for cyst count in different categories are given below and presented in Table 4.8.

4.6.1 Cyst count

Cross P 12210/Raj MR 1

Parent P 12210 out of total 15 plants, three plants were susceptible and 12 were highly susceptible (Table 4.8; Figure 4.2). The average number of cysts found in P 12210 was 33.7 with range of 13-61 cysts in a single plant. While in Raj MR 1 all 15 plants were resistant for cereal cyst nematode (Table 4.8; Figure 4.4). The average number of cysts *per* plant found in Raj MR 1 was 0.0.

In F₁ generation, out of total 15 plants, seven plants were susceptible and eight plants were highly susceptible (Table 4.8; Figure 4.5). The average number of cysts found in F₁ generation was 19.4 with range of 10-33 cysts in a single plant. In F₂ generation, out of total 120 plants, 30 plants were resistant, seven plants were moderate resistant, 44 plants were

susceptible and 39 plants were highly susceptible. The average number of cysts *per* plant found in F₂ generation was 16.3 with range of 0-78.

In B₁ generation, out of total 30 plants, one plant was resistant, 17 plants were susceptible and 12 plants were highly susceptible plants. The average number of cysts found in B₁ generation was 20.4 with range of 4-49 cysts in a single plant. In B₂ generation, out of total 30 plants, eight plants were resistant, five plants were moderate resistant, 11 plants were susceptible and six plants were highly susceptible. The average number of cysts *per* plant found in B₂ generation was 14.8 with range of 0-61.

Table 4.8: Observations for cyst nematode count in different generations for crosses P 12210/ Raj MR 1 and P 12231/Raj MR 1 in bread wheat

Generations	Number of plants observed					Number of cyst found	
	Total	R (0-4)	MR (5-9)	S (10-20)	HS (>20)	mean	range
Cross P 12210 /Raj MR 1							
P₁	15	0	0	3	12	33.7	13-61
P₂	15	15	0	0	0	0.0	0
F₁	15	0	0	7	8	19.4	10-33
F₂	120	30	7	44	39	16.3	0-78
B₁	30	1	0	17	12	20.4	4-49
B₂	30	8	5	11	6	14.8	0-61
Cross P 12231 /Raj MR 1							
P₁	15	0	0	1	14	28.0	14-48
P₂	15	14	1	0	0	0.1	0-1
F₁	15	0	0	5	10	19.9	10-41
F₂	120	33	2	38	47	19.0	0-72
B₁	30	0	2	15	13	25.3	6-71
B₂	30	10	4	9	7	13.4	0-65

R : (resistant); MR : (moderate resistant); S : (susceptible); HS :(highly susceptible)

Cross P 12231/Raj MR 1

Parent P 12231, out of total 15 plants, one plant was susceptible and 14 were highly susceptible (Table 4.8; Figure 4.3). The average number of cysts found in P 12231 was 28.0 with range of 14-48 cysts in a single plant. While, in Raj MR 1 out of total 15 plants, 14 plants were resistant and one plant was moderate resistance for cereal cyst nematode. The average number of cysts *per* plant found in Raj MR 1 was 0.1 with range of 0-1.

In F₁ generation, out of total 15 plants, five plants were susceptible and 10 plants were highly susceptible (Table 4.8; Figure 4.6). The average number of cysts found in F₁ generation was 19.9 with range of 10-41 cysts in a single plant. In F₂ generation, out of total 120 plants, 33 plants were resistant, two plants were moderate resistant, 38 plants were susceptible and 47 plants were highly susceptible. The average number of cysts *per* plant found in F₂ generation was 19.0 with range of 0-72.

In B₁ generation, out of total 30 plants, two plants were moderate resistant, 15 plants were susceptible and 13 plants were highly susceptible plants. The average number of cysts *per* plant found in B₁ generation was 25.3 with range of 6-71. In B₂ generation, out of total 30 plants, 10 plants were resistant, four plants were moderate resistant, nine plants were susceptible and seven plants were highly susceptible. The average number of cysts *per* plant found in B₂ generation was 13.4 with range of 0-65.

4.6.2 Mode of segregation for resistance to *H. avenae*

Cross P 12210/Raj MR 1

Data revealed that (Table 4.9) in parent P 12210, out of total 15 plants, all the 15 plants were susceptible to cereal cyst nematode and in parent Raj MR 1 out of total 15 plants, all the 15 plants were resistance to cereal cyst nematode. In F₁ generation, out of total 15 plants, all the 15 plants were susceptible to cereal cyst nematode, but in F₂ generation out of 120 plants, 37 plants were resistance and 83 plants were susceptible to cereal cyst nematode. In backcross generations, in B₁ generation out of 30 plants, one plant was resistant, 29 plants were susceptible and in B₂ generation out of 30 plants, 13 plants were resistant and 17 plants were susceptible.

Cross P 12231/Raj MR 1

Data revealed that in parent P 12231, out of total 15 plants, all the 15 plants were susceptible to cereal cyst nematode and in parent Raj MR 1, out of total 15 plants, all the 15 plants were resistance to cereal cyst nematode. In F₁ generation out of total 15 plants, all the

15 plants were susceptible to cereal cyst nematode, but in F₂ generation out of 120 plants, 35 plants were resistance and 85 plants were susceptible to cereal cyst nematode. In backcross generations, in B₁ generation out of 30 plants, two plants were resistant, 28 plants were susceptible and in B₂ generation out of 30 plants, 14 plants were resistant and 16 plants were susceptible.

Table 4.9: Mode of segregation for resistance to *H. avenae* in the different generations for crosses P 12210/Raj MR 1 and P 12231/Raj MR 1 in bread wheat

Sr no	Cross/Generation	Number of plants observed			chi-square value	Mode of segregation
		Total	R	S		
Cross P 12210/Raj MR 1						
1	P12210 (P ₁)	15	0	15		
2	Raj MR 1(P ₂)	15	15	0		
3	P 12210/Raj MR 1 (F ₁)	15	0	15		
4	P12210 × Raj MR 1 (F ₂)	120	37	83	1.88	3:1
5	P12210 × F ₁ (P12210 × Raj MR 1) (B ₁)	30	1	29		
6	Raj MR 1 × F ₁ (P12210 × Raj MR 1) (B ₂ (test cross))	30	13	17	0.30	1:1
Cross P 12231/Raj MR 1						
1	P12231 (P ₁)	15	0	15		
2	Raj MR 1 (P ₂)	15	15	0		
3	P12231 × Raj MR 1 (F ₁)	15	0	15		
4	P12231 × Raj MR 1 (F ₂)	120	35	85	0.90	3:1
5	P12231 × F ₁ (P12231 × Raj MR 1) (B ₁)	30	2	28		
6	Raj MR 1 × F ₁ (P12231 × Raj MR 1) (B ₂ (test cross))	30	14	16	0.04	1:1

R: (resistant); S: (susceptible)

Genetic analysis of discrete categories worked out by chi-square analysis and presented in Table 4.9. The F₁ plants of both crosses (P 12210/Raj MR 1 and P 12231/Raj MR 1) were susceptible to *H. avenae* indicating that susceptibility was dominant over resistance for this

nematode infection. The F_2 plants for both the crosses segregated in the ratio of 3 susceptible: 1 resistant, indicating the monogenic recessive nature of the inheritance of the gene.

