STUDIES ON GENE EFFECTS FOR VARIOUS FORAGE AND GRAIN CHARACTERISTICS IN OAT

THESIS

By

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(A-2010-30-33)

Submitted to

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Is there anything I can say,

anything I can give

or do for you.....

Because all that I'm

all that I have

I owe to you.....

Affectionately Dedicated to my Revered Grandparents and Parents

Who sacrificed

their present

to make my future better

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CERTIFICATE – I

This is to certify that the thesis entitled **"Studies on gene effects for various forage and grain characteristics in oat"** submitted in partial fulfilment of the requirements for the award of the degree of **Master of Science (Agriculture)** in the discipline of **Plant Breeding and Genetics** of CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur is a bonafide research work carried out by **Mr. Lakshit Choudhary (Admission No. A-2010-30-33)** son of **Dr. Subhash Chand Choudhary**, under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

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

13/07/12

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Place: Palampur
Dated: 13th July, 2012

CERTIFICATE- II

This is to certify that the thesis entitled, **"Studies on gene effects for various forage and grain characteristics in oat"**, submitted by **Mr. Lakshit Choudhary (Admission No. A-2010-30-33)** son of **Dr. Subhash Chand Choudhary** to the CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur in partial fulfilment of the requirements for the degree of **Master of Science (Agriculture)** in the discipline of **Plant Breeding and Genetics** has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.

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LIST OF ABBREVIATIONS USED

AOAC	:	Association of Official Analytical Chemist
°C	:	Degree Centigrade
°E	:	Degree East
°N	:	Degree North
CD	:	Critical Difference
cm	:	Centimeter
g	:	Grams
Kg	:	Kilograms
mm	:	Millimeters
NS	:	Non-Significant
P_1	:	Female parent
P_2	:	Male parent
*	:	Significant
CFBD	:	Compact Family Block Design
%	:	Per cent
D	:	Duplicate
C	:	Complementry
MP	:	Mid-parent
BP	:	Better parent
CV	:	Check variety
R	:	Resistance
S	:	Susceptible
χ^2	:	Chi-square

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ABSTRACT

The choice of an efficient breeding methodology depends to a large extent on the knowledge of the genetic systems controlling the character to be selected. The objectives of this study were to study the nature and magnitude of gene effects for various forage and grain traits and to study the inheritance of powdery mildew resistance. The research was carried out in the Department of Crop Improvement, CSK HPKV, Palampur during *rabi* 2010-11 and 2011- 12 using generation means analysis derived from crosses of PLP-1 × *A. sterilis* and Kent× *A. sterilis* to transfer disease resistance and quality traits from wild oat to the cultivated oat.

The results obtained in the present investigation with respect to generation mean analysis suggested that both additive and dominance effects were important for most of the traits but dominance was predominant as compared to additive effects. Duplicate type of gene action was observed for days to 50 per cent flowering, leaves per plant, leaf: stem ratio, flag leaf area, green fodder and dry matter yield per plant, seed yield per plant, days to maturity, dry matter per cent for PLP-1 x *A. sterilis*, these observation implies the use of biparental approach and selection to be delayed to later generations. Complementary type of gene action was observed for plant height, tillers per plant, 100 seed weight and harvest index for PLP-1 x *A. sterilis,* implies the use of biparental approach and early generation selection to be followed.

A monogenic type of gene action was recorded for the resistance to powdery mildew (*Erysiphe graminis* f. sp. *Avenae*). PLP-1 was found to be resistant and *Avena sterilis* was highly susceptible to powdery midew. The segregation pattern studies indicated that the powdery mildew disease in oat is controlled by single dominant gene, and inherited in the ratio of 3:1

Thus study reveals that PLP-1 x *Avena sterilis* was found to be the promising cross because of its crude protein yield per plant, green fodder yield per plant, early flowering and disease resistance among the two crosses studied and thus could be utilized in future breeding programme.

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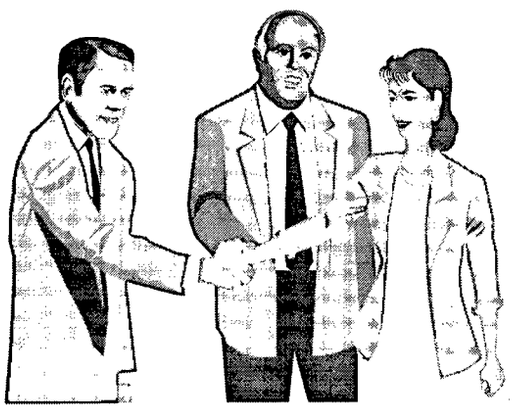


INTRODUCTION

1. INTRODUCTION

Oat (*Avena sativa* L.) is a cool season, annual crop grown mainly in moist areas of temperate climates of the world serving as a food for mankind and forage for cattle. It ranks 6th among cereals in world for annual production. Russia was the world production leader at 5.3 million metric tonnes in 2008-09, followed by Canada at 4.3 million metric tonnes (Statistics Canada, 2010). Preference to oat cultivation as a grain crop in Central and Western Europe and as fodder in Asia Minor is available since Christian era (Vavilov, 1926), however, some workers (Zade, 1918, Trabut, 1914 and Malzew, 1930) include Mediterranean region as centre of origin especially the cultivated red oat (*A. byzantina*).

About 50 species of oat are known (Hackel, 1890) and have been summarized in three groups, having n=7, n=14 and n=21 respectively (Stanton, 1936). Common oat (*A. sativa* L.) belongs to hexaploid group. *A. sativa* is more likely evolved from *A. sterilis* (Koch, 1848 and Trabut, 1914) instead of *A. fatua* (Haussknecht, 1885; Thellung, 1912 and Zade, 1918). *A. sativa* is an allo-hexaploid having three distinct genomes, designated as A, B and C (Nishiyama, 1929 and Rajhathy and Morrison, 1960). Progenitor of A genome is one of the *strigosa* group (Nishiyama, 1929). *A. ventricosa* is donor of C genome (Rajhathy, 1966 and Thomas, 1970). B genome is possibly a modified form of A genome (Sadasivaiah and Rajhathy, 1968). It is an important *rabi* fodder crop in India.

Crops like berseem and lucerne remain dormant in hilly areas during winter months, whereas oat can easily be grown during this period because of its good regeneration capacity, drought and cold tolerance ability. Ever increasing population has led to competition between human and livestock for food. The competition for utilization of land for food grains and fodder necessitates intensified efforts toward more efficient forage production which involves development of high yielding, fast growing, multicut with good regeneration capacity, dual purpose, nutritious and resistant varieties of fodder crops through genetic improvement.

The wild ancestor of *Avena sativa* is the hexaploid wild oat, *A. sterilis. Avena sterilis* (wild oat), having same genome is easily crossable with *A.sativa* (cultivated oat) and possess desirable traits such as high protein, earliness and 100-seed weight which can be introgressed into cultivated oat through interspecific hybridization.

Qualitative characters controlled by one or few major genes are more readily manipulated in a breeding programme as compared to quantitative traits controlled by many genes. Nevertheless, the breeder is concerned mainly with quantitative characteristics which could be of use in both formulating and performing the breeding programme. The inheritance of characteristics chosen has a major influence on the statergy employed for cultivar development.

Most of the forage and grain yield traits are quantitative in nature, and thus the choice of parents for hybridization and selection of desirable lines for direct use as a variety or as a parent in hybridization programme is a difficult task for a breeder. Besides high grain and fodder yield, emphasis should also be given for improving the oat plants with respect to some of the morphological traits for harnessing it to full potential. In order to combine various desirable attributes along with better yield and responsiveness to intensive cultivation, the most appropriate approach is to adopt recombinant breeding. In such an approach, the efficiency of breeding programme would, mainly depend upon the genetic architecture of the traits under improvement (Cockerham, 1961). Moreover in such a breeding programme, an objective judgement about heterotic cross combinations, likely to produce transgressive segregants in self pollinated crops like oat would, mainly depends upon the relative importance of various genic effects (Jinks, 1983).

Oat crop itself suffers from a wide range of diseases and pests. Powdery mildew (*Erysiphe graminis* f. sp. *avenae*) is one of the most deleterious foliar diseases of cultivated oat. An estimated loss of up to 32% in yield due to this pathogen has been reported (Jones et al. 1987). Because oats are often grown as a low input crop, the most economical and environmentally safe method for controlling powdery mildew is by growing resistant cultivars. To effectively breed for disease resistance, information on the genetics and mode of inheritance is essential.

Therefore, in order to have rapid genetic amelioration of the oat (*Avena sativa* L.) based on sound biometrical approaches, the present investigation entitled "Studies on gene effects for various forage and grain characteristics in oat" was undertaken with following objectives:

I. To study the nature and magnitude of gene effects for various forage and grain traits and ;

II. to study the inheritance of powdery mildew resistance.

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

Plant breeder is mainly concerned with quantitative traits showing continuous variation such as yield. Therefore, it is imperative for a breeder to have the information on the complexity and its component traits for an effective genetic improvement programme in various crop species.

The relevant literature reviewed on various aspects of the present investigation entitled "Studies on gene effects for various forage and grain characteristics in oat" has been given under the following heads as below:

2.1 Studies on gene action for various forage and grain traits in oat.

2.2 Studies on heterosis in oat.

2.3 Studies on inheritance of powdery mildew resistance in oat.

2.1 *Studies on gene action for various forage and grain traits*

The characterization of genetic components using appropriate mating designs and field experimentation is imperative as it helps in estimation and partitioning of various components, which eventually determine the applicability and success of breeding programmes. Fisher (1918) and Wright (1922) provided the basic framework for characterizing and partitioning genetic variance into physically assignable components. Fisher (1918) was the first to divide the genetic variance into three components, *i.e.* additive, dominance and epistatic variance.

Dickerson (1963), Dudley and Moll (1969) and Mather and Jinks (1971) outlined the following components of genetic variance, which are of practical consideration in crop improvement programmes.

Additive genetic variance associated with the average effects of individual genes. It measures the breeding value of various genotypes and is fixable for effective selection.

Dominance variance associated with intra-allelic interactions of genes at segregating loci and measures breeding behaviour of alleles in heterozygotes. It is of practical application to proceed for hybridization.

