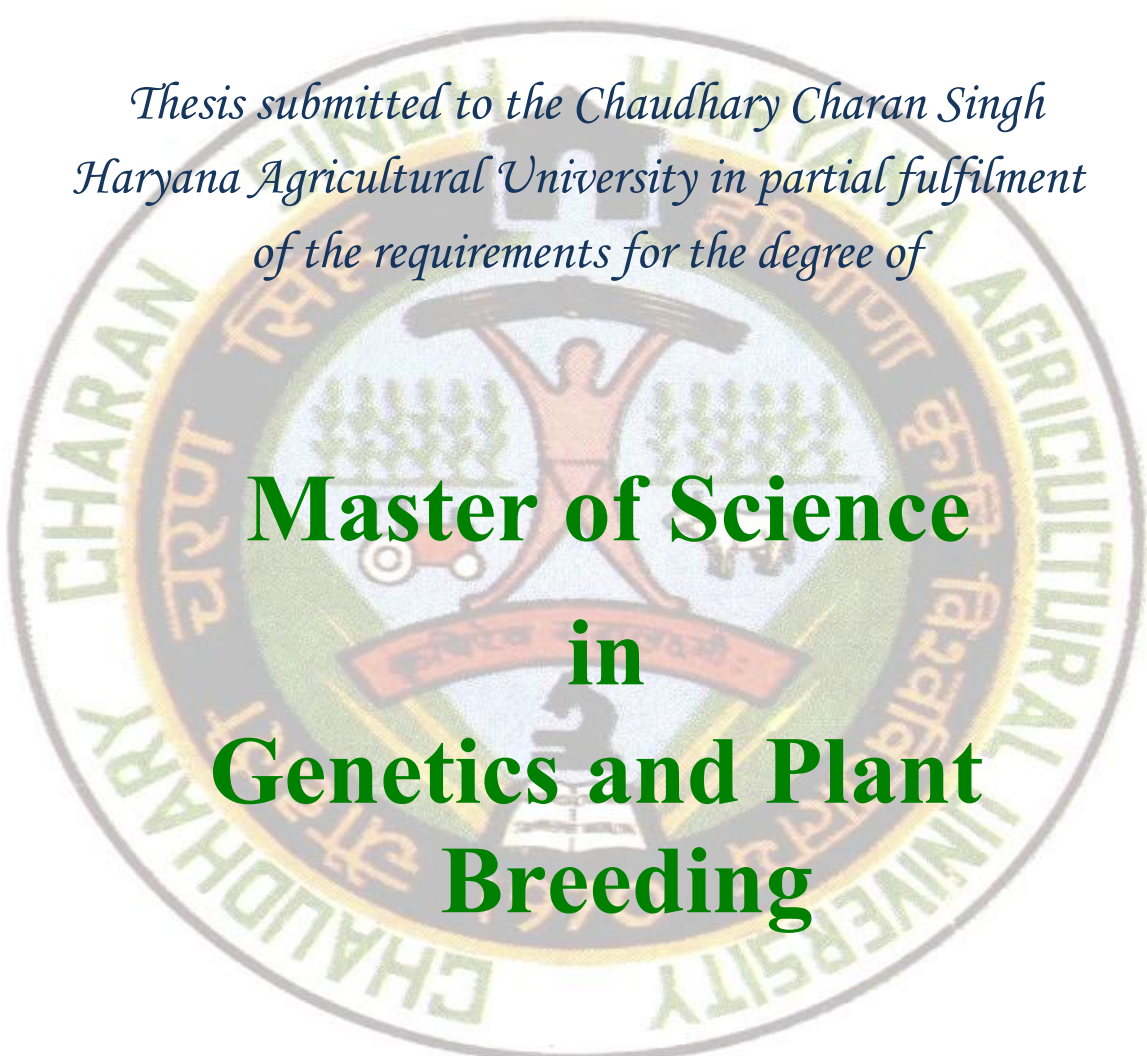


Evaluation of Oat (*Avena sativa* L.) genotypes for yield and quality characters

BY
ATMAN POONIA
(2015A71M)