The chi-square value calculated on the observed segregation ratio of the susceptible versus resistant plants in the F_2 generation of both crosses, viz., P 12210/Raj MR 1 and P 12231/Raj MR 1 was found in the ratio of 3:1. This indicated that the inheritance was governed by a single recessive gene. The observed chi-square value for test cross ($F_1 \times$ recessive parent) was also found in the ratio of 1 susceptible: 1 resistant. The back cross of F_1 plants with the susceptible parents gave all susceptible progeny in both the crosses (Table 4.9) again conferred recessive nature of the genes governing resistance against *H. avenae*.



Figure 4.1: Pot experiments of two crosses conducted for cereal cyst nematode resistance during year 2013-14



Figure 4.2: Observation on cereal cyst nematode infestation in susceptible parent P12210



Figure 4.3: Observation on cereal cyst nematode infestation in susceptible parent P 12231



Figure 4.4: Observation on cereal cyst nematode infestation in resistant parent Raj MR 1



Figure 4.5: Observation on cereal cyst nematode infestation in F_1 of P 12210/Raj MR 1



Figure 4.6: Observation on cereal cyst nematode infestation in F_1 of P 12231/Raj MR 1

Cereal cyst nematode (*Heterodera avenae* Woll.), the cause of ‘molya’ diseases is a problem in Rajasthan, Haryana, Punjab, western Uttar Pradesh, Himachal Pradesh and Jammu & Kashmir states of India. Crop rotation and nematicides may be effective for controlling this nematode (Nicol and Rivoal, 2007). However, nematicides may leave residual toxicity which causes health hazards and very expensive if used on a large scale in wheat cultivation. Instead, breeding for resistance is an economical option for managing *H. avenae* (Cook, 2004). Study of inheritance pattern is a pre-requisite step before undertaking a project to breed wheat varieties resistant to *H. avenae*. Genetics of this trait can greatly facilitate the breeders to select the suitable breeding programmes. In addition, genetics of the yield and its components needs to be thoroughly understood. The nature of gene action governing the expression of various traits could be helpful in formulating an effective and sound breeding programme. The knowledge of heritability and genetic gain of the characters is necessary to determine the extent to which they can be transmitted from their parents to offspring and the extent to which they can be improved through selection. More specifically, the plant breeder is interested in the estimation of gene effects in order to formulate the most advantageous breeding procedures for improvement of the attribute in question. Therefore, breeders need information about genetic variability, nature of gene action and heritability for nematode resistance, grain yield and its components for development of high yielding nematode resistance wheat varieties. Results of various experiments are discussed under the following head.

5.1 Analysis of variance

The analysis of variance revealed that the progenies were highly significant for all the characters in both the crosses. This suggested that the genotypes selected were genetically variable and considerable amount of variability generated in their filial generations, which facilitate possibility of selection in a breeding programme. This is in agreement with genetic variation reported by Tammam (2005), Farshadfar *et al.* (2008), Amin (2013) in wheat. Sufficient amount of genetic variability in wheat was also reported by Bergale *et al.* (2001), Asif *et al.* (2004) and Tripathi *et al.* (2011). Furthermore, Zaazaa *et al.* (2012), Shankarrao *et*

al. (2010) and Kalimullah *et al.* (2012) reported high variability in the filial and backcross generations of wheat for yield and its component traits.

5.2 Mean performance

The *per se* performance of F_1 generation was higher than its better parent for grain yield *per plant*, tillers *per plant*, days to heading and days to maturity indicated overdominance. Also the mean performance F_2 generation for grain yield *per plant*, tillers *per plant* and days to maturity was higher than its better parent suggested the opportunities to get transgressive segregants for better recombinants. Similarly, Akhtar and Chowdhary (2006) reported overdominance for grain yield *per plant*, spike length and 1000-grain weight. While, Azam *et al.* (2013) revealed that mean values for days to heading were greater for parents, indicating lack of dominance for days to heading. Mahamood *et al.* (2006) reported overdominance for grain yield *per plant*, biomass, plant height, days to heading, days to maturity, spikelets *per spike* and 1000-grain weight.

Spikelets *per spike* and biomass *per plant* the *per se* performance of the F_1 and F_2 generations were equal to their better parent indicated dominance effect involved in the expression. This suggested that the genes should be fixed through inbreeding and selection should be performed in later generations. Similarly, Inamullah *et al.* (2006), Singh and Rai (1987), Yadav and Narsinghani (1999) also reported the similar findings in generation mean analysis studies. Mean performance of F_1 and F_2 generations of grains *per spike*, plant height and harvest index were intermediate to their parents that showed lack of dominance or partial dominance and selection from early generations suggested for these types of gene expressions.

The average performance of backcross generations were higher than their respective parents for grain yield *per plant*, tillers *per plant*, spike length, spikelets *per spike*, biomass *per plant*, harvest index, days to heading and days to maturity indicated epistatic interactions may involved in expressions of these traits. Number of researcher *i.e.* Naidu *et al.* (1984), Chatrath *et al.* (1986), Pawar *et al.* (1988), Jitender Kumar *et al.* (1994), Dhiman and Dawa (1999), Chowdhary *et al.* (2001) reported such type expressions in backcross generations and suggested biparental mating approach for epistatic interactions. The mean performance of F_2 was lower than F_1 for spike length, plant height, harvest index and days to heading indicated inbreeding depression for these traits. Naidu *et al.* (1984), Sharma and Sain (2004) also reported inbreeding depression in wheat crosses for yield component traits.