Epistatic variances associated with inter-allelic (non-allelic) interaction of genes at two or more segregating loci. Epistasis involving additive effects is fixable and as such exploited in intra-population improvement. Other epistatic effects are exploited in hybridization programme.

Nijhawan *et al.* (1970) observed that additive effects were greater than dominant in the inheritance of number of panicles per plant, where as dominant gene effects were more important than additive effects for grain yield and number of spikelets per panicle.

Campbell and Frey (1972) found both additive gene action and duplicate epistasis for kernel protein content in interspecific crosses between two A. *sativa* cultivar and six high protein *A. sterilis* lines.

Arora *et al.* (1974) using seven parental diallel of exotic and local oat reported predominantly non-additive type of gene action for green fodder yield, tillers per plant and plant height which can be exploited through hybridization.

Bhandari (1974) reported that additive gene effects were more important for days to 50 per cent flowering and protein percentage, where as non-additive gene effects were predominant for plant height, leaf width, tillers number per plant, fresh and dry matter yield per plant which were under the influence of complementary type of gene action in oat.

Paroda *et al.* (1974) observed that green fodder and dry matter yields in oat were governed by both additive and non-additive gene effects with preponderance of the latter indicated the importance of effective selection after hybridization.

Sraon (1974) reported additive gene action and partial dominance for protein content in a diallel analysis of four cultivars of oat.

Sraon *et al.* (1975) observed additive gene action for groat protein percentage and partial dominance conditioned low protein percentage in interspecific crosses of *A. sterilis* and *A. sativa* lines crossed in a diallel fashion including reciprocals.

Lawerence and Frey (1976) in the inheritance study of grain yield in the interspecific crosses of *A. sterilis* and *A. sativa* lines found that effective factors for grain yield exihibited additive gene action, epistasis and linkage.

Mishra and Ahlawat (1977) studied inheritance of grain yield and certain other quantitative characters in oat crosses and reported significantly additive gene action for heading date, yield and number of tillers per plant.

Manga and Sidhu (1979) studied combining ability and inheritance of yield and yield components in crosses involving *A. sativa* and *A. byzantina* and found both additive and non-additive gene action with over dominance for plant protein to be prevalent in oat indicating the importance of both hybridization and selection for its improvement.

Solanki and Kishor (1979) reported predominance of additive gene action for green and dry fodder yield and the number of leaves and non-additive gene action for tillers and plant height in forage oat.

Akbar and Abdullah (1980) revealed the evidence of overdominance for plant height, additive gene action and partial dominance for leaf area; and overdominance and gene interaction for number of days to flowering, days to maturity and plant dry weight in a diallel of six varieties in oat.

Sarswat (1981) reported complementary type of epistasis for plant height, fresh fodder and dry matter yield. He also found both additive and non-additive type of gene action with partial dominance for days to 50% flowering and per cent crude protein indicating the importance of hybridization and selection for its improvement.

Kuenzel (1982) found that additive gene effects were important in control of grain yield and additive and non-additive gene effects were important in control of groat protein percentage and protein yield.

Dwivedi *et al.* (1984) observed that plant height, tiller number, green and dry matter yields were governed by both additive and non-additive type of gene effects. Predominance of additive gene effects for plant height and tiller number and non-additive gene effects for green and dry matter yields were also observed.

Manga and Sidhu (1984) reported both additive and non-additive gene action, partial dominance for days to 50% flowering and number of leaves per plant, overdominance for leaf size and complete dominance for leaf: stem ratio.

Jhorar *et al.* (1988) in his study for the estimation of gene effects for number of leaves in three oat crosses by making use of generation mean analysis revealed that additive gene effects were significant in all three crosses, while dominance gene effects were significant in one cross only. Complementary type of epistasis was observed in all the crosses.

Kozlenko and Egorova (1989) found that additive genes predominated in the control of plant height and 1000 grain weight, while grain weight per plant was mainly controlled by non-additive genes.

Mishra and Verma (1989) observed significant and maximum F_2 deviation for tiller number and grain yield among the two crosses, indicating the presence of epistasis.

Soldatov and Batalova (1990) reported overdominance effects for tillering and grain yield, and recommended that selection for these traits should be deferred until later generations.

Kishor *et al.* (1992) found complementary as well as duplicate gene effects for green fodder and dry matter yield in triple test cross analysis in F_2 population of forage oat, where as only duplicate type epistasis was observed for protein content.

De Koeyer and Stuthman (1998) observed additive × additive epistasis for grain yield in 6^{th} cycle progeny due to significant σ^2 sca, while studying the continued response through seven cycles of recurrent selection for grain yield in oat.

Reuben-Sowm (1999) reported that both additive and dominance variances were significant in the control of flowering, plant height and tillering in hybridization of seven oat parents from different parts of world in full diallel fashion.

Singh (1999) observed predominance of additive gene effects for number of tillers per plant and green forage yield.

Dogra *et al.* (2003) while studying six generations of six crosses of oat observed the predominant role of dominant genic effects for tillers per plant, leaves per plant, days to 50 per cent flowering, plant height, fresh fodder yield per plant, dry matter yield per plant and grain yield per plant indicating importance of hybridization for its improvement.

Sood *et al.* (2006) observed that non-additive genetic variances were high in oat for both fodder and grain yield and their related traits, where as both additive and non- additive variances were equally important for leaf: stem ratio and biological yield per plant. They further observed that additive variances were higher than the non- additive genetic variances for 100-seed weight.

Prajapati *et al.* (2009) observed that the estimates of variances due to specific combining ability (σ^2 sca) were higher than general combining ability (σ^2gca) and their ratio (σ^2sca: σ^2gca) indicated predominance of non-additive *i.e.* non-fixable type of gene action for the characters studied.

2.2 Studies on heterosis

The term heterosis was first used by Shull in 1909. Heterosis may be defined as superiority of F_1 hybrid over its both the parents in terms of yield or some other attributes. The term heterosis is generally used only when the hybrid is either superior or inferior to both its parents. In general, cross-pollinated species show more heterosis, particularly when inbreds are used as parents. In self-pollinated species like rice, heterosis has been commercially exploited in China (Singh, 1990).

Manga and Sidhu (1981) studied heterosis for dry matter yield and its components in 45 F_1 hybrids obtained from a ten-parent diallel set. For dry matter yield, the heterosis ranged from -46.40 to 79.70 per cent over better parent. They

suggested multiple crossing followed by pedigree method of selection in segregating generation's for the development of high yielding cultivars in oat.

Cowen and Frey (1987) estimated heterosis for grain yield, straw yield, harvest index, plant height and heading date in crosses obtained from more distantly related parents in a diallel design without reciprocals.

Mishra and Verma (1989) studied hybrid vigour in two crosses of oat for plant height, days to 50 per cent heading and tiller number. Significant heterosis ranging from -8.79 to 93.74 per cent over mid-parent was observed for all the characters. Significant heterobeltiosis (-21.31 to 29.25 per cent) was also observed for all the traits except tillers number.

Akici and Ozgen (1991) reported heterosis for plant height, number of tillers per plant and 100 seed weight in F_1 hybrids from a five parent diallel set of crosses in oat.

Tyagi *et al.* (1995) in ten-parent diallel reported 84.34 and 76.73 per cent heterosis over better parent in oat for green and dry matter yield, respectively. The maximum of 78.13 per cent heterosis was observed in hybrid TOS 96 × TOS 63 over OS 6, the check variety for green fodder yield, while maximum heterosis of 72.35 per cent was observed in hybrid Chauripatti × TOS 63 over OS-6 for dry matter yield.

Babbar *et al.* (1997) reported heterobeltiosis for dry matter yield per plant and green fodder yield per plant in a line × tester mating design in oat. They emphasized that the genetic diversity among the parents plays a key role in genetic improvement of oat through hybridization.

Dogra (2002) observed positive heterosis for fresh fodder, grain and dry matter yields in a six-parent diallel in oat.

Thukral and Verma (2003) while studying heterosis and inbreeding depression in 5 crosses of oat observed that the range of heterosis varied substantially among various crosses and characters, except for days to 50%

heading and maturity, indicating the wide variability in the test material. Mean heterosis was high for grain yield per plant and number of tillers per plant; moderate for plant height, number of spikelets per panicle and panicle length; and low for days to 50 per cent heading, 100-grain weight and days to maturity. The average inbreeding depression over all crosses was favourable for days to heading and grain yield per plant; low for days to maturity; and moderate for 100-grain weight.

Prajapati *et al.* (2009) observed maximum significant heterosis over better parent (BP) in cross OL 1389 x OS 6 followed by JHO 2000-4 x Kent and Sabzar x Kent while, maximum standard heterosis was found in OS 311 x Kent for green forage yield per plant. The highest heterobeltiosis for grain yield and dry matter yield per plant was recorded in cross JHO 2000-4 x Kent followed by OS 311 x Kent and JHO 2000-5 x Kent.

Vishwakarma *et al.* (2010) studied heterosis in 27 different crosses of forage oat resulting from lines x testers mating design grown in two environments. The extent of heterosis over better parent and standard variety ranged from -33.43 to 37.88 per cent and -30.12 to 38.70 per cent for green forage yield per plant and -15.45 to 50.08 per cent and -32.11 to 53.28 per cent for grain yield per plant, respectively.

2.3 Studies on inheritance of powdery mildew resistance

The component of resistance and their phenotypic and genetic characteristics can be determined only by genetic analysis. On the basis of mode of inheritance three main kinds of resistance have been identified: (a) monogenic resistance, in which resistance is controlled by a single gene, (b) oligogenic resistance, where resistance is governed by few genes and (c) polygenic resistance, where resistance is controlled by many genes. Genes with large effect on the expression of resistance are said to be major genes and genes which individually have only a small effect on the expression of resistance are called minor genes (Russel, 1978).

Roderick and Jones (1991) during evaluation of adult plant resistance to powdery mildew (*Erysiphe graminis* f.sp. *avenae*) in transgressive lines of oats found that previously identified segregant lines of oat with levels of adult plant

resistance to powdery mildew better than the resistance parent maintained at this high level of resistance in field nurseries over two growing seasons. This enhancement was not expressed on inoculated detached leaves under laboratory conditions where no difference between the more resistant parent cv. Maldwyn and the most resistance segregants was detected.