*Thesis submitted to the Chaudhary Charan Singh
Haryana Agricultural University in partial fulfilment
of the requirements for the degree of*

The seal of Chaudhary Charan Singh Haryana Agricultural University is a circular emblem. It features a central figure of a person holding a sickle, with a banner below it. The text 'CHAUDHARY CHARAN SINGH HARYANA AGRICULTURAL UNIVERSITY' is written around the perimeter. In the center, there is a smaller emblem with a book and a torch.

Master of Science in Genetics and Plant Breeding

**COLLEGE OF AGRICULTURE
CCS HARYANA AGRICULTURAL UNIVERSITY
HISAR - 125004 (HARYANA)**

2017

CERTIFICATE - I

This is to certify that this thesis entitled, “**Evaluation of Oat (*Avena sativa* L.) genotypes for yield and quality characters**” submitted for the degree of **Master of Science** in the subject of **Genetics and Plant Breeding** from Chaudhary Charan Singh Haryana Agricultural University, Hisar, is a bonafide research work carried out by **Mr. Atman Poonia** 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.

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CERTIFICATE - II

This is to certify that this thesis entitled, “**Evaluation of Oat (*Avena sativa* L.) genotypes for yield and quality characters**” submitted by **Mr. Atman Poonia** to the Chaudhary Charan Singh Haryana Agricultural University, Hisar, in partial fulfilment of the requirements for the degree of **Master of Science** in the subject of **Genetics and Plant Breeding** has been approved by the Student’s Advisory Committee after an oral examination on the same.

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Hisar

May, 2017

(Atman Poonia)

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ABBREVIATIONS

- Plant height (cm) - PH
- Number of days to 50% flowering - DF
- Number of days to maturity - DM
- Flag leaf length (cm) - FLL
- Internode length (cm) - IL
- Number of Tillers/plant - TPL
- Peduncle length (cm) - PL
- Axis length - AL
- No. of Spikelets /panicle - NOS
- Seed yield (g)- SY
- 100-Seed weight (g) - SI
- Leaf length (cm) - LL
- Leaf width (cm) - LW
- Green fodder yield (kg) - GFY
- Dry matter yield (kg) - DMY
- No. of leaves/plant - NOLS
- Germination - GP
- Seedling length (cm) - SL
- Seedling dry weight (mg) - SDW
- Seed vigour index I - SVI
- Seed vigour index II - SVII
- Forage Crude Protein (%) in single cut– CP(F)
- Forage Crude Protein (%) at 1st cut of multicut – CPM
- Forage Crude Protein (%) at 2nd cut of multicut– CPMC
- Seed Crude Protein(%) – CP(G)
- Electrical conductivity (dS/m/seed)- EC
- Gram – g
- Kilogram – kg
- Percentage--%
- Centi meter--cm

CHAPTER - I

INTRODUCTION

Oat (*Avena sativa* L.) is an important winter cereal crop in the world used as food, feed and fodder. It belongs to the family Poaceae & ranks sixth in the world cereal production following wheat, maize, rice, barley and sorghum. The bulk of the oats produced in the world are used extensively as feed for livestock (cattle, sheep, poultry and horses). Only 17% of the world production (grain) is used as human food. It is considered to be a valuable component in agriculture as oat reduces disease pressure in cereal crop rotations and is therefore highly suited for sustaining, extensive production systems. Oat is a dual purpose crop of temperate and subtropical areas. Being a highly nutritious cereal, especially rich in fat, protein, vit B₁, phosphorous and iron. It is used for human consumption as well as for poultry, dairy cattle and other animals. Livestock feeding is the main use of oat forage. Oat forage (whole crop green oats) may be grazed by cattle, can be converted into hay and silage for further use of animals. Oat fodder is mostly fed as green and surplus is converted into silage or hay for further use during fodder deficit period (Suttie and Reynolds, 2004). It is preferred feed of all animals and its straw is soft and superior to wheat and barley.