The mean performance of F_1 , F_2 , B_1 , and B_2 were better than their parents for grain yield *per plant* and tillers *per plant*. This indicated over dominance and epistasis for these traits. For spikelets *per spike* and biomass *per plant* the mean performance of F_1 and F_2 were equal to the parents while, performance of B_1 , and B_2 were better to parents, which showed dominance gene action and epistasis for these traits. The mean performance of F_1 , F_2 , B_1 , and B_2 were intermediate to their parents for grains *per spike* and plant height which indicated partial or no dominance for these traits.

5.3 Genetic variability parameters

Development of any plant breeding program is dependent upon the existence of genetic variability. The efficiency of selection and expression of heterosis also largely depend upon the magnitude of genetic variability present in the plant population (Singh and Narayanan (1993), Singh and Chaudhary (1999), Farshadfar *et al.* (2001), Amin (2013)). Moreover Johanson *et al.* (1955) reported that heritability values along with estimates of genetic gain were more useful than heritability alone in predicting the effect of selection.

In present study the high genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) followed by high heritability and genetic advance were recorded for grain yield *per plant*, tillers *per plant*, biomass *per plant*, harvest index, days to heading and days to maturity indicated presence of high magnitude of variability and heritability. Under such type of situations selection may be practiced for improvement of these traits provided there was high additive genetic variance. Results are in confirmation with Singh and Yunus (1988) and Ehdaie and Waines (1989). Similar findings were also reported by Virk *et al.* (1972) for plant height, tillers *per plant* and grain yield *per plant*; Singh *et al.* (1987) for plant height; Munir *et al.* (2009) for days to heading; Singh *et al.* (2013) for days to heading and days to maturity; Korkut *et al.* (2001) for plant height, grain yield; Shabana *et al.* (2007) for plant height. Also, El-Hennawy (1997); Arya *et al.* (2005) and Ranjana and Kumar (2013) reported high genetic variability parameters for grain yield and its component traits. While Muhammad Yaqoob (2016) showed low variability and heritability estimates for days to maturity.

High to moderate values of GCV, PCV, broad sense heritability and genetic advance were recorded for 1000-grain weight and plant height. This suggested that there was moderate level of variability and heritability for these traits. Therefore selection may practiced up to some extent for these traits. In previous studies, Zaazaa *et al.* (2012) also reported moderate GCV and PCV with high heritability values for grain yield and its

component traits in wheat. Also, Kaushik *et al.* (1997) observed moderate heritability for 1000-grain weight, tillers *per* plant and grains *per* ear and suggested that selection based on main component traits was effective in improving both heritability and genetic advance for most of the characters. While in contradiction, high genetic variability parameters were recorded by Singh *et al.* (1987) for plant height; Singh and Yunus (1988) for grain weight; Begum *et al.* (2002) for 1000-grain weight; Shabana *et al.* (2007) for plant height.

Low values of GCV and PCV with moderate to low broad sense heritability and genetic advance were recorded for grains *per* spike, spike length and spikelets *per* spike indicating low scope of selection. Similar results were reported by Ehdaie and Waines (1989), Singh and Yunus (1988) in 60 families of bread wheat (*T. aestivum* L.) developed by triple test cross. In contradiction, Shabana *et al.* (2007) reported high variability parameters for these traits.

High GCV and PCV followed by high heritability and genetic advance were recorded for grain yield *per* plant, tillers *per* plant, biomass *per* plant and harvest index indicated presence of high magnitude of variability and heritability. This suggested the better opportunities for selection to improve these traits. High to moderate values of GCV, PCV, broad sense heritability and genetic advance were recorded for 1000-grain weight and plant height. This suggested that there was moderate level of variability and heritability for these traits. Therefore selection may be practiced up to some extent for these traits. Low values of GCV and PCV with moderate to low broad sense heritability and genetic advance were recorded for grains *per* spike, spike length and spikelets *per* spike. This indicated lesser scope of selection for these traits.

5.4 Inheritance of grain yield and its components

Basic assumptions involved in the generation mean analysis are: (i) diploid segregation, (ii) homozygous parents, (iii) absence of multiple alleles, (iv) absence of linkage, (v) absence of lethal genes, (vi) constant viability for all genotypes and (vii) environmental effects are additive with the genotypic value.

Hexaploid wheat is an amphidiploid but behaves as a diploid thereby fulfilling the assumptions of diploid segregation. The parents used in the present study were advanced generations which had been selfed for several generations and thus they should be homozygous. The assumptions of absence of multiple alleles and absence of linkage could not be tested. However these are hardly realistic and difficult to verify as well, though unavoidable, if any analysis is at all to be possible.

The lethal genes were not likely to be present in the crosses as the parents used have been maintained by selfing for many generations. Viability was also perhaps constant for all the genotypes in the present material. In the present study, different genetic estimates varied from one environment to the other suggesting considerable amount of genotype-environment interaction. Moreover, genotype-environment interaction is a common phenomenon present in most of the populations. Hence, in present study all the assumptions were fulfilled, thus, it is possible to make the estimates of genetic parameters for polygenic traits.

The present study revealed that grain yield *per plant* was governed by both additive and dominance components of gene effects however the dominance component was in negative direction. Also the additive $\times$ additive and dominance $\times$ dominance interactions were significant in majority of the crosses. In both crosses duplicate type of interactions was observed. This revealed that the progress through direct selection will be very limited. Under such cases the effect of dominance and duplicate type interaction should be minimized by selfing the material up to few generations. Shekhawat *et al.* (2000) also reported dominance and dominance $\times$ dominance type of gene effects, with higher magnitude but they were unexploitable due to duplicate type of epistasis. Satyavart *et al.* (1999) reported both additive and non-additive components were important for grain yield *per plant* and also duplicate type of epistasis was observed for grain yield *per plant*. Fatehi *et al.* (2004) observed higher value of additive gene effect as compared with dominant gene effect for this trait. Singh and Rai (1987) reported that dominance component was positive and highly significant for yield *per plant*. Chowdhry *et al.* (2001) noted yield *per plant* was governed by over dominance type of gene action. Inamullah *et al.* (2006) noted significance of dominant component for this trait. Amaya *et al.* (1972) reported the relatively more importance of dominance gene effects than additive gene effects for this trait. Sharma and Ahmad (1980) observed both additive and dominance components were significant for grain yield *per plant*. Jitender Kumar *et al.* (1994) also reported importance of additive as well as dominance gene effects for governing the grain yield *per plant*. Naidu *et al.* (1984), Dhiman and Dawa (1999) reported similar type of gene interactions for grain yield *per plant*. While, Chatrath *et al.* (1986) reported that additive type of gene effects and additive $\times$ additive type of epistasis were of more importance for yielding ability in wheat.