Sebesta *et al.* (2000) while studying genetic basis of oat resistance to fungal diseases observed that race specific resistance to fungal diseases is governed by single dominant gene, partially dominant or complementary gene interaction.

Yu and Herrmann (2006) introgressed successfully powdery mildew resistance gene from *Avena macrostachya* into hexaploid oat (*A. sativa*). Genetic analysis of F_1, F_2, F_3 and BC_1 populations from two powdery-mildew resistant introgressed lines revealed that the resistance is controlled by a dominant gene.

MATERIALS AND METHODS

3. MATERIALS AND METHODS

The present investigation was carried out at Experimental Farm of the Department of Crop Improvement, CSKHPKV Palampur (HP) during *rabi* 2010-11 and 2011-12. The details of the materials used and the methods employed in the present investigation are presented below:

3.1 Experimental Site

The Experimental farm is situated at $32^0 6'$ N latitude, $76^o 3'$ E longitude at an elevation of 1290.8 m (a.m.s.l). Agro-climatically the location represents the mid-hill zone of Himachal Pradesh (zone-II) and is characterized by humid sub-temperate climate with high rainfall (2500 mm). The soil is acidic in nature with pH ranging from 5.0 to 5.6 and soil texture is silty clay loam.

3.2 Experimental Materials

The experimental material consisted of two diverse genotype of cultivated oat viz., PLP-1 and Kent and one local collection of wild oat (*Avena sterilis*). F_1 seeds of two crosses namely, PLP-1 × *A. sterilis* and Kent × *A. sterilis* were developed during *rabi* 2009-10. Fresh F_1's of these crosses were developed during *rabi* 2010-11 and available F_1's were simultaneously backcrossed to both its parents P_1 and P_2 and also advanced to F_2 generation.

3.3 Layout of the experiment

The experimental material comprising of different generations *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 of two crosses were evaluated in Compact Family Randomized Block Design with three replications, during *rabi* 2011-12. Parents were grown in double rows of 2m length while another non segregating generations F_1's were grown in single row of 2m length. The segregating, F_2 generations were grown in four rows and BC_1 and BC_2 were grown in three rows. The row to row distance was 25 cm with plant to plant distance of 5 cm apart. Recommended package of practices were followed for raising the crop.

***Avena sativa* (PLP-1)**

***Avena sativa* (Kent)**

Avena sterilis

Plate: 3.1 Parents used in crossing programme

3.4 Recording of observations

Ten randomly taken plants in case of parents and their F_1's, 25 in case of backcrosses (BC_1 and BC_2) and 50 plants in case of F_2 generation in each replication were used for recording the following data:

3.4.1 Morphological and yield characters

1. Days to 50 per cent flowering

It was expressed as number of days from sowing to 50 per cent flowering on plot basis.

2. Plant height (cm)

The plant height was measured in centimeters from base upto the end of the main tiller at the time of maturity.

3. Number of leaves per plant

Total numbers of leaves in each plant were counted at the time of 50 per cent flowering.

4. Number of tiller per plant

Total number of tillers in each plant were counted before harvesting the plants.

5. Leaf: stem ratio

Leaves and stem were separated and weighed individually. Leaf:stem ratio was calculated by dividing the leaf weight by stem weight.

6. Flag leaf area (cm^2)

Flag leaf was separated and leaf area was measured by using leaf area meter.

7. Fresh fodder yield per plant (g)

Selected plants from each plot were harvested at 50 per cent flowering and were weighed immediately for fresh fodder yield.

Plate: 3.2 Experimental plot at Palampur

8. Dry matter per cent

One hundred grams of green fodder was kept in oven in brown paper bags at 60°C for three days for drying and dry matter per cent was recorded.

9. Dry matter yield per plant (g)

Dry matter per cent was used to determine dry matter yield per plant.

$$DMY = \frac{\text{Dry matter per cent} \times \text{Green fodder yield per plant (g)}}{100}$$

10. Crude protein content (%)

Per cent crude protein content (N × 6.25) in forage was estimated by Macro Kjeldahl method (AOAC 1970).

11. Crude protein yield per plant (g)

Crude protein yield per plant was computed by multiplying crude protein content with dry matter yield.

12. Days to maturity

The numbers of days taken from the sowing to 75 per cent maturity of the plants in a plot were recorded.

13. Seed yield per plant (g)

The average yield of selected plants was recorded in grams after threshing.

14. Harvest index (%)

It was calculated as below:

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

15. 100-seed weight (g)

Randomly 100 seeds of parents and their six generations were counted and weighed.

3.4.2 Disease reaction

The genotypes were screened for powdery mildew reaction and observations were recorded as per cent area infected on the basis of visual observations. Screening of F_1'sand F_2's was done against powdery mildew under field conditions (Mayee and Datar, 1991)

Scale used to evaluate oat genotypes for disease reaction to powdery mildew

Grade	Level of resistance	Disease reaction
0	Highly Resistant	No symptoms on the leaf
1	Resistant	Small specks of whitish grey dots covering 1% or less of the leaf area
3	Moderately Resistant	White powdery patches covering 1-10% of the leaf area
5	Moderately Susceptible	Powdery patches big, covering 11-25% of the leaf area
7	Susceptible	Powdery patches big, covering 26-50% of the leaf area
9	Highly Susceptible	Powdery patches big, coalescing to cover 51% or more of the leaf area

3.5 Biometrical analysis

Estimation of Mather's simple scaling test (1949), joint scaling test of Cavalli (1952) and estimation of genic effects (Jinks and Jones, 1958) were carried out as per the procedure given in detail by Mather and Jinks (1982) using SPAR1 programme (Doshi and Gupta, 1991). Heterosis and inbreeding depression for each cross was also estimated.

Estimation of the chi-square values were worked out with respect to inheritance of powdery mildew disease for testing the goodness of fit.

3.5.1 Simple scaling tests

Following scaling tests were carried out for the detection of non-allelic interactions:

$$A = 2\overline{B_1} - \overline{P_1} - \overline{F_1}$$

$$B = 2\overline{B_2} - \overline{P_2} - \overline{F_1}$$

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

$$D = 2\overline{F_2} - \overline{B_1} - \overline{B_2}$$

The deviation of these scaling tests from zero was tested using the respective standard errors. The deviations from zero of these quantities indicate the inadequacy of additive-dominance model. The standard errors of the above scaling test were calculated as follow:

$$SE(A) = \pm \{4\, V(\overline{B_1}) + V(\overline{P_1}) + V(\overline{F_1})\}^{1/2}$$

$$SE(B) = \pm \{4\, V(\overline{B_2}) + V(\overline{P_2}) + V(\overline{F_1})\}^{1/2}$$

$$SE(C) = \pm \{16V(\overline{F_2}) + 4V(\overline{F_1}) + V(\overline{P_1}) + V(\overline{P_2})\}^{1/2}$$

$$SE(D) = \pm \{4\, V(\overline{F_2}) + V(\overline{B_1}) + V(\overline{B_2})\}^{1/2}$$

The significance of the deviation of these quantities was tested by 't' test

t'_A = A/SE (A), and similarly for others

The additive-dominance model was adequate, if all these scaling tests were equal to zero within the limits of their sampling errors. Any value of these

scaling tests i.e. beyond the limits of error was an indication of epistasis. The significant deviation of A and B scaling tests from zero indicated the presence of additive x dominance [j] type of interaction. However, the deviation of C scaling test revealed the presence of dominance x dominance [l] type of interaction, whereas that of D scaling tests indicated the presence of additive x additive [i] interaction.

3.5.1.1 Estimation of genic effects and joint scaling test

Estimation of various genic effects and test of fitness of appropriate genetic model was done according to joint scaling test of Cavalli (1952), as described in detail by Mather and Jinks (1982). Joint scaling test in general consists of estimating various genetic parameters from means of available type of generations followed by the comparison of observed generation means with the expected values, derived from the estimates of genetic parameters (genic effects), using weighted least square technique, taking as goodness of fit of a particular model was carried out by using weighted chi-square analysis. The observed and expected generation means were compared by chi-square test with the degree of parameters (p) estimated.

In the present study, the estimation of genic effects and chi-square test of goodness of fit was carried out by using 6 parameters model.

In 6-parameter model (digenic interaction model), following genic effects were estimated:

m = Inbred population mean

(d) = additive

(h) = dominance

(i) = additive x additive

(j) = additive x dominance

(l) = dominance x dominance

The genetic expectation of different generation means, used in the present study for the estimation of various genic effects in the presence of digenic interactions, was as follow:

$P_1 = m + d + i$

$P_2 = m - d + i$

$F_1 = m + h + l$

$F_2 = m + \frac{1}{2} h + 1/4l$

$B_1 = m + \frac{1}{2} d + \frac{1}{2} h + 1/4i + 1/4j + 1/4l$

$B_2 = m - \frac{1}{2} d + \frac{1}{2} h + 1/4i - 1/4j + 1/4l$

3.5.2 Heterosis and Inbreeding depression

Heterosis is expressed as per cent deviation from mid parent specifically called average heterosis. Heterobeltiosis is the per cent deviation towards desirable side over better parent and standard heterosis is the per cent deviation towards desirable side over best check. The formulae used for their estimation and for testing of significance were as follows:

$$\text{Heterosis over mid parent (\%)} = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

$\overline{MP}$ = mean mid parental value

$\overline{F_1}$ = mean of F_1

$$\text{Heterosis over better parent (\%)} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

where,

$\overline{BP}$ = mean better parental value

$\overline{F_1}$ = mean of F_1

$$\text{Standard heterosis (\%)} = \frac{\overline{F_1} - \overline{CV}}{\overline{CV}} \times 100$$

where,

$\overline{CV}$ = mean value of check variety.

$\overline{F_1}$ = mean of F_1

The significance of heterosis for each observation and each cross was ascertained by their respective critical difference (CD) value.

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

RESULTS AND DISCUSSION

4. RESULTS AND DISCUSSION

The objectives of the present investigation were to detect the presence of non-allelic interactions along with the estimation of various genetic effects namely, additive, dominance and epistasis using generation means approach in two different crosses of oat. Generation mean analysis is used to estimate the components of variance which provides information about the nature and magnitude of gene action for the important characters of various crop species (Ganesh and Sakila, 1999). Therefore, the present study was undertaken to determine the relative magnitude of genic effects governing some quantitative traits in oat.