Oat is a self pollinated hexaploid crop ($2n= 6x=42$) with basic chromosome number $x= 7$ having genomic constitution of AACCCDD (Rines *et al.* 2006). The genus *Avena* is very large and diverse and includes diploid and tetraploid species. Oat is thought to be originated in Asia Minor (Gibson and Benson, 2002). The cultivated oat is derived from another hexaploid species *Avena sterilis*. It is corroborated by the fact that the hybrid between them is fully fertile. The genus *Avena* comprises about 70 species; a few are cultivated. *Avena sativa* L. and *Avena byzantina* K sometimes known as white oat and red oat, respectively, are the main oats grown for fodder and grain. They are hexaploids and modern cultivars may contain genetic material from both these species. *Avena strigosa*, the bristle-pointed oat or black oat, is a diploid. Recently, *A. strigosa* has become very important in subtropical and temperate situations as a winter cover crop and a forage crop. The diploid *A. strigosa* Schreb ($2n=14$) is hulled, but also has a naked type. There is also a diploid naked oat, *A. nuda* L. ($2n=14$), but it is not commonly cultivated. Oats belongs to the genus *Avena* established by Tournefort, a French explorer and botanist, and is classified as, Phylum-Spermatophyta, Sub-class-Monocotyledons, Family-Gramineae, Tribe-Aveneae. There are two division of the genus *Avena*, annuals and perennials. Predominantly two species *i.e.*, (*Avena sativa* L.) and (*Avena byzantina* C.) are cultivated in the world. Of these two *Avena sativa* L. is most important, contributing over 80 per cent of the total world acreage.

Fodder oat is used as a multipurpose crop worldwide. They are usually winter sown, grazed prior to stem elongation and taken to maturity for use as feed and/or milling grains.

Multiple cuts are usually taken, after which part or all of the crop may be saved for seed. Oat has adequate soluble carbohydrates and fibres (Peterson *et al.* 2005). Oat provides one of the richest sources of the dietary soluble fibre beta-glucan, providing 5.0 g (oatmeal) to 7.2 g (oat bran) per 100 g serving (Glore *et al.* 1994). Nutrition experts believe that beta-glucan, inhibit cholesterol build up and hence help in the prevention of heart disease (Whitehead *et al.* 2014). Oat have assumed considerable importance in India as fodder as well as grain for animal feed particularly calves and young stock, horses, poultry and sheep. On dairy farms oat fodder is a must, as it can be fed green and the surplus converted into silage or hay for use during the scarcity period.

Oat is basically a European and North American crop. It is best grown in temperate regions of the world as they are winter hardy in nature. Oat requires cool and moist climate. The total area, production and productivity of oat during 2015 were about 9.58 million hectares, 22.60 million metric tons and 2.36 metric tons per hectare, respectively in the world (USDA, 2016). European Union is the largest producer of oat followed by Russian Federation, Canada, USA and Australia (USDA, 2016). Europe accounts for 64.2% of total oat produced in the world (FAOSTAT, 2015). In India, oat is grown on 100,000 hectares of area with productivity of 35-40 tonnes of green fodder per hectare. In India, it is mainly grown in *rabi* season mostly for fodder in U.P, Punjab, Bihar, Haryana and M.P. (Anonymous, 2014).

Livestock is a vital subsector of agriculture in India, with a large bovine population which includes 155.3 million cattle and 108.7 million buffaloes (National Dairy Development Board, 2016). India supports 20% of the livestock population of the world on 2.3% geographical area only (Tonapi *et al.* 2011). Livestock provides milk, butter and other products of animal origin for human nutrition. Despite this large bovine population, the scenario of milk production and productivity is far below the world's average. At present, the country faces a net deficit of 63% green fodder, 24% dry crop residues and 64% feeds (Kumar *et al.* 2012).