Dominance component of gene effect was more prevalent for tillers *per plant*, but in negative direction. Additive $\times$ additive and additive $\times$ dominance were also important for genetic control of tillers *per plant*. This is in agreement with earlier study by Kularia and

Sharma (2005) in barley. Shekhawat *et al.* (2006) also reported dominance gene action controlling the inheritance of tillers in wheat. On contrary, Verma and Yunus (1986), and Pawar *et al.* (1988) reported that the tillers *per* plant governed by additive gene effects. Under such type of situation the dominance component should be reduced to facilitate the selection. therefore, selection should be practised after a few generations of selfing. Chatrath *et al.* (1986) reported that additive $\times$ additive (i) gene effects were more important in genetic control of all characters in wheat. Akhtar and Chowdhary (2006) revealed that additive $\times$ additive (i), additive $\times$ dominance (j), dominance $\times$ dominance (l) type of epistasis effects together which indicate complex inheritance of this traits. Singh *et al.* (1986) studied tillering ability under favourable, rainfed and saline environments and reported importance of both additive and non-additive types of gene effects were important in the inheritance of tillering ability, but dominant gene effects were of more prevalent.

In present study, both additive and dominance gene effects were significantly predominant for inheritance of 1000-grain weight. Additive $\times$ additive and dominance $\times$ dominance interactions were also important for inheritance of 1000-grain weight. Inamullah *et al.* (2006) also reported the relative importance of additive type of gene action for 1000-grain weight. Results are in confirmation with Kumar *et al.* (1994), Shekhawat *et al.* (2000) and Rahman *et al.* (2003). While Kapoor and Luthra (1990) reported existence of high order interactions or linkages in the expression of 1000-grain weight and spike number *per* plant. Akhtar and Chowdhary (2006) indicated that additive, dominance and epistatic genetic effects seemed to have played role in the inheritance of this character. Similarly, Dhaduk and Shukla (1998) reported that both additive and non-additive type of gene action played an important role for inheritance of 1000-grain weight. Hence, for improvement of 1000-grain weight the breeding strategy would be growing large segregating populations and delayed selection in later generations after selfing.

In cross P 12210/Raj MR 1 during both years three parameter model was found adequate and only additive effect was controlling the inheritance of number of grains *per* spike. This was in agreement with the study by Ketata *et al.* (1976a), who reported that estimate of gene effects were free from non-allelic interactions. But for cross P 12231/Raj MR 1 during both years additive and dominance effects were prevalent for inheritance of this trait, however the dominance component was in negative direction. Sharma *et al.* (1986) reported that additive as well as dominance gene effect both are governing the inheritance of number of grains. Present study showed that additive $\times$ additive interaction was more

important in the genetic architecture of this trait. Pawar *et al.* (1988) also reported predominance of fixable type of gene effects and interaction for number of grains *per* spike. Whereas significant additive, dominance effects along with additive $\times$ additive and dominance $\times$ dominance interactions reported in a numerous studies (Naidu *et al.* (1984), Chatrath *et al.* (1986), Pawar *et al.* (1988), Jitender Kumar *et al.* (1994), Dhiman and Dawa (1999) and Chowdhry *et al.* (2001)).

In present study, both additive and dominance gene effects were in preponderance for inheritance of spike length. Also the role of additive $\times$ additive and dominance $\times$ dominance interactions were important in the genetic control of this trait. Similarly, Inamullah *et al.* (2006) also reported the additive and dominance both type of gene action for spike length. Singh and Rai (1987) reported additive $\times$ additive component for spike length. Yadav and Narsinghani (1999) reported both additive and dominance gene effects, and complementary interaction for spike length. Rabbani *et al.* (2009) investigated that spike length exhibited over-dominance type of gene action under irrigated conditions and additive type of gene action under rainfed conditions.

The additive and dominance both types of gene effect were in preponderance for number of spikelets *per* spike however the dominance component was in negative direction in majority of the cases. Among epistatic interactions additive $\times$ additive and dominance $\times$ dominance were more important. Negative significant dominance gene effect and significant positive dominance $\times$ dominance gene interaction indicated duplicate type of interactions for number of spikelets *per* spike. This was in agreement with the study by Ojaghi and Akhundova (2010), who reported dominance gene action and duplicate interaction for number of spikelets for spike. Akhtar and Chowdhary (2006) reported both additive and dominance component for this trait, but epistasis was not observed in their study for number of spikelets *per* spike. Ketata *et al.* (1976a) reported that there was not significant role of epistasis in inheritance of number of spikelets *per* spike.

Present study revealed that the plant height was governed by additive gene effect in majority of the cases. In cross P 12231/Raj MR 1 during year 2014-15 the plant height was governed by dominance gene action. Gene interactions were mostly nonsignificant for this trait. Thus due to the predominant role of additive effect selection in early generation will be effective for plant height. Similar results were reported by Haleem (2009), while Tonk *et al.* (2011) reported both additive and dominance effect with additive $\times$ additive and dominance $\times$ dominance interaction. Ketata *et al.* (1976a) reported the relative importance of dominance

gene effects for plant height and stated that epistasis may be non-trivial factor in inheritance of plant height. Bhatiya *et al.* (1986) in biparental crosses of macroni wheat noticed higher magnitude of dominance effects for plant height and they suggested cyclic method of breeding involving selection and crossing of desirable segregants may helpful in wheat improvement. Ahmad *et al.* (2007) are also opined that dominant effect was the most contributor factor to the inheritance of majority of traits in spring wheat, while Rahman *et al.* (2003) reported importance of partial dominance for plant height character.

For biomass *per plant*, both additive and dominance were significant, but the dominance component was in negative direction in majority of the crosses. In respect to epistatic interactions additive $\times$ additive and additive $\times$ dominance were significant in majority of the crosses. This indicated that selection should be delayed to later generations for biomass *per plant*. Kularia and Sharma (2005) also reported both additive and dominance gene actions and suggested biparental mating approach to get best combination with fixable genes. In present study harvest index was governed by additive and dominance types of gene actions. The non fixable dominance $\times$ dominance type of epistatic interaction was more important as it was significant in majority of the crosses. Shrikant *et al.* (2004) studied the inheritance of harvest index and observed both additive and dominance gene effects were were significant but epistasis was absent in the study. Inamullah *et al.* (2006) reported that the additive component was significant for harvest index.