4.1 Studies on gene effects for morphological and yield characters

The selection of a suitable breeding methodology on the basis of genetic variability generated through hybridization programme would largely depend on the nicking ability and practical utility of the parents in a cross and the genetic architecture of economic traits under consideration (Cockerham 1961; Sprague 1966). Fasoulas (1981) proposed the genetic theory of gene action which is logical and in a consistent manner explains the evolution of gene action which takes place through the combined action of recombination and selection. The knowledge of the type of gene action controlling various traits is helpful in choosing an efficient breeding program.

A. sterilis (wild oat), having same genome is easily crossable with *A. sativa* (cultivated oat) and possess desirable traits such as high protein, earliness and 100-seed weight which can be introgressed into cultivated oat through interspecific hybridization.

To understand the type of breeding procedure to be followed, it is essential to estimate the type of gene effects in plant population. In order to increase the yield potential, it is imperative to utilize the available genetic potential efficiently. The nature and magnitude of genetic variation present in population is elucidated by genetic analysis of the quantitative traits. The

predominance of additive gene effects signifies the development of homozygous lines while dominance gene effects are used for exploitation of hybrid vigour. The generation mean analysis is the most common tool employed for the estimation of gene effects and components of genetic variance (Hayman and Mather, 1955).

4.2 Estimates of simple scaling tests and genic effects

Simple scaling tests (A, B, C and D) as per Mather (1949) and Mather and Jinks (1982) were carried out to test the adequacy of additive-dominance model. Joint scaling test as per Cavalli (1952) was used to estimate the genic effects by using three parameter model and further verifying the same by χ^2 test. Failure of additive-dominance model was interpretated under situation, when either of the scaling test, or χ^2 was significant. In crosses where there was failure of additive-dominance model, six parameter model was used to estimate the various genic effects including non-allelic interactions due to additive x additive [i], additive x dominance [j] and dominance x dominance [l] as per Jinks and Jones (1958). The results obtained on estimates of scaling test and various genic effects for two crosses studied with respect to fifteen characters are documented in tables 4.1 to 4.8 and are described character-wise here under:

4.2.1 Days to 50% flowering

The estimates of simple scaling tests A, B, C and D are given in Table 4.1. B and D scaling tests were significant in cross PLP-1 × *A. sterilis* indicating the presence of [i], [j] and [l] type of interactions. In Kent × *A.sterilis* A,B,C and D scaling tests were non-significant indicating the absence of [i], [j] and [l] type of interactions.

Additive effects [d] were positive and significant in cross PLP-1 × *A. sterilis* however non-significant [d] was observed for Kent × *A. sterilis*. While dominance effect [h] were negative and non-significant in both the crosses. Opposite signs of [h] and [l] were present in PLP-1 × *A. sterilis*. This indicated the presence of duplicate type of gene action. The significant chi-square value in case of PLP-1 × *A.sterilis* indicated the failure of additive-dominance model and presence of digenic and higher order interactions. These are the only source of genetic variation in this cross. The non-significant values of A, B, C and D scaling test and also chi-square in cross Kent × *A.sterilis* indicated the fitting of additive-

dominance model. Duplicate type of epistasis in PLP-1 × *A.sterilis* can be utilized by growing large populations in segregating generations and adopting biparental mating approach in early segregating generations in order to isolate desirable segregants. Bhandari (1974) observed additive genic effects to be more important for days to 50% flowering. Presence of positive and significant dominance genic effect along with duplicate type of epistasis was observed in PLP-1 × *A. sterilis* and Kent × *A. sterilis* crosses as recorded by some earlier workers (Akbar and Abdullah, 1980; Sarswat. 1981; Manga and Sidhu, 1984 and Reuben-Sowm, 1999).

4.2.2 Plant height

The estimates of simple scaling tests A, B, C and D are given in Table 4.1. A and B scaling tests were significant in cross PLP-1 × *A. sterilis* indicating the presence of [j] type of interaction. In Kent × *A. sterilis* only A scaling test was significant indicating the presence of [j] type of interaction.

Table 4.1 Estimates of scaling tests and genic effects for days to 50 per cent flowering and plant height in oat

Cross Parameters → ↓	Days to 50 % flowering		Plant height	
	PLP-1 x *A.sterilis*	Kent x *A.sterilis*	PLP-1 x *A.sterilis*	Kent x *A.sterilis*
A	0.67±3.28	-3.67±2.73	-10.33**±3.61	18.33*±7.77
B	-6.67*±2.91	-3.00 ±4.15	16.33**±3.67	-6.00±7.72
C	9.33±7.46	4.00±12.63	7.33±8.96	4.33±8.88
D	7.67*±3.13	5.33±6.22	0.67±4.63	-4.00±5.38
[m]	132.33**±1.45	128.33**±2.96	99.00**±2.08	103.33**±1.33
[d]	7.00** ±1.16	2.00 ±1.89	-10.67**±2.03	10.67*±4.67
[h]	-11.33±6.68	-7.33±12.63	-6.33±9.41	-1.17±11.32
[i]	-15.33*±6.25	-	-1.33 ±9.26	8.00±10.75
[j]	3.67*±1.68	-	-13.33**±2.53	12.17*±5.06
[l]	21.33* ±8.78	-	-4.67 ±12.08	-20.33±20.67
χ^2 (3d.f)	11.26*	3.34	29.18**	7.02
Type of interaction	D	-	C	C

*P≤0.05; and **P≤0.01

Additive effects [d] were negative and significant for cross PLP-1 × *A. sterilis* however positive and significant [d] was observed for cross Kent × *A. sterilis*. While dominance effect [h] were negative and non-significant in both the crosses. Same signs of [h] and [l] were present for cross PLP-1 × *A. sterilis* and Kent × *A. sterilis*. This indicated the presence of complementary type of epistasis. The significant chi-square value in case of PLP-1 × *A. sterilis* indicated the failure of additive-dominance model and presence of digenic and higher order interactions. These are the only source of genetic variation in this cross. The non-significance of chi-square in cross Kent × *A. sterilis* indicated the fitting of additive-dominance model. Kozlenko and Egarova (1989) reported predominance of additive genic effects for plant height. However, PLP-1 × *A. sterilis* had both negative additive and dominance genic effects as reported by Reuben – Sowm (1999) in oats.

4.2.3 Leaves per plant

The estimates of simple scaling tests A, B, C and D are given in Table 4.2. In PLP-1 × *A. sterilis* only A scale was significant indicating the presence of [j] type of interaction. A, B, C and D scales were non-significant for the cross Kent × *A. sterilis* indicating the absence of all three types of interactions. Positive and significant additive effects were observed in cross Kent × *A. sterilis.* Non-significant negative dominant effects were observed in PLP-1 × *A. sterilis* and non-significant positive effects were recorded in Kent × *A. sterilis*. However predominant dominance genic effects were observed by Jhorar *et al.* (1988). Manga and Sidhu (1984) observed partial dominance for number of leaves per plant. Duplicate type of genic interaction was present in PLP-1 × *A. sterilis* as signs of [h] and [l] were in opposite direction.

4.2.4 Tillers per plant

The estimates of simple scaling tests A, B, C and D are given in Table 4.2. In PLP-1 × *A. sterilis* only C scale was significant indicating the presence of [l] type of interaction. A, B, C and D scales were non-significant for the cross Kent × *A. sterilis* indicating the absence of all three types of interactions. The additive [d] gene effect was found to be negative for cross PLP-1 × *A.sterilis.* The

dominance [h] effect was found to be positive and non-significant for both the crosses. Complementary type of epistasis was found for this trait for PLP-1 × *A. sterilis.* The additive x additive interactions are the outcome of complementary epistasis and lead to transgressive segregation. The significant chi-square value in case of PLP-1 × *A. sterilis* implied the presence of digenic or higher order interactions due to failure of additive-dominance model. Dominance genic effects were positive and non-significant in both the crosses. Earlier Bhandari (1974) and Soldatov and Batalova (1990) found the predominance role of genic effects for this trait.

Table 4.2 Estimates of scaling tests and genic effects for leaves per plant and tillers per plant in oat

Cross → / Parameters ↓	Leaves per plant		Tillers per plant	
	PLP-1 x *A.sterilis*	Kent x *A. sterilis*	PLP-1 x *A. sterilis*	Kent x *A.sterilis*
A	-10.00*±4.92	-3.67±6.57	-3.67±2.06	-1.00±1.92
B	-12.67±6.80	-11.67±8.23	-3.67±2.16	-0.67±1.56
C	-3.33±9.68	-17.33±13.40	-8.00*±3.16	-3.67±2.77
D	9.67±5.04	-1.00±6.60	-0.33±1.83	-1.00±1.49
[m]	46.33**±1.86	42.33**±2.60	11.33**±0.67	11.00**±0.58
[d]	3.00±3.42	9.67*±4.06	-0.33±1.25	1.67±0.94
[h]	-9.00±10.56	0.67±13.86	2.67±3.75	0.83±3.08
[i]	-19.33±10.08	-	0.67±3.65	-
[j]	1.33±3.73	-	0.00±1.47	-
[l]	42.00*±16.75	-	6.67* ±2.91	-
χ^2(3d.f)	7.29	4.14	9.53*	1.83
Type of interaction	D	-	C	-

*P≤0.05; and **P≤0.01

4.2.5 Leaf: stem ratio

The estimates of simple scaling tests A, B, C and D are given in Table 4.3. In case of cross PLP-1 × *A. sterilis*, the significance of A type of scaling test indicated the presence of [j] and [l] type of interactions while A, B, C and D tests confirmed non-significance in Kent × *A.sterilis* which indicated absence of all type of interactions. The chi-square values for additive-dominance model were significant for PLP-1 × *A. sterilis* which indicated the presence of epistasis. However for the cross Kent × *A. sterilis* the chi-square values were non-significant which suggested the absence of epistasis in this cross. The six parameter model showed that the value of [d] was negative and significant for cross PLP-1 × *A. sterilis*, the value of [d] was non- significant and positive for the cross Kent × *A. sterilis* . The significant chi-square value in case of PLP-1 × *A. sterilis* indicated the failure of additive- dominance model and presence of digenic and higher order interactions. Duplicate type of genic interaction was present in PLP-1 × *A. sterilis* as signs of [h] and [l] were in opposite direction.