Availability of good quality forage along with sufficient quantity is essential to maintain high level of milk and meat production. Oat forms an exceptional fodder crop because of its excellent growth habit, quick regeneration ability, high palatability, succulence and high nutritive value for both milch and draft animals. It has gained importance due to its multi-cut nature and quick regeneration habit which ensures regular supply of green fodder over a period of time. It forms an excellent combination when fed along with cold season legumes like berseem or Egyptian clover, alfalfa, Indian clover, Persian clover and pea (Nadeem *et al.* 2010). It has dry matter digestibility in excess of 75% (Burgess *et al.* 1972). Oat has adequate soluble carbohydrate to make good silage. Oat straw is soft and is used as bedding material due to its dust free and absorbent nature. In dairy farms, oat as a fodder is

inevitably adopted, as it can be fed green and surplus converted into silage and hay for use during lean period. A large number of varieties are being grown by the farmers all over the country based on local preferences and agro-climatic conditions. Each of the variety differs from other varieties in one or more specific characteristics. These characteristics may be morphological or physiological in nature. The work on cultivar breeding has also become of paramount importance. Genetic improvement of a crop depends upon the extent and magnitude of genetic variability present in the economic characters.

The first step in breeding programme is to determine the amount of variation that is present in the characters of agronomic importance within large collection of material in order to define the valuable populations to be considered further. Assessment of the genetic variability can be achieved using morphological measurements and phenotypic characterization (Greene *et al.* 2008). Genetic diversity arises due to geographical separation or due to genetic barriers to cross ability or due to different patterns of evolution. Several workers have emphasized the need of parental diversity in optimum magnitude to obtain superior genotypes in the segregating generations. To measure this extent of diversity, the idea of D^2 statistics was used to measure group distance based on multiple characters. It was originally developed by Mahalanobis (1928) and it has become one of the important techniques to assess genetic divergence on the basis of multiple traits. Rao (1952) suggested the application of these techniques for the assessment of genetic diversity in plant breeding.

Introduction, hybridization and mutation are methods for creating variability in the population. Introduction does not create variability Mutation no doubt is one of the important agencies of creating variability but surity and direction of variability are not definite. Hybridization is the most potent method of creating variability. The pre-requisite of any breeding programme is the evaluation of existing genetic stock. The success of a systematic breeding programme depends mainly on judicious selection of promising parents from the gene pool. Which depends upon the knowledge regarding the nature and magnitude of gene effects of various characters. Therefore the coefficient of variability, genetic diversity, heritability and genetic advance which help the breeders in deciding the appropriate breeding procedures to increase the genetic potentialities as well as to make a dent in the yield barrier were carried out.

Therefore, present investigation, **“Evaluation of Oat (*Avena sativa* L.) genotypes for yield and quality characters”** has been under taken to evaluate the germplasm with following objectives:-

1. To determine variability parameters in oat genotypes for morphological & yield traits
2. To estimate the genetic diversity of oat genotypes for various yield & quality traits
3. To estimate the association between yield & quality traits

CHAPTER-II

REVIEW OF LITERATURE

Evaluation refers to the agronomic description of the genotypes, for the traits, that are generally crucial to breeders and researchers in crop improvement. Germplasm evaluation, in the broad sense and in the context of genetic resources, is the description of the material in a collection. It covers the whole range of activities starting from the receipt of the new samples by the curator and growing these for seed increase, characterization and preliminary evaluation, and also for further or detailed evaluation and documentation. It is needed to understand the genetic relationship among the genotypes so that they may be deployed effectively in oat breeding programme. So it is crucial for varietal improvement and development, identification and release. Genetic diversity or variation is the main ingredient in every breeding programme. Genetic diversity assessment is important to identify and evaluate potential genotypes for further use in the breeding programmes.