Present study revealed that the days to heading and days to maturity were governed by additive gene effect in majority of the cases. Additive $\times$ additive type of gene interaction was mostly significant for these traits. Thus due to the predominant role of additive effect and additive $\times$ additive interaction selection in early generation will be effective for days to heading and days to maturity. Similarly, Kathiria *et al.* (1997) found that both additive as well as dominance gene effects were involved in the inheritance of days to heading and maturity with preponderance of additive gene effects. Also, Sood *et al.* (2009) observed that the additive dominance model was found to be adequate for days to maturity, and reported the presence of additive gene effect for this trait. Munir *et al.* (2009) reported that days to heading was controlled by additive genes coupled with high heritability. Sood (2004) observed preponderance of dominance gene action for days to maturity.

Additive gene effect in general, was predominant for 1000-grain weight, plant height, days to heading and days to maturity. Thus the presence of additive gene effects and additive $\times$ additive type of interaction indicated that direct selection may effective for these traits.

Moreover, for grain yield *per* plant and spikelets *per* spike had both additive and dominance gene effects as well as additive $\times$ additive and duplicate type of interactions were prevalent. Whereas, grains *per* spike, spike length, biomass *per* plant and harvest index had both additive and dominance gene effects and additive $\times$ additive type and dominance $\times$ dominance type of interaction were prevalent in majority of the cases. Therefore, under this type of situation selection should be started after a few generations of selfing. For tillers *per* plant negative dominance effect and additive $\times$ additive, additive $\times$ dominance and duplicate type interactions were prevalent. The predominance of duplicate type of interaction and dominance gene effect suggested that selection should be performed after a few generations of selfing.

5.5 Components of variances

The magnitude of additive component of genetic variance was, in general, higher than the dominance component of genetic variance in over the crosses and years for grain yield *per* plant. This revealed the ample scope of selection for this trait. Similarly Singh *et al.* (1986) reported that the magnitude of additive genetic variance was higher than dominance genetic variance for grain yield *per* plant while, Hussain *et al.* (2008) observed both additive and dominance variance for this trait. In contradiction, Dere and Yildirim (2006) reported dominance variance for grain yield *per* plant. Both additive and dominance genetic variances were prevalent in tillers *per* plant. Meena and Sastry (2003) observed similar results for tillers *per* plant. Also Akhtar and Chowdhary (2006) reported both additive and dominance variance for tillers *per* plant. Therefore, selection for this trait may be effective in early segregating generations.

The magnitude of additive genetic variance was lower than the dominance in majority of the crosses for 1000-grain weight. This revealed that selection for this trait should be carried out after a few generations of selfing. This was in agreement with the earlier reports by Akhtar and Chuodhary (2006), while Singh *et al.* (1986) observed that the magnitude of additive variance was higher than dominance genetic variance for 1000-grain weight. Likewise, the magnitude of additive genetic variance was lower than the dominance genetic variance in majority of the crosses for grains *per* spike. This revealed that selection for this trait should be carried out after a few generations of selfing. In contradiction, Ojaghi and Akhundova (2010); Rahman *et al.* (2003); Inamullah *et al.* (2006); Singh *et al.* (1986) reported that the magnitude of additive genetic variance was higher than dominance gentic variance grains *per* spike. The magnitude of additive component of genetic variance was

lower than the dominance component of genetic variance in majority of the crosses for spike length. This revealed that selection for this trait should be carried out after a few generations of selfing. Similarly Meena and Sastry (2003) reported higher magnitude of dominance genetic variance than additive genetic variance for spike length.

For spikelets *per* spike, the magnitude of additive genetic variance was higher than the dominance genetic variance only for two out of four crosses over the years. This indicated a poor scope of direct selection, therefore, the selection should be carried out after a few generations of selfing. This was in agreement with the earlier reports by Akhtar and Chowdhary (2006) and Singh *et al.* (1986) observed higher magnitude of additive genetic variance than dominance genetic variance for spikelets *per* spike. While, for plant height both additive and dominance genetic variances were prevalent in over the crosses and years and there was no clear trend. Therefore, selection for this trait may be deferred for a few generations to reduce the dominance gene action. Similarly, Ojaghi and Akhundova (2010) and Meena *et al.* (2003) reported both additive and dominance variance for plant height however the magnitude of additive variance was higher in these studies. Also, for biomass *per* plant both additive and dominance genetic variances were prevalent. Therefore, selection for this trait may be differed for a few generations to reduce the dominance gene action. Meena and Sastry (2003) observed that the magnitude of dominance genetic variance was higher than additive genetic variance for biomass *per* plant. The magnitude of additive genetic variance was higher than the dominance genetic variance in majority of the crosses for harvest index. This revealed the ample scope of selection for this trait. In contradiction Singh *et al.* (1986) and Akhtar and Chowdhary (2006) observed dominance variance was higher in magnitude than additive genetic variance for harvest index.

The magnitude of additive genetic variance was higher than the dominance component of genetic variance in all the crosses over the years for days to heading and days to maturity. This revealed the ample scope of selection for these traits. Similarly, Tefera and Peat (1997) reported that the additive genetic variances was higher than the respective dominance component of genetic variance for days to heading and days to maturity and suggested that selection for these traits would be effective in early generations. Khan (2009) showed that the magnitude of additive genetic variance was higher than dominance genetic variance for days to heading and days to maturity. Further, Abd El-Rahman (2013) also revealed that additive genetic variance was larger than dominance genetic variance for days to heading and days to maturity. In contradiction, Moussa (2010) reported that the magnitude of dominance genetic

variance was higher than the additive genetic variance for days to heading and days to maturity which makes improving it through selection in the early generations could not be effective. Abd El Rahman and Hammad (2009) reported that the magnitude of dominance genetic variance was higher than the additive genetic variance for days to heading and days to maturity and advised to delay selection for these traits to later generations with increased homozygosity.

Thus components of genetic variances showed that the dominance component of genetic variance was, in general, higher in magnitude than additive component of genetic variance. The discrepancy in the expression of gene effect and genetic component of variances may be either due to gene dispersion in the parents or cancellation effect of genes. Therefore high magnitude of dominance genetic variance suggested that selection for these traits should be carried out after a few generations of selfing.