4.2.6 Flag leaf area

The estimates of simple scaling tests A, B, C and D are given in Table 4.3. In case of cross PLP-1 × *A.sterilis*, the significance of B type of scaling test indicated the presence of [j] type of interaction. In Kent × *A. sterilis* B, C and D scaling tests were significant indicating the presence of [i] and [j] type of interactions. The additive [d] and dominance [h] gene effects were found to be negative and significant for cross Kent × *A.sterilis.* Significance of chi-square for the crosses PLP-1 × *A.sterilis* and Kent × *A.sterilis* indicated the failure of additive- dominance model which suggested that the source of variation in these crosses for this trait is because of digenic or higher order interactions. Complementary type of gene interaction was observed in Kent × *A.sterilis.* Duplicate type of epistasis was found for this trait for PLP-1 × *A.sterilis.* The cross Kent × *A.sterilis* had additive and dominance genic effects for this trait as reported earlier by Akbar and Abdullah (1980) and Manga and Sidhu (1984).

Table 4.3 Estimates of scaling tests and genic effects for Leaf: stem ratio and Flag leaf area in oat

Cross → / Parameters ↓	Leaf:stem ratio		Flag leaf area	
	PLP-1 x *A. sterilis*	Kent x *A.sterilis*	PLP-1 x *A. sterilis*	Kent x *A. sterilis*
A	-0.23**±0.07	-0.05±0.08	-3.33±3.11	-3.33±3.76
B	-0.03±0.06	-0.05±0.06	12.67**±2.16	31.33**±2.49
C	-0.14±0.16	-0.05±0.15	8.00±7.71	48.67**±5.13
D	0.06±0.06	0.03±0.08	-0.67±4.08	10.33**±2.49
[m]	0.55**±0.03	0.53**±0.03	18.67**±1.86	29.33**±0.88
[d]	-0.07**±0.02	0.03±0.04	0.67±1.70	-4.33*±1.76
[h]	-0.08±0.13	0.02±0.16	8.67±8.23	-19.00**±5.33
[i]	-0.12±0.12	-	1.33±8.17	-20.67**±4.99
[j]	-0.10**±0.03	-	-8.00**±1.79	-17.33**±1.89
[l]	0.38*±0.18	-	-10.67±10.28	-7.33±8.72
χ^2(3d.f)	20.40**	3.73	37.61**	218.24**
Type of interaction	D	-	D	C

*P≤0.05; and **P≤0.01

4.2.7 Green fodder yield per plant

The estimates of simple scaling tests A, B, C and D are given in Table 4.4. For this trait, Scale A was found to be significant for cross PLP-1 × *A.sterilis* which indicated [j] type of interaction and scale A,B,C and D were found to be non-significant in Kent × *A.sterilis*, indicated the absence of all types of interactions. The value of additive effect [d] was found to be significant for the cross Kent × *A.sterilis*. The opposite signs of [h] and [l] for PLP-1 × *A.sterilis* revealed the presence of duplicate type of epistasis. The non-significant values of A, B, C and D scaling test and also chi-square in cross Kent × *A.sterilis* indicated the fitting of additive-dominance model. The cross Kent × *A.sterilis* had

mainly additive genic effects for this trait as reported earlier by Solanki and Kishor (1979); Dwivedi *et al.* (1984) and Singh (1999). In both crosses, duplicate epistatic gene effect was observed for this trait as reported earlier by Kishor *et al.* (1992).

4.2.8 Dry matter per cent

The estimates of simple scaling tests A, B, C and D are given in Table 4.4. B, C, and D scaling tests were significant in cross PLP-1 × *A.sterilis* indicating the presence of all three types of interaction. In Kent × *A.sterilis* only B scaling test was significant indicating the presence of [j] type of interaction.

Table 4.4 Estimates of scaling tests and genic effects for green fodder yield per plant and dry matter percent in oat

Cross → / Parameters ↓	Green fodder yield per plant		Dry matter per cent	
	PLP-1 x *A. sterilis*	Kent x *A.sterilis*	PLP-1 x *A. sterilis*	Kent x *A. sterilis*
A	-41.67**±8.33	13.33±13.01	-2.03±3.34	-0.40±3.14
B	-10.00±25.17	-30.00±26.25	12.37**±2.91	4.03*±1.57
C	35.00±42.39	-16.67±29.67	-18.67*±7.04	-3.43±8.92
D	43.33±23.33	0.00±18.86	-14.50**±3.60	-3.53±4.34
[m]	180.00**±10.00	166.67**±6.67	20.13**±1.58	24.50**±2.1
[d]	-16.67±12.02	46.67**±13.33	-5.17**±1.74	2.53*±1.07
[h]	-65.83±47.19	-28.33±38.27	32.73**±7.37	7.88±8.80
[i]	-86.67±46.67	-	29.00**±7.21	7.07±8.67
[j]	-15.83±12.56	-	-7.20**±2.09	-2.22±1.67
[l]	138.33*±64.10	-	-39.33**±9.90	-10.70±9.90
χ^2(3d.f)	-	2.70	30.37**	7.88*
Type of interaction	D	-	D	D

*P≤0.05; and **P≤0.01

Additive effects [d] were negative and significant for cross PLP-1 × *A.sterilis* however positive and significant [d] was observed for cross Kent × *A.sterilis*. While dominance effect [h] were positive and significant in PLP-1 × *A.sterilis*. Opposite signs of [h] and [l] were present for cross PLP-1 × *A.sterilis* and Kent × *A.sterilis*. This indicated the presence of duplicate type of epistasis. The significant chi-square value in case of PLP-1 × *A.sterilis and* Kent × *A.sterilis* indicated the failure of additive-dominance model and presence of digenic and higher order interactions. These are the only source of genetic variation in this cross.

4.2.9 Dry matter yield per plant

The estimates of simple scaling tests A, B, C and D are given in Table 4.5. A and B scaling tests were significant in cross PLP-1 × *A. sterilis* indicating the presence of [j] type of interaction. In Kent × *A. sterilis* A, B, C and D scaling tests were non-significant indicating the absence of [i], [j] and [l] type of interactions. The chi-square values were significant for cross PLP-1 × *A. sterilis* while for the cross Kent × *A. sterilis* chi-square value was non-significant which indicated that additive-dominance model was adequate. Additive effect *i.e* [d] was significant and negative for cross PLP-1 × *A. sterilis* and significant and positive for Kent × *A. sterilis*. Dominance effect [h] was significant for PLP-1 × *A. sterilis*. Signs of [h] and [l] were in opposite directions in PLP-1 × *A.sterilis*, which indicated the presence of duplicate type of gene interaction thus suggested the use of biparental mating and recurrent selection for exploiting both fixable and non fixable gene effects for improving this trait. The cross PLP-1 × *A. sterilis* had mainly or predominantly positive genic effects as reported earlier by Akbar and Abdullah (1980); Bhandari (1974); Paroda *et al.*(1974); Dwivedi *et al.(*1984) and Singh *et al.* (1985) in oats.

4.2.10 Crude protein per cent

Scaling tests B and D were found to be significant for cross PLP-1 x *A. sterilis* indicated [i] and [j] type and A and C scaling tests were significant in Kent x *A. sterilis* indicated [j] and [l] type of interactions (Table 4.5). The significance of chi-square values for both the crosses revealed the inadequacy of additive-

dominance model. The values of additive gene effects [d] were found to be significant and positive for both the crosses. The values of dominance effect were significant and negative for cross PLP-1 x *A. sterilis*. Duplicate type of epistasis was observed in both crosses as the values of [h] and [l] attained opposite signs. It implies that improvement of crude protein per cent might be made by intermating among selected plants followed by selection in later generations. In cross PLP-1 x *A. sterilis* dominance genic effects were negative and significant along with some amount of positive additive genic effects as reported by Kishor *et al.* (1992).

Table 4.5 Estimates of scaling tests and genic effects for dry matter yield per plant and crude protein per cent in oat

Cross → / Parameters ↓	Dry matter yield per plant		Crude protein per cent	
	PLP-1 x *A. sterilis*	Kent x *A.sterilis*	PLP-1 x *A. sterilis*	Kent x *A. sterilis*
A	-14.59*±5.27	1.83±3.36	1.31±1.49	5.65**±0.50
B	15.37*±6.69	-1.23±6.85	-14.47**±0.80	-1.96±2.20
C	-25.99±13.90	-11.07±7.19	-1.57±2.88	2.27*±1.12
D	-13.38±7.36	-5.83±3.81	5.80**±1.53	-0.71±1.14
[m]	36.17**±3.23	41.07**±1.24	12.23**±0.67	12.54**±0.18
[d]	-11.88**±3.54	16.37**±2.90	7.21**±0.73	3.67**±1.08
[h]	38.15*±14.95	4.67±8.06	-8.62*±3.10	0.72±2.32
[i]	26.76±14.72	-	-11.59**±3.06	1.41±2.28
[j]	-14.98**±4.13	-	7.89**±0.79	3.80**±1.10
[l]	-27.53±19.84	-	24.75**±4.10	-5.10±4.45
χ^2(3d.f)	16.88**	4.84	367.26**	187.93**
Type of interaction	D	-	D	D

*P≤0.05; and **P≤0.01

4.2.11 Crude protein yield per plant

A, B and C scaling tests were significant in cross PLP-1 x *A. sterilis* and thus indicated the presence of all three [j] and [l] types of interactions (Table 4.6). In cross Kent x *A. Sterilis,* A and D scaling test were significant thereby indicated [i] and [j] type of interactions. Significance of chi-square for the crosses PLP-1 × *A.sterilis* and Kent × *A.sterilis* indicated the failure of additive- dominance model which suggested that the source of variation in these crosses for this trait is because of digenic or higher order interactions. The values of additive gene effects [d] were found to be significant and positive for Kent × *A.sterilis.* The opposite signs of [h] and [l] for both crosses revealed the presence of duplicate type of epistasis. The cross Kent × *A.sterilis* had appreciable amount of genic effects along with duplicate type of epistasis as indicated by opposite signs of [h] and [i]. Earlier workers also reported more or less same findings (Saron. 1974; Manga and Sidhu, 1979 and Saraswat, 1981).