A limited number of studies have been conducted to evaluate different oat species in India and abroad. A brief account of research work done on these aspects is being reviewed as under:

- 2.1 Genetic variability
- 2.2 Heritability and Genetic advance
- 2.3 Correlation analysis
- 2.4 Genetic divergence analysis
- 2.5 Principal component analysis

2.1 Genetic variability

Availability of genetic variability is the rule of nature and is prerequisite for guiding a breeder to look forward for improving crop varieties. Whole breeding pursuit related to creation and management of genetic variability. It is inherent and not changed by environmental conditions. A brief review of work done in India and abroad on above aspect in oat is given below:

Bind *et al.*, (2016) studied 30 diverse genotypes of oat and observed 11 quantitative traits. High estimates of heritability (broad sense) were obtained for all the characters. The magnitude of PCV as expected was more than the corresponding GCV for all the characters indicating importance of environment in expression of characters.

Shekhawat and Jaipal (2016) studied genetic variability for grain and fodder production in thirty genotypes of oats and found that Analysis of variance indicated that sufficient amount of genetic variability was present among the genotypes for all characters.

High heritability with high genetic advance was observed for tillers per metre row length and green fodder yield (q/ha).

Surje *et al.*, (2014) studied 15 oat genotypes and estimated the mean performance of yield and other morpho-physiological characters. This reveals that the genotype NDO-609 produced the highest and significantly higher mean for green forage yield, and dry matter yield. The mean values for different characters of cut and uncut management of oat genotype Kent and JHO-99-2 had highest total grain yield per plant and number of grains per panicle.

Chakraborty *et al.* (2014) observed high GCV, PCV, heritability along with genetic advance for green fodder yield, dry fodder yield, seed yield per plant, spikelets per panicle, flag leaf width, peduncle length and reducing sugar.

Dubey *et al.*, (2014) estimated Genetic variability among 34 genotypes of M6 generation were derived from oat genotypes (Kent and JO-1). They found High phenotypic and genotypic coefficient of variation for crude protein yield followed by leaf area, total green fodder yield and total dry matter yield which indicated the presence of high amount of variation for these characters.

Khan *et al.* (2014) conducted an experiment to compare the forage yield and quality of ten oat (*Avena sativa* L.) genotypes. They showed that varieties were differed significantly ($P \leq 0.05$) in yield, growth and quality parameters.

Sofi *et al.* (2014) studied variability parameters and revealed that the range of variation was high in traits like seed yield/ha, seed breadth, tillers/meter², seed length and green fodder yield as indicated by higher values of Coefficient of Variation. The PCV and GCV values were higher for all traits except days to maturity. In all cases the PCV values were higher than their corresponding values of GCV understandably due to influence of environment on these traits.

Arora (2013) characterized and evaluated 108 germplasm accessions of oat under one harvest and two harvest systems separately for various morphological traits. Wide range of genetic variability was recorded for green fodder yield per metre row (650-1850 g) and for dry matter yield per metre row (60-180 g) in one harvest.

Kapoor *et al.* (2013) studied forty F₁ hybrids, obtained by crossing eight lines and five testers selected from oat germplasm. Analysis revealed significant gca and sca mean squares for most of the traits.

Bibi *et al.* (2012) characterized and evaluated 180 accessions of oats (*Avena sativa* L.) for green fodder yield. The highest values of genotypic variance, phenotypic variance, genotypic and phenotypic coefficients of variation were recorded for number of tillers per meter row while lowest for number of leaves per plant.

Sangwan *et al.* (2012) conducted study on variability and character association in fodder oat. The results revealed that the magnitude of genotypic and phenotypic coefficient of variation was moderate for dry mater yield, number of tiller/m and green fodder yield.

Shehzad *et al.* (2011) performed an experiment to compare the forage yield and quality of oat (*Avena sativa* L.). Varieties differed significantly ($P < 0.05$) for yield, growth and quality parameters.