5.6 Selection strategy

In present study, generation mean analysis showed that grain yield *per* plant was governed by additive component of mean in two crosses out of four, while in remaining two crosses dominance component of mean was significant. Analysis of components of variance indicated that additive genetic variance was higher than the dominance genetic variance in three out of four crosses. This might be due to high degree of dispersion of positive alleles in parents or cancellation of gene effects of positive and negative loci. Therefore, high additive component of genetic variance revealed that selection would be effective in early generations for grain yield *per* plant. For tillers *per* plant dominance, additive $\times$ additive and additive $\times$ dominance components of gene effects were significant in all the crosses, but in analysis of components of variances, additive genetic variance was higher than dominance genetic variance in two out of four crosses and in remaining crosses high dominance genetic variance was observed. This may due to high magnitude of dominance in both components *i.e.*, mean and variances. Therefore, selection for this trait may be deferred for a few generations to reduce the dominance gene effect.

Additive gene effect was significant in all the crosses for 1000-grain weight, while dominance gene effect and additive $\times$ additive and dominance $\times$ dominance type of interactions were significant in two out of four crosses. But the magnitude of additive genetic variance was lower than the dominance genetic variance in three out of four of the crosses for 1000-grain weight. This revealed that selection for this trait should be carried out after a few generations of selfing. Additive gene effect was significant in three out of four crosses, while

dominance gene effect and additive $\times$ additive interaction were significant in two out of four crosses for grains *per* spike. But magnitude of additive genetic variance was lower than the dominance genetic variance in all four crosses for grains *per* spike. Similarly for spike length additive gene effect was significant in all four crosses, while dominance gene effect and additive $\times$ additive interaction were significant in two out of four crosses. The magnitude of additive genetic variance was lower than the dominance genetic variance in three out of four crosses for spike length. Therefore, dominance component of genetic variance need to be reduced for selection these traits after a few generations of selfing.

In the case of spikelets *per* spike, dominance effect was significant in all the four crosses and additive gene effect, as well as additive $\times$ additive, additive $\times$ dominance, dominance $\times$ dominance and duplicate interactions were significant in two out of four crosses. Likewise, analysis of component of genetic variances also showed higher magnitude of dominance genetic variance than additive genetic variance in majority of the crosses indicated that selection would not be effective in early generations. For plant height, additive gene effect and additive genetic variance both were prevalent in majority of the crosses, indicating a clear cut trend of preponderance of additive genetic variance for inheritance of this trait. Thus selection can be effectively utilized in early segregating generations for this trait.

Biomass *per* plant showed preponderance dominance effect in majority of the crosses. With regards to variances, both additive and dominance components of genetic variances were equally important. This revealed that dominance component of genetic variance need to be reduced through selfing before starting the process of selection of biomass *per* plant. For harvest index, additive gene effect was significant in two out of four crosses, similarly dominance gene effect was also significant in two out of four crosses. But the magnitude of additive genetic variance was higher than the dominance genetic variance in three out of four crosses for harvest index. This might be due to high degree of dispersion of positive alleles in parents or cancellation effect of positive and negative loci. Therefore, selection would be effective in early generations for harvest index.

Additive gene effect was significant in all the crosses for days to heading and days to maturity, while additive $\times$ additive type of interactions was significant in majority of the crosses over the years. Also the magnitude of additive genetic variance was higher than the dominance genetic variance in all the crosses over the years for days to heading and days to

maturity. This revealed that selection for this trait would be effective in early segregating generations.

The discrepancies in inheritance on the basis of gene effects and genetic variances in some of above traits may be due to cancellation effects of genes at mean level (Dhanda and Sethi, 1996). The majority of the characters had high magnitude of dominance component, which indicated that selection would not be effective in early segregating generations for these traits. Therefore, it is necessary to reduce dominance component through selfing for a few generations before selection. Abbasi *et al.* (2014) also reported similar findings in bread wheat for grain yield and its component traits.

5.7 Inheritance of resistance to cereal cyst nematode

Breeding for resistance is an economical option for managing *H. avenae* (Cook, 2004). Study of inheritance pattern is a pre-requisite step before undertaking a project to breed wheat varieties resistant to *H. avenae*. Since the genetic basis of resistance to this nematode can greatly facilitate the breeders to utilize the a suitable breeding programme, but very limited reports are available on inheritance of cereal cyst nematode on wheat. Pankaj *et al.* (2008) suggested that resistance was governed by single dominant gene. In order to reach consensus on gene action the inheritance studies should be conducted over the wide range of genetic material, sources of resistance, different environmental conditions (Crowder *et al.* 2003), because nematode reproduction rate of development, size of cysts and number of eggs and larvae in cysts were highly influenced by soil environmental conditions including temperature thereby effecting resistance mechanism (Adams *et al.* 1982). Although, the inheritance studies on nematode, in general, and cereal cyst nematode in particular are limited, yet several reports on disease resistance suggested the contradiction of inheritance in view of different sources of resistance used and environmental conditions. For example, studies on inheritance of resistance to tobacco cyst nematode were in contradiction.

In present study, the source of resistance was used variety Raj MR 1, and the sources of susceptible genotypes were used P 12210 and P 12231. The F₁ plants of both the crosses (P 12210/Raj MR 1 and P 12231/Raj MR 1) were susceptible to *H. avenae* indicating that susceptibility was dominant over resistance for this nematode resistance. The F₂ plants segregated in the ratio of 3 susceptible verses 1 resistant, indicating the monogenic recessive nature of the inheritance of the gene. The observed chi-square value for test cross (F₁ × recessive parent) data was also found to be nonsignificant when compared with theoretical ratio 1 susceptible : 1 resistant. The back cross of F₁ plants with susceptible parents gave all

susceptible progeny again confers recessive nature of the gene governing resistance against *H. avenae*.