4.2.12 Days to maturity

For days to maturity, scaling tests B, C and D were significant for PLP-1 x *A. Sterilis* and Kent x *A. sterilis* (Table 4.6). Significance of B, C and D tests showed the presence of [i], [j] and [l] type of non-allelic interactions. Additive effects [d] were significant in both the crosses. The dominance genic effects were significant and negative for both crosses. Opposite and significant signs of [h] and [l] components in PLP-1 x *A. Sterilis* and Kent x *A. sterilis* indicated the presence of duplicate epistasis. The significant chi-square values in both crosses indicated the failure of additive-dominance model and presence of digenic and higher order interactions. These are the only source of genetic variation in these crosses for this trait. Presence of dominance genic effect along with duplicate type of epistasis was observed for both crosses as recorded earlier by Akbar and Abdullah (1980).

Table 4.6 Estimates of scaling tests and genic effects for crude protein yield per plant and days to maturity in oat

Cross → / Parameters ↓	Crude protein yield per plant		Days to maturity	
	PLP-1 x *A. sterilis*	Kent x *A.sterilis*	PLP-1 x *A. sterilis*	Kent x *A. sterilis*
A	-3.31*±1.68	3.86**±1.17	-7.33±4.07	-7.00±3.99
B	-5.04**±0.46	-0.83±1.14	-30.00**±4.00	-13.00**±3.87
C	-4.14*±1.96	0.37±1.50	28.67**±6.74	20.00**±5.12
D	2.11±1.24	-1.33*±0.65	33.00**±3.54	20.00**±2.62
[m]	4.42**±0.47	5.15**±0.19	167.33**±1.33	159.33**±0.67
[d]	0.95±0.83	3.72**±0.52	24.33**±2.33	14.67**±2.26
[h]	-1.49±2.51	1.95±1.45	-49.00**±7.38	-26.67**±5.69
[i]	-4.21±2.49	2.67*±1.30	-66.00**±7.09	-40.00**±5.25
[j]	0.87±0.86	2.35**±0.81	11.33**±2.57	3.00±2.36
[l]	12.57**±3.84	-5.70**±2.56	103.33**±11.51	60.00**±10.39
χ^2(3d.f)	121.47**	25.56**	103.41**	65.39**
Type of interaction	D	D	D	D

*P≤0.05; and **P≤0.01

4.2.13 Seed yield per plant

Higher seed yield potential is the ultimate goal of any breeding programme but it cannot be achieved unless a good genotype with resistance to insect, pest and diseases is obtained otherwise it will achieve little or no success. The simple

scaling test in case of PLP-1 x *A. sterilis* revealed significance of C and D thereby indicating the presence of [i] and [l] type of interactions (Table 4.7). A,B,C and D scaling test were significant in case of cross Kent x *A. sterilis* thereby revealed the presence of [i], [j] and [l] type of interactions. The significant positive additive gene effects and significant negative dominance gene effects were seen in both the crosses. Duplicate type of gene action was observed in cross PLP-1 x *A. sterilis* and Kent x *A. sterilis*. The significant chi-square values in case of cross PLP-1 x *A. sterilis* and Kent x *A. sterilis* implied the presence of digenic or higher order interactions due to failure of additive-dominance model. For grain yield in oat earlier workers (Nijhwan *et al.* 1970; Kozlenko and Egarova, 1989 and Soldatov and Batalova, 1990) have also indicated the predominant role of dominance. For this trait in present study, mainly additive × additive non-allelic interaction genic effects were noticed in both crosses, as observed earlier by Lawrence and Frey (1976) and De koeyer and Stuthman (1998). However, additive gene effects for grain yield were also reported by Kuenzel (1982) and Cox (1983).

4.2.14 100 seed weight

For this trait, Scale B, C and D were found to be significant for cross PLP-1 x *A. sterilis* which indicated [i], [j], [l] type of interactions and scale B and D were found to be significant in Kent x *A. sterilis*, indicated [i] and [j] type of interactions (Table 4.7). The chi-square values for additive-dominance model were significant for both crosses indicating the presence of epistasis .The values of additive effect [d] was found to be significant and positive for cross PLP-1 x *A. sterilis*. The values of additive effect [d] were found to be significant and negative for cross Kent x *A. sterilis*. The significant negative dominance gene effects were seen in Kent x *A. sterilis*. The opposite signs of [h] and [l] for cross Kent x *A. sterilis* revealed the presence of duplicate type of epistasis while PLP-1 x *A. sterilis* showed complementary type of epistasis. For this trait in the present study, presence of additive genic effects were observed as reported earlier by Kozlenko and Egarova (1989) and Sood *et al.* (2006).

Table 4.7 Estimates of scaling tests and genic effects for seed yield per plant and 100 seed weight in oat

Cross → / Parameters ↓	Seed yield per plant		100 seed weight	
	PLP-1 x *A.sterilis*	Kent x *A. sterilis*	PLP-1 x *A. sterilis*	Kent x *A.sterilis*
A	0.23±2.43	-32.07**±2.07	-0.01±0.46	0.30±0.70
B	-2.29±2.46	-16.99**±1.95	-8.97**±0.56	-4.81**±0.51
C	93.23**±7.89	56.61**±5.81	-14.90**±1.13	-0.26±0.66
D	47.65**±3.63	52.84**±2.91	-2.96**±0.60	2.12**±0.37
[m]	58.26**±1.75	58.93**±1.35	2.32**±0.26	5.04**±0.05
[d]	19.29**±0.98	15.12**±1.09	1.21**±0.30	-0.79*±0.35
[h]	-100.05**±7.49	-95.40**±5.92	4.15**±1.22	-7.79**±0.80
[i]	-95.29**±7.26	-105.68**±5.83	5.91**±1.19	-4.25**±0.73
[j]	1.26±1.29	-7.54**±1.31	4.48**±0.35	2.56**±0.38
[l]	97.36**±8.82	154.75**±7.25	3.07±1.64	8.76**±1.56
χ^2(3d.f)	173.69**	500.87**	342.40**	123.99**
Type of interaction	D	D	C	D

*P≤0.05; and **P≤0.01

4.2.15 Harvest index

In case of cross PLP-1 x *A. sterilis*, the significance of B and C type of scaling tests indicated the presence of [j] and [l] type of interactions while C test confirmed significance in Kent x *A. sterilis* which indicated [l] type of interactions (Table 4.8). The chi-square values for additive-dominance model were significant for both crosses which indicated the presence of epistasis. The six parameter model showed that the values of [d] were negative and non-significant for both

crosses.Dominace effects [h] were also negative and non- significant for crosses PLP-1 x *A. sterilis* and Kent x *A. sterilis.* Same signs of [h] and [l] were present for cross PLP-1 × *A.sterilis* and Kent × *A.sterilis*. This indicated the presence of complementary type of epistasis.

Table 4.8 Estimates of scaling tests and genic effects for harvest index in oat

Cross → / Parameters ↓	PLP-1 x *A. sterilis*	Kent x *A. sterilis*
A	1.07±1.71	0.82±2.63
B	10.51**±2.81	4.99±2.11
C	11.41*±5.09	6.10*±3.40
D	-0.08±2.50	0.59±2.00
[m]	27.37**±1.09	27.19**±0.69
[d]	-0.51±1.22	-1.39±1.45
[h]	-0.60±5.16	-0.26±4.13
[i]	0.17±4.99	-1.19±4.01
[j]	-4.72**±1.48	-2.08±1.62
[l]	-11.76±7.05	-4.62±6.71
χ^2(3d.f)	16.33**	7.95*
Type of interaction	C	C

***P≤0.05; and **P≤0.01**

Table 4.9 Gene interactions for various traits in oat

Cross ⟶ /Character ↓	PLP-1 x *A. sterilis*	Kent x *A. sterilis*
Days to 50 per cent flowering	D	-
Plant height	C	C
Leaves per plant	D	-
Tillers per plant	C	-
Leaf:stem ratio	D	-
Flag leaf area	D	C
Green fodder yield per plant	D	D
Dry matter per cent	D	D
Dry matter yield per plant	D	-
Crude protein per cent	D	D
Crude protein yield per plant	D	D
Days to maturity	D	D
Seed yield per plant	D	D
100 seed weight	C	D
Harvest index	C	C

D- Duplicate Epistasis, C- Complementary Epistasis

4.3 Estimation of heterosis and Inbreeding depression

Manifestation of hybrid vigour in crop plants has been observed by Plant Breeders mainly in cross pollinated crops. But in self pollinated crops also hybrid vigour has been reported (Tandon 1980 and Gill 1987) and is being utilized commercially in many crops like rice etc.

The commercial exploitation of heterosis in crop plants is regarded as a major breakthrough in plant breeding especially in cross pollinated crops as compared to self pollinated crops where it has so far not been exploited much because artificial hybridization is cumbersome and unless some cytoplasmic male sterility system as in rice is available. Breeder's interest lies in hybrids only if they are superior to standard varieties. In the present study, some of the parents involved are also the standard varieties. Therefore, it will be desirable to compare the potentiality of these crosses in relation to the standard varieties also (Table 4.9). The estimates of heterosis and inbreeding depression for different traits are presented as below:

4.3.1 Days to 50 per cent flowering

Significant heterosis both over mid-parent and better parent was observed in both crosses. The cross combination PLP-1 x *A. sterilis* (3.12) exhibited the highest average heterosis. The cross PLP-1 x *A. sterilis* (5.88) also exhibited the highest heterobeltiosis. Non-significant negative heterosis over standard check in Kent x *A. sterilis* whereas non-significant positive heterosis in PLP-1 x *A.sterilis* was observed. The non-significant inbreeding vigour for days to 50 per cent flowering was found in both the crosses. Significant heterosis for days to 50 per cent flowering was found over mid-parent and better parent in PLP-1 x *A. sterilis* and Kent x *A. sterilis* as reported earlier by Mishra and Verma (1989).