Singh *et al.* (2011) evaluated 70 oat genotypes and concluded that high phenotypic and genotypic coefficient of variation coupled with high heritability and genetic advance as (%) of mean were reported for green fodder productivity, plant height, tillers/plant, dry matter yield and green fodder yield.

Bahadur *et al.*, (2008) reported the extent of variability and genetic diversity on oat for various fodder yield and quality traits and considerable variability for all the characters was found. The magnitude of genotypic coefficient of variation (GCV) was quite close to the estimates of phenotypic coefficient of variation (PCV) for almost all the traits.

Kumar *et al.* (2007) reported highly significant differences among the genotypes for all traits and also recorded high estimates of coefficient of variation for number of tillers, flag leaf length, green fodder yield, number of leaves, longest internode length, number of spikelets per panicle, seed yield per panicle, peduncle length, number of nodes on the main stem and dry matter yield.

Vishwakarma *et al.* (2007) reported that a wide range of variability existed for the various forage yield characters studied. High GCV and PCV was observed for green forage, grain yield per plant, number of tillers, number of grain/panicle and plant height.

Mall *et al.* (2005) evaluated forty eight oats genotypes for genetic variations, heritability and genetic advance for ten characters. High genotypic and phenotypic coefficients of variation were observed for dry matter yield plant⁻¹, green fodder plant⁻¹ and harvest index.

Pundir *et al.* (2003) observed that attribute like GFY per plant and leaf breadth had the maximum and minimum genotypic and phenotypic coefficients of variation, respectively.

Shankar *et al.* (2002) evaluated genotypes of oat for genetic variability and estimated inter-relationship among various desirable characters. High estimates of genotypic and phenotypic coefficient of variation (GCV and PCV respectively) were observed green fodder yield, dry matter yield, number of grains/panicle, 1000 grain weight, and grain yield.

2.2 Heritability and Genetic advance

Heritability estimation along with genetic advance is very crucial in predicting the grain under selection. Heritability is a property not only of characters but also of the environmental circumstances to which the individuals are subjected. Since the value of

heritability depends on the magnitude of all the components of the genetic and environmental variances a change in any one of these will affect heritability. Fisher (1918) reported the relative importance of genetic and environmental variances, Lush (1940) coined the term broad sense heritability for the genetic variance to total variance.

Genetic advance denotes the improvement in the genetic value of selected single plants over the base population. High heritability along with high genetic advance indicated that improvement could be effective by simple phenotypic performance.

A brief account of review work on Heritability and Genetic advance estimates for various morphological characters is being reviewed as under:

Bind *et al.*, (2016) studied 30 diverse genotypes of oat and observed that high heritability coupled with high genetic advance as *per cent* of mean for seeds per panicle, dry matter yield per plant, green fodder yield per plant and harvest index which suggests that these four traits might be under control of additive gene effects and therefore they are more reliable for effective selection.

Shekhawat and Jaipal (2016) reported high heritability with high genetic advance for tillers per metre row length and green fodder yield (q/ha).

Surje *et al.*, (2014) studied 15 oat genotypes and estimated the green forage and grain yield and observed high heritability, genetic advance along with genetic gain as a *per cent* of mean for the characters like number of grains per panicle, grain yield per plant, crude protein content and weight of flag leaf.

Chakraborty *et al.* (2014) estimated high of heritability along with genetic advance for green fodder yield, dry fodder yield, seed yield per plant, spikelets per panicle, flag leaf width, peduncle length and reducing sugar.

Dubey *et al.*, (2014) studied 34 genotypes of M6 generation derived from oat genotypes Kent and JO-1. They revealed that high values of heritability coupled with high expected genetic advance were observed for the characters like, leaf area and axis length indicating the scope for selection.

Sofi *et al.* (2014) studied heritability and genetic gain for green fodder yield/ha, plant height and tillers/meter², seed yield/ha, seed breadth, 1000-seed weight and seed length. Since these traits have high GCV, heritability and genetic gain, these can be utilized for seeking improvement in green fodder and seed yield.