These results are in contrast with genetic studies by Nielsen (1982), Yadav *et al.* (1987), Pankaj *et al.* (1995) and Pankaj *et al.* (2008), who reported single dominant gene for resistance against *Heterodera avenae* in wheat with respect to F₁, F₂, and backcross progenies of cross combinations Raj 1482 × CCNRV 4, Raj 1482 × Raj MR 1, and Raj 1482 × AUS 15854. The contradiction may be due to environmental conditions which may vary from one location to another and the use of susceptible line were different from that of earlier report by Pankaj *et al.* (2008). Another, CCN resistance is controlled by a single gene but this single gene is differed over places (virulence spectrum). In different wheat species, several single genes *i.e.* *Cre* 1 (*Triticum aestivum*; AUS 10894/Loros), *Cre* 2 (*Aegeolopas ventricosa*; AP-1, H-93-8), *Cre* 3 (AUS 18913), *Cre* 4 (*Aegeolopas tauschii*; CPI 110813), *Cre* 5 (*Aegeolopas ventricosa*; VPM 1), *Cre* 6 (*Aegeolopas ventricosa*; AP-1, H-93-8, H-93-35), *Cre* 7 (*Aegeolopas triunclatis*; TR-353), *Cre* 8 (*Triticum aestivum*) and *Cre* R (*Secale cereale*) have been identified over the places for resistance against cereal cyst nematode (Rivoal *et al.* (2001), Mokabli *et al.* (2002), Vanstone *et al.* (2008), Smiley and Nicol (2009)). Moreover, the *Cre* 1 gene reported in *T. aestivum* showed resistance against almost all pathotypes (Imren *et al.*, 2013).

In addition, discrepancies in inheritance of resistance due to different sources of resistance, susceptibility, their interactions criteria of evaluation and variation in environment. This was also reported by Crowder *et al.* (2003) and Hayes *et al.* (1995) for tobacco cyst nematode. The results of Spasoff *et al.* (1971), Miller *et al.* (1972), LaMondia *et al.* (1991) and LaMondia *et al.* (2002) were also contradictory on the mode of inheritance of tobacco cyst nematode.

CHAPTER –VI

SUMMARY AND CONCLUSIONS

The present investigation entitled, “Inheritance of grain yield, its components and resistance to cereal cyst nematode in wheat (*Triticum aestivum* L.)” was conducted with the objectives, namely, (i) to estimate additive, dominance and epistatic parameters, (ii) to estimate variability, heritability and genetic advance for grain yield and its components and (iii) to develop the selection strategy for grain yield, its components and nematode resistance in wheat. The study was carried out during the period of *rabi* 2013-14 and *rabi* 2014-15 on six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of two cross combinations (P 12210/Raj MR 1 and P 12231/Raj MR 1). The experiment was laid out in compact family block design with three replications in the Department of Genetics and Plant Breeding at Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana, India. Observation were recorded on grain yield *per* plant, number of tillers *per* plant, 1000-grain weight, number of grains *per* spike, spike length, number of spikelets *per* spike, plant height, biomass *per* plant, harvest index, days to heading and days to maturity. The results are summarized as given below.

Majority of genetic variability parameters, heritability and genetic advance were high for grain yield *per* plant, tillers *per* plant, harvest index, biomass *per* plant, days to heading and days to maturity in both crosses. Plant height, 1000-grain weight and grains *per* spike had low to moderate values, while spike length and spikelet *per* spike had low estimates for these parameters in both crosses.

Mean performance of F_1 and F_2 generations were either higher or at par to the better parent for grain yield *per* plant, tillers *per* plant, 1000-grain weight, spikelets *per* spike, biomass *per* plant, harvest index, days to heading and days to maturity indicated dominance/overdominance over the crosses and years. This indicated the presence of high magnitude of heterosis for these traits. Mean performance of B_1 and B_2 generations were better than their recurrent parents for grain yield *per* plant, tillers *per* plant, 1000-grain weight, spikelets *per* spike, biomass *per* plant and harvest index in majority of the cases, this may be due to the influence of non-additive gene effects. Grains *per* spike, spike length and plant height in the generations F_1 , F_2 , B_1 and B_2 were either intermediate or lower than the parents which may be due to lack of dominance and/or epistasis.

Adequacy of three parameter model showed that only additive gene effect was significant for grains *per* spike, spike length, plant height and harvest index, while dominance gene effect was significant for biomass *per* plant and both additive and dominance were significant for 1000-grain weight in some crosses or years.

The six parameter model indicated that 1000-grain weight, grains *per* spike, spike length, plant height, days to heading and days to maturity were, in general, predominantly governed by additive gene effect, while grain yield *per* plant, tillers *per* plant, spikelets *per* spike, biomass *per* plant and harvest index were, in general, predominantly governed by dominant type of gene effect.

Analysis of genetic components of variances revealed that the magnitude of additive component of genetic variance was, in general, higher than the dominance component of genetic variance along with high narrow sense heritability for grain yield/plant, harvest index, days to heading and days to maturity in majority of the crosses and years. Improvement in these traits may be carried out through selection in early segregating generations. The magnitude of additive component of genetic variance was, in general, lower than the dominance component of genetic variance with low to moderate narrow sense heritability for 1000-grain weight, grains *per* spike and spike length. This indicated preponderance of non additive components of variances for these traits, while for tillers *per* plant, spikelet *per* spike and plant height both additive and dominance type of variances were important. This suggested that a few generations of selfing should be carried out to reduce the dominance effect before initiation of selection for improvement of these traits.

This revealed that majority of the traits were governed by dominance genetic component. Therefore, the dominance genetic component needs to be reduced through selfing before initiation of selection of these traits. Discrepancies in inheritance of grain yield *per* plant, 1000-grain weight, grains *per* spike, spike length and harvest index may be due to cancellation of gene effects at mean level.

Chi-square analysis on discrete categories of resistance and susceptible for cereal cyst nematode showed that the F_2 plants for both the crosses segregated in the ratio of 3 susceptible verses 1 resistant, indicating monogenic inheritance and susceptibility was dominant over resistance for this nematode infection. The observed chi-square value for test cross ($F_1 \times$ recessive parent) was also found in the ratio of 1 susceptible: 1 resistant, while the back cross of F_1 plants with the susceptible parents gave all susceptible progeny in both the crosses, further confirmed these results.

CONCLUSIONS:

1) Genetic variability and heritability parameters indicated that grain yield *per plant*, tillers *per plant*, plant height, biomass *per plant*, harvest index, days to heading and days to maturity had, in general, high PCV, GCV, heritability in broad sense and genetic advance, while 1000-grain weight, grains *per spike*, spike length and spikelets *per spike* indicated low to moderate estimates of variability, heritability and genetic advance over the crosses and years.