4.3.2 Plant height

No significant positive heterosis both over mid-parent and better parent was observed in two crosses *viz.*, PLP-1 x A. *sterilis* and Kent x *A. sterilis.* Mishra and Verma (1989) and Akici and Ozgen (1991) also reported significant heterosis and heterobeltiosis. Significant negative heterosis over standard check was

observed in cross PLP-1 x *A. sterilis*. Non-significant negative heterosis over standard check was observed in cross Kent x *A. sterilis*. Non-significant inbreeding vigour for height was found in both crosses under study.

4.3.3 Leaves per plant

Significant and positive heterosis both over MP and BP was observed in PLP-1 x *A. sterilis*. In case of Kent x *A. sterilis* significant negative heterosis over BP was observed. The cross PLP-1 x *A. sterilis* exhibited the highest heterobeltiosis. Significant positive heterosis over standard check was observed in PLP-1 x *A. sterilis*. Highest heterosis was observed over standard check to the extent of 19.85 for cross PLP-1 x *A. sterilis*. Significant inbreeding vigour for leaves per plant was found in PLP-1 x *A. sterilis*.

4.3.4 Tillers per plant

Out of the two crosses, significant negative heterosis was observed in the cross Kent x *A. sterilis* over both MP and BP where as in PLP-1 x *A. sterilis* significant positive heterosis was observed both over MP and CV. The cross combination PLP-1 x *A. sterilis* (16.22) exhibited the highest average heterosis. The cross Kent x *A. sterilis* exhibited the highest heterobeltiosis. Significant inbreeding vigour for tillers was found in PLP-1 x *A. sterilis*. Mishra and Verma (1989) also observed significant heterosis for the above trait but he also observed non-significant heterobeltiosis for this trait.

4.3.5 Leaf: stem ratio

The non-significant positive heterosis both over MP and BP was observed in PLP-1 x *A. sterilis*. While significant positive heterosis over MP was observed in cross Kent x *A. sterilis*. Non-Significant heterosis over standard check was observed in both the crosses.

4.3.6 Flag leaf area

The significant positive heterosis was observed in PLP-1 x *A. sterilis* over MP. While significant negative heterosis over BP was observed in Kent x *A. sterilis*. Significant negative heterosis was observed over standard check to the extent of -16.90 in Kent x *A. sterilis*. Non-significant inbreeding depression was observed in both the crosses.

4.3.7 Green fodder yield per plant

The significant positive heterosis was observed in PLP-1 x *A. sterilis* over MP and BP. While significant negative heterosis was observed in Kent x *A. sterilis* over MP and BP. The significant positive heterosis over standard check was observed in PLP-1 x *A. sterilis*. Highest heterosis was observed over standard check to the extent of 13.54 in PLP- 1 x *A. sterilis*. Significant inbreeding vigour for green fodder yield was found in cross Kent x *A. sterilis*. Significant inbreeding vigour and inbreeding depression for green fodder yield per plant was found in both crosses. Tyagi *et al.* (1995), Babbar *et al.* (1997) and Dogra (2002) obtained the significant values of heterosis and heterobeltiosis for the same character.

4.3.8 Dry matter per cent

Significant heterosis over MP was observed in PLP-1 x *A. sterilis*. The cross combination PLP-1 x *A. sterilis* (16.22) exhibited the highest average heterosis. The non-significant positive heterosis over standard check was observed in both the crosses. Significant inbreeding vigour for dry matter percent was found only in case of PLP-1 x *A. sterilis*.

4.3.9 Dry matter yield per plant

Significant positive heterosis over MP and BP was observed in PLP-1 x *A. sterilis*. While significant negative heterosis was observed in Kent x *A. sterilis* over MP and BP. The cross combination PLP-1 x *A. sterilis* (30.82) exhibited the highest value of average heterosis. The significant positive heterosis over standard check was observed in PLP-1 x *A. sterilis*. Highest heterosis was observed over standard check to the extent of (20.70) in PLP-1 x *A. sterilis*. Significant inbreeding depression was observed in cross PLP-1 x *A. sterilis*. Babbar *et al.* (1997) and Dogra (2002) found significant positive heterosis and heterobeltiosis which is in accordance with the present findings.

4.3.10 Crude protein per cent

Significant positive heterosis over MP and BP was observed in PLP-1 x *A. sterilis*. Non-significant negative heterosis over MP and BP was observed in kent

x *A. sterilis*. The significant positive heterosis over standard check was observed in PLP-1 x *A. sterilis*. Significant inbreeding vigour for CP per cent was found in cross PLP-1 x *A. sterilis*.

4.3.11 Crude protein yield per plant

. The significant positive heterosis over MP and BP was observed in cross PLP-1 x *A. sterilis*. Significant negative heterosis over BP was observed in cross Kent x *A. sterilis*. The significant positive heterosis over standard check was observed PLP-1 x *A. sterilis*. The cross combination PLP-1 x *A. sterilis* (66.46) exhibited the highest value of average heterosis. Significant inbreeding vigour for crude protein yield was found for the cross PLP-1 x *A. sterilis*.

4.3.12 Days to maturity

Out of two crosses significant negative heterosis over standard check in Kent x *A. sterilis* was observed. Significant positive heterosis was observed in PLP-1 x *A. sterilis* over MP and BP. While significant positive heterosis over MP was observed in Kent x *A. sterilis*. The cross combination PLP-1 x *A. sterilis* exhibited the highest average heterosis and heterobeltiosis. The significant positive heterosis over standard check in PLP-1 x *A. sterilis* was observed. Non-significant inbreeding vigour for days to maturity was found in both crosses.

4.3.13 Seed yield per plant

The significant negative heterosis over MP and BP was observed in cross PLP-1 x *A. sterilis* whereas significant positive heterosis over MP and significant negative heterosis over BP was observed in Kent x *A. sterilis*. The cross Kent x *A. sterilis* exhibited the highest average heterosis. Significant negative heterosis over standard check was observed in both the crosses. Significant inbreeding vigour for seed yield per plant was found in both crosses *viz.*, PLP-1 x *A. sterilis* and Kent x *A. sterilis*. Cowen and Frey (1987) and Dogra (2002) also reported significant heterosis heterobeltiosis for this trait.

Table. 4.10 Estimates of Heterosis, Heterobeltiosis and Inbreeding depression for various characters in oat

E1	PLP-1 × *A. sterilis*				Kent × *A. sterilis*			
	MP	BP	CV	Inbreeding depression	MP	BP	CV	Inbreeding depression
Days to 50 per cent flowering	3.12**	5.88**	0.51	-0.25	2.65*	4.60**	-1.77	0.52
Plant height	-5.02*	-7.49*	-7.49**	-4.58	-8.58**	-9.85**	-4.55	-5.80
Leaves per plant	24.60**	19.85**	19.85**	11.47*	-2.81	-13.20*	5.34	7.97
Tillers per plant	16.22*	13.15	19.44*	20.93*	-9.33*	-20.93**	-5.58	2.94
Leaf : stem ratio	7.33	1.10	1.11	9.29	14.75*	7.36	-3.33	8.57
Flag leaf area	56.41**	-6.15	-6.15	8.20	10.20	-38.64**	-16.90*	-62.96
Green fodder yield per plant	12.95*	12.37*	13.54*	0.92	-15.32**	-25.40**	-2.08	6.38**
Dry matter percent	16.28*	6.81	6.81	24.50**	3.27	-13.24	3.20	4.92
Dry matter yield per plant	30.82**	20.70**	20.70*	25.21**	-14.80*	-35.12**	0.65	-1.82
Crude protein per cent	26.67**	19.41**	34.86**	13.30*	-5.65	-6.69	11.19	-7.88
Crude protein yield per plant	66.46**	63.08**	63.08**	35.16**	-13.31	-30.85*	12.44	-9.65
Days to maturity	11.21**	2.43**	2.43**	0.79	9.02**	1.05	-2.23**	1.04
Seed yield per plant	-12.75**	-41.16**	-41.16**	-78.86**	25.94**	-19.87**	-9.84**	-18.06**
100 seed weight	-25.45**	-49.38**	41.37**	55.10**	-51.54**	-67.41**	-8.77	-51.20**
Harvest index	-3.11	-17.11**	-17.11**	-13.43*	3.73	0.95	-10.99**	-4.95

***P≤0.05; and **P≤0.01**

MP- Mid-parent , BP- Better parent, CV- Check variety

4.3.14 100 seed weight

Significant negative heterosis over MP and BP was observed in both crosses *viz.,* PLP-1 x *A. sterilis* and Kent x *A. sterilis*. Significant positive heterosis over standard check was observed in PLP-1 x *A. sterilis*.Highest heterosis was observed over standard check to the extent of 41.37 in PLP-1 x *A. sterilis.* Significant inbreeding vigour for 100 seed weight was found both crosses. Akici and Ozgen (1991) also reported heterosis for 100 seed weight for this trait.

4.3.15 Harvest index

Significant negative heterosis over BP was observed in PLP-1 x *A. sterilis*. The cross PLP-1 x *A. sterilis* exhibited the highest heterobeltiosis. Significant negative heterosis over standard check was observed in both the crosses. Significant inbreeding vigour for harvest index was found in cross PLP-1 x *A. sterilis.* Cowen and Frey (1987) also found significant heterosis which is in accordance with the present findings.

The mean performance of two crosses for various traits and generations in oat is given in the Appendix I and II.

4.4 Inheritance of powdery mildew disease resistance in oat

Powdery mildew (*Erysiphe graminis* f. sp. *avenae*) is a major disease of oat. The fungus is an obligate parasite appearing as patches of white fluffy mycelium on the lower leaves and leaf sheaths. As the disease progresses, the patches become powdery and turn gray or brown.

In the present study, the segregation of resistant and susceptible plants in F_2 generation of cross PLP-1 x *A. sterilis*, revealed the good fit to 3:1 ratio. In cross PLP-1 × *A. sterilis* parent PLP-1 was resistance and parent *A. sterilis* was highly susceptible to powdery mildew disease. The segregation pattern studies indicated that the powdery mildew disease in oat is controlled by single dominant gene, and inherited in the ratio of 3:1.

Pathogen	F_1 (Phenotype)	F_2			
		R	S	Ratio	P<0.05
Erysiphe graminis* f.sp. *avenae	R	70	25	3:1	0.03

This confirms that single dominant gene is responsible for resistance against powdery mildew. The results of powdery mildew are in conformity with earlier workers Sebesta *et al.* (2000) and Yu and Herrmann (2006) who have also reported that inheritance of resistance was dominant and monogenic.