Ahmed *et al.* (2013) assessed seventy-five germplasm lines of oat for 10 morphological traits to determine the interrelationships and effects among fodder and grain yield traits of oat. Days to percent flowering, plant height, number of spikelets/panicle, leaf width and green fodder yield showed high heritability and genetic advance.

Bibi *et al.* (2012) studied 180 accessions of oat for green fodder yield and found high heritability (broad sense) for almost all the traits studied *viz.*, number of tillers, days to 50%

flowering, days to 50% maturity, plant height, intermodal length, leaf area, number of leaves, green fodder yield and dry matter yield, indicating that selection of high fodder yielding oat genotypes would be helpful for further improvement of fodder yield.

Pundir *et al.* (2007) observed high heritability accompanied by high genetic advance for green fodder yield, dry fodder yield, number of leaves per plant, leaf length, leaf breadth, green leaf weight and dry leaf weight indicating the effectiveness of simple selection for the improvement of these traits.

Gautam *et al.* (2006) reported high heritability coupled with high genetic advance for green fodder yield, leaf:stem ratio, grain yield, tillers per plant and flag leaf length in forage oat.

Shekhawat *et al.* (2006) studied 69 genotypes of oats for green fodder yield and eleven related characters 30.5 to 74.9 *per cent* for heritability (broad sense) and 8.4 to 46.8 *per cent* for genetic advance (as % of mean) was found. The heritability was maximum (74.9%) for days to 50 *per cent* panicle emergence and the genetic advance as *per cent* of mean was maximum (46.8%) for leaf: stem ratio.

Mall *et al.* (2005) observed high broad sense heritability coupled with high genetic advance for dry matter yield per plant, green fodder yield per plant, harvest index, number of grains per panicle, number of tillers per plant, biological yield per plant and grain yield per plant, whereas, low heritability coupled with low genetic advance was observed for 1000-grain weight indicating that the environment highly affected this character.

Bertan *et al.* (2004) determined the genotypic gain through selection in segregating generations of oat. Data were recorded for vegetative cycle, stature of plant, weight of panicle, number of grains per panicle, average weight of grains and percentage of caryopses in white oat crosses.

Pundir *et al.* (2003) studied thirty-six diverse genotypes of oat for variation in terms of forage characters and results revealed that high heritability estimates with high genetic advance for green and dry fodder yield, number of leaves per plant, leaf length and leaf breadth.

Shankar *et al.* (2002) studied the variability in forage oats and observed the inter-relationship between various desirable characters. They observed high heritability estimates associated with greater genetic advance (as *per cent* of mean) for green fodder yield, dry matter yield, number of grains per plant, 1000-grain weight and grain yield.

Mittelman *et al.* (2001) evaluated eight crosses among oat lines to estimate heritability and to verify the effect of selection for plant height and heading date.

2.3 Correlation analysis

Krishna *et al.* (2014) evaluated fifty genotypes of fodder oat (*Avena sativa* L.) to measure the correlation, path and diversity. Path coefficient analyses determine maximum positive direct effect on green fodder yield was contributed by leaf stem ratio, dry matter, spike length and number of spikelets per panicle. However indirect effect on improvement in green fodder yield was exerted by most of the traits studied. So a direct selection for all these traits will helps in improvement of green fodder yield. Green fodder yield was positively correlated with most of the traits studied except number of leaves and stem girth. Among different traits, plant height and leaf length showed positive correlation with most of the traits studied.

Sofi *et al.* (2014) reported that green fodder yield/ha was highly correlated with plant height and tillers/meter², while seed yield/ha had significant positive correlation with seed breadth, 1000-seed weight, plant height and seed length.