2) Mean performance of different segregating generations indicated overdominance for grain yield *per plant*, 1000-grain weight, tillers *per plant*, spikelets *per spike*, days to heading, days to maturity, biomass *per plant* and harvest index, while grains *per spike*, spike length and plant height showed lack of dominance.

3) Results regarding gene effects indicated that 1000-grain weight, grains *per spike*, spike length, plant height, days to heading and days to maturity were predominantly governed by additive gene effects, while grain yield *per plant*, tillers *per plant*, spikelets *per spike*, biomass *per plant* and harvest index were predominantly governed by dominance gene effects.

4) Results of components of genetic variances indicated that for grain yield *per plant*, harvest index, days to heading and days to maturity additive component of genetic variance was higher than dominance component of genetic variance. Dominance component of genetic variance was higher than additive component of genetic variance for 1000-grain weight, grains *per spike*, spike length and biomass *per plant*, while both additive and dominance component of genetic variance for tillers *per plant*, spikelets *per spike*, plant height and harvest index in majority of the cases. This revealed that majority of the traits were governed by dominance genetic component. Therefore, the dominance genetic component needs to be reduced through selfing before initiation of selection of these traits. Discrepancies in inheritance of grain yield *per plant*, 1000-grain weight, grains *per spike*, spike length and harvest index may be due to cancellation of gene effects at mean level.

5) Results of inheritance of nematode resistance indicated that resistance to cereal cyst nematode was governed by a single recessive gene.

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ABSTRACT

Title of thesis	: Inheritance of grain yield, its components and resistance to cereal cyst nematode in wheat (<i>Triticum aestivum</i> L.)
Name of degree holder	: Niketa Yadav
Admission No.	: 2012A38D
Major Advisor	: Dr. S.S. Dhanda, Principal Scientist, Department of Genetics and Plant Breeding
Title of degree	: Doctor of Philosophy
Year of award of degree	: 2016
Degree awarding University	: Chaudhary Charan Singh Haryana Agricultural University, Hisar, India
Major subject	: Genetics and Plant Breeding
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Key words: Cyst Nematode, resistance, variability, inheritance, yield components

The present investigation was conducted to estimate additive, dominance and epistatic parameters, to develop the selection strategy for various traits and to determine resistance to cereal cyst nematode in bread wheat. The study was carried out during the period of *rabi* 2013-14 and *rabi* 2014-15 on six generations (P₁, P₂, F₁, F₂, B₁ and B₂) of two cross combinations (P 12210/Raj MR 1 and P 12231/Raj MR 1) in the Haryana Agricultural University, Hisar. The experiment was laid out in compact family block design with three replications. Observation were recorded on grain yield *per* plant, number of tillers *per* plant, 1000-grain weight, number of grains *per* spike, spike length, number of spikelets *per* spike, plant height, biomass *per* plant, harvest index, number of days to heading, and number of days to maturity. The results indicated that grain yield *per* plant, tillers *per* plant, plant height, biomass *per* plant, harvest index, days to heading and days to maturity had, in general, high PCV, GCV, heritability in broad sense and genetic advance over the crosses and years. Higher mean performance of F₁ and F₂ generations than their respective better parents showed overdominance for grain yield *per* plant, tillers *per* plant, 1000-grain weight, spikelets *per* spike, biomass *per* plant, harvest index, days to heading and days to maturity. Gene effects indicated that 1000-grain weight, grains *per* spike, spike length, plant height, days to heading and days to maturity were predominantly governed by additive gene effects, while grain yield *per* plant, tiller *per* plant, spikelet *per* spike, biomass *per* plant and harvest index were predominantly governed by dominance gene effects. Components of genetic variances indicated that for grain yield *per* plant, harvest index, days to heading and days to maturity additive component of genetic variance was important, while dominance component of genetic variance was, in general, responsible inheritance of 1000-grain weight, grains *per* spike, spike length and biomass *per* plant. Both additive and dominance component of genetic variances had major role in inheritance for tillers *per* plant, spikelets *per* spike, plant height and harvest index over the crosses and years. This indicated preponderance of dominance genetic component for inheritance for majority of traits and selfing for a few generations will be required for improvement of these traits through selection. Results of inheritance of nematode resistance indicated that resistance to cereal cyst nematode was governed by a single recessive gene.

MAJOR ADVISOR

SIGNATURE OF DEGREE HOLDER

HEAD OF THE DEPARTMENT

CURRICULUM VITAE

- (a) Name : Niketa Yadav
(b) Date of Birth : 27. 09. 1991
(c) Mother's Name : Mrs. Nirmala Yadav
(d) Father's Name : Dr. Rajkanwar Yadav
(e) Spouse's Name : Satbeer Singh, Ph.D
(f) Permanent Address : V.P.O.-Neerpur, Tehsil.- Narnaul,
District.- Mahinder Garh (Haryana)-123001
(g) Mobile : +919466020073
(h) E-mail : y.niketa@gmail.com
(i) Academic Qualification:



Degree	University/B oard	Year of Passing	Percentage of marks	Subjects
Ph.D.	CCS HAU, Hisar	2016	79.80	Major: Genetics and Plant Breeding Minor: Seed Science & Technology
M.Sc. (Agri.)	CCS HAU, Hisar	2012	72.50	Major: Genetics and Plant Breeding Minor: Seed Science & Technology
B.Sc. (Hons.) Agri.	SK RAU, Bikaner	2010	73.50	All agriculture and allied subjects
Senior secondary	RBSE, Ajmer	2006	63.85	Physics, Chemistry, Biology, Hindi, English
Matriculation	RBSE, Ajmer	2004	77.50	Hindi, English, Science, Maths, Social Science, Sanskrit

(j) Publications:

Niketa Yadav, R S Kanwar, S S Dhanda and Satbeer Singh; Inheritance of resistance for cereal cyst nematode (*Heterodera avenae* woll.) in wheat (*Triticum aestivum* L.) National Symposium on Nematode Management: A challenge to Indian Agriculture in the Changing Climate, Pune, 8th -10th Jan. 2015, pp-101-102.

Niketa Yadav and S S Dhanda; Inheritance of yield and its component traits in bread wheat (*Triticum aestivum* L.). National Seminar on *Omic Technologies for Better Food and Nutrition*, Telangana University, Nizamabad, 25th Feb. 2016.

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I also undertake that, patent, if any, arising out of the research work conducted during the programme shall be filed by me only with due permission of the competent authority of CCS Haryana Agricultural University, Hisar.

Niketa Yadav