4.1 Powdery mildew infected plant of cross PLP-1 × *A.sterilis*

SUMMARY AND CONCLUSIONS

5. SUMMARY AND CONCLUSIONS

The present investigation entitled "Studies on gene effects for various forage and grain characteristics in oat " was undertaken to get the information on the nature and magnitude of gene action for seed yield and quality traits, and to study the inheritance of powdery mildew resistance. The investigation was carried out at the Experimental Farm of the Department of Crop Improvement, CSK HPKV Palampur.

The experimental material comprising P_1, P_2, F_1, F_2, BC_1 and BC_2 generations of two crosses *viz.*, PLP-1 x *A. sterilis* and Kent x *A. sterilis* was evaluated in Compact Family Randomized Block Design with three replications during *rabi* 2011-12. The observations were recorded on ten randomly taken plants per entry per replication in case of parents and F_1s, twenty- five in case of back crosses (BC_1 and BC_2) and fifty plants in case of F_2 generations. The data was analyzed by using simple scaling test given by Mather (1949) and Joint scaling test of Cavalli (1952), and the estimation of various genic effects by Jinks and Jones (1958).

For inheritance studies, separate experiment consisting of F_1, F_2 was raised. Inoculation of each plant was done from powdery mildew infected plants. The mode of inheritance was ascertained by applying chi-square test of goodness of fit.

The results of scaling tests revealed that additive-dominance model was fit in cross Kent x *A. sterilis* for days to 50% flowering, plant height, tillers per plant, leaves per plant, leaf: stem ratio, green fodder yield per plant, dry matter yield per plant which suggested the absence of epistasis in this cross. Dominance component was found to be predominant over additive component hence breeding strategy should be hybridization in above cross followed by deffering selection to later generations. The above model was a failure thereby indicating presence of non allelic interactions for remaining traits in this cross.

Complementary type of gene action was observed for plant height, tillers per plant, 100 seed weight, and harvest index in cross PLP-1 x *A. sterilis* and plant height, flag leaf area, harvest index in cross Kent x *A. sterilis*. Such type of gene action was not observed for remaining traits in both the crosses. The traits for which the above gene action was observed, the breeding strategy should be selection in early generation by adopting biparental matings for isolation of transgressive segregants.

Duplicate type of gene action was observed for days to 50% flowering, leaves per plant, leaf: stem ratio, flag leaf area, green fodder yield per plant, dry matter yield per plant, crude protein per cent, crude protein yield per plant, seed yield per plant, days to maturity, dry matter per cent in cross PLP-1 x *A. sterilis*; green fodder yield per plant, crude protein per cent, crude protein yield per plant, seed yield per plant, 100 seed weight, days to maturity, dry matter per cent in cross Kent x *A. sterilis*. Duplicate type of gene action was not observed for the remaining traits in both the crosses. The traits for which the above gene action was observed, the breeding strategy would be by growing large segregating populations and adopting biparental mating to get transgressive segregants in oat.

All the components of gene action *i.e.*, d, h, i, j and l in cross PLP-1 x *A. sterilis* and Kent x *A. sterilis* were found to be significant for crude protein per cent, days to maturity, dry matter per cent and seed yield per plant, 100-seed weight respectively. In addition significantly positive value of d and significantly negative value of [i] for the traits crude protein per cent, days to maturity in PLP-1 x *A. sterilis* and for seed yield per plant in Kent x *A. sterilis* were observed. This indicates negative alleles are dispersed in the parents for the inheritance of these traits which suggests that the selection should be delayed to later generations in oat.

Out of the two crosses PLP-1 x *A. sterilis* is the best cross. Therefore, the results obtained in the present investigation with respect to the above best cross for generation mean analysis suggested that both additive and dominance gene

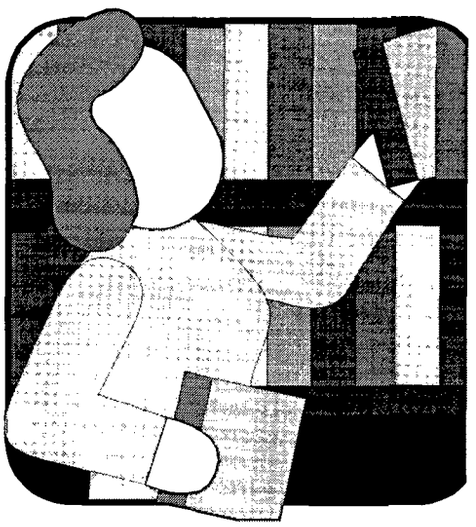
effects were important for most of the traits but dominance was predominant as compared to additive effects. Duplicate type of gene action was observed in the expression of days to 50% flowering, leaves per plant, leaf: stem ratio, flag leaf area, green fodder yield per plant, dry matter yield per plant, crude protein per cent, crude protein yield per plant, seed yield per plant, days to maturity, dry matter per cent for the above cross which implies the use of biparental approach and selection to be deferred to later generations. Complementary type of gene action was observed in plant height, tillers per plant, 100 seed weight, harvest index which implies the use of biparental approach and early generation selection.

Moreover, for cross PLP-1 x *A. sterilis*, additive x additive (i), additive x dominance (j) and dominance x dominance (l) interaction effects with duplicate nature are contributing in the inheritance of these traits *viz.,* Days to 50% flowering, crude protein per cent, days to maturity, dry matter per cent indicating recurrent selection could be employed for genetic improvement of these traits. The method is helpful in breaking up of undesirable linkages.

The results of this study demonstrated that gene effects obtained by generation mean analysis differed with genetic backgrounds of the crosses. There is an involvement of epistasis in genetic control of some of the traits studied in the present findings which revealed separate breeding strategies crosswise.

For powdery mildew the results obtained revealed that PLP-1 was resistant and *A. sterilis* was highly susceptible to powdery midew. The segregation pattern studies indicated that the powdery mildew disease in oat is controlled by single dominant gene, and inherited in the ratio of 3:1

Thus above study reveals that PLP-1 x *A. sterilis* was found to be the promising cross because of its crude protein yield per plant, green fodder yield per plant; early flowering and disease resistance among the two crosses studied and thus could be utilized in future breeding programme. The outcome of the present endeavour suggests different breeding strategy crosswise because of different gene actions in studied crosses.



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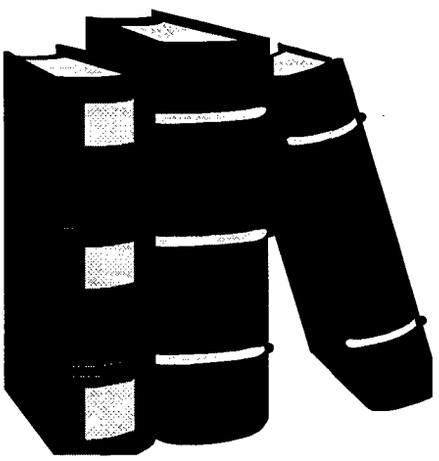

APPENDICES

Appendix I

Mean performance of cross PLP-1 x *Avena sterilis* for various traits in oat

Generations ↓	Days to 50 per cent flowering	Plant height (cm)	Leaves per plant	Tillers per plant	Leaf : stem ratio	Flag leaf area	Green fodder yield per plant	Dry matter percent
P1	131.33	102.33	43.67	12.00	0.60	21.67	160.00	24.97
P2	114.67	97.00	40.33	12.67	0.53	4.33	161.67	20.90
F1	132.00	94.67	52.33	14.33	0.61	20.33	181.67	26.67
F2	132.33	99.00	46.33	11.33	0.55	18.67	180.00	20.13
BC1	132.00	93.33	43.00	11.33	0.49	19.33	150.00	24.80
BC2	115.00	104.00	40.00	11.67	0.56	18.67	166.67	29.97

Generations ↓	Dry matter yield per plant	Crude protein percent	Crude protein yield per plant	Days to maturity	Seed yield/ plant (g)	100 Seed weight (g)	Harvest index (%)
P1	40.07	10.46	4.18	164.67	55.36	3.65	29.11
P2	33.87	11.81	4.01	138.67	19.31	10.19	20.70
F1	48.36	14.11	6.82	168.67	32.57	5.16	24.13
F2	36.17	12.23	4.42	167.33	58.26	2.32	27.37
BC1	36.92	12.94	3.84	163.00	44.08	4.40	27.15
BC2	48.80	8.73	2.89	138.67	24.79	3.19	27.67

Appendix II

Mean performance of cross Kent x *Avena sterilis* for various traits in oat

Generations ↓	Days to 50 per cent flowering	Plant height (cm)	Leaves per plant	Tillers per plant	Leaf : stem ratio	Flag leaf area	Green fodder yield per plant	Dry matter percent
P1	128.00	105.33	53.00	14.33	0.54	29.33	210.00	29.70
P2	113.33	108.33	41.67	10.67	0.47	3.33	160.00	20.20
F1	129.00	97.67	46.00	11.33	0.58	18.00	156.67	25.77
F2	128.33	103.33	42.33	11.00	0.53	29.33	166.67	24.50
BC1	126.67	110.67	47.67	12.33	0.54	22.00	190.00	27.53
[illegible]	114.67	100.00	38.00	10.67	0.50	26.33	143.33	25.00

Generations ↓	Dry matter yield per plant	Crude protein percent	Crude protein yield per plant	Days to maturity	Seed yield/ plant (g)	100 Seed weight (g)	Harvest index (%)
P1	62.17	12.19	6.80	159.33	62.29	3.53	25.67
P2	32.50	12.46	4.05	136.00	16.97	10.23	24.29
F1	40.33	11.63	4.70	161.00	49.91	3.33	25.91
F2	41.07	12.54	5.15	159.33	58.93	5.04	27.19
BC1	52.17	14.73	7.68	156.67	40.07	3.58	26.20
BC2	35.80	11.06	3.96	142.00	24.95	4.37	27.59

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B.Sc. Agri.	2010	COA, CSKHPKV, Palampur	7.62/10.00 O.G.P.A	1st	All Agril. Courses
M.Sc.(Ag)	2012	COA, CSKHPKV, Palampur	8.00/10.00 O.G.P.A	1st	Plant Breeding and Genetics