Surje and De (2014) studied the green forage and grain yield of fifteen oat genotypes under two different modes; one to determine the yield when the crop is subjected to one cut as fodder and then left to regenerate and produce seed and the other to produce seed only without taking any cut. The grain yield per plant exhibited significant positive correlation with plant height, tiller number per plant, length of panicle, number of spikelet per panicle in both cut and uncut managements. Besides, in the uncut management, number of grain per panicle, chlorophyll b content and total chlorophyll content also showed significant positive correlation.

Ahmed *et al.* (2013) reported that grain yield was found to be positively correlated with days to 50 percent flowering, plant height, number of leaves/plant, leaf length, leaf width, leaf/stem ratio and green fodder yield. For fodder yield, leaf length had maximum positive direct effect followed by number of leaves/plant and plant height. The high positive correlation between fodder yield and days to 50 percent flowering, plant height, number of spikelets/panicle, leaf/stem ratio was obtained mainly through indirect effect via number of leaves/plant, leaf length and leaf width.

Bahadur *et al* (2008) observed the genotypic correlations were higher than their corresponding phenotypic correlation. The characters green and dry fodder yield were positively and significantly correlated with plant height, stem diameter, number of leaves/plant, leaf length and leaf breadth.

Lorencetti *et al.* (2006) reported that the number of panicles per plant (NPP) expressed highest correlation with individual plant grain yield (GY) both through single correlations and through direct effects on grain yields.

Kumar *et al.*, (2004) reported that plant height was found significantly and positively correlated with all the characters. The number of leaves and tillers per plant were positively correlated with plant height, number of nodes on main stem and dry matter yield, and negatively associated with flag leaf length and width. Green fodder yield per plant was found to be strongly and positively correlated with plant height, number of leaves and number of tillers per plant, flag leaf length and width, stem thickness and dry matter yield per plant.

Kurek *et al.* (2002) revealed that coefficients of phenotypic correlation were significant and high between panicle weight and grain per panicle.

Ziya *et al.*, (2001) reported that grain yield was negatively correlated with plant height. The effects of these traits were higher than those of 1000 grain weight and grain number per panicle.

2.4 Genetic Divergence

In plant breeding programmes, assessment of the genetic diversity is done by the D^2 statistics devised by Mahalanobis in 1928. Now this technique is extensively used in variability related plant breeding studies. This is one of the patent techniques of measuring genetic divergence. Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding. Genetic diversity plays a very important role, because hybrids derived from lines of diverse origin, generally display a greater heterosis compared to closely related parents.

Kumar *et al.* (2016) studied genetic diversity among 50 genotypes using Mahalanobis D^2 statistics for 16 characters. Based on the D^2 values, all genotypes were grouped into seven clusters depending upon the similarity in the expression of their genetic divergence. Maximum numbers of genotypes were grouped in cluster VI (12) followed by cluster IV (11), I (9), II (8), III (4) and clusters V and VII had three genotypes each. The highest intra cluster D^2 value was observed for cluster V (5.304) followed by cluster I (5.174), cluster III (5.054), cluster VI (4.771), cluster II (4.470), cluster VII (4.501) and cluster IV (4.104). The average inter cluster distance was found to be highest between cluster V and VII (8.558), cluster III and V (7.165), cluster III and VI (5.919) whereas the lower inter-cluster distance was observed between clusters II and IV (5.075), followed by clusters IV and VI (5.328).

Krishna *et al.* (2014) grouped the 50 genotypes of oat into ten clusters based on distance ranges. Cluster I includes 37 numbers of lines, Cluster IV and IX includes three lines and Cluster II, III, V, VI, VII, VIII and X included one line in each. The cluster with higher number of lines means that low genetic diversity among the lines and they are more closely related. The inter-cluster distances were higher than intra-cluster distances suggesting presence of high genetic diversity between lines of any two clusters than the lines present within the cluster.

Ahmed *et al.* (2011) computed 75 genotypes of oat into 9 characters. Cluster IV consisted of 21 lines, cluster I & II had 20 lines each, cluster V had 9 lines. Highest intra cluster distance was observed for cluster IV followed by cluster II, I and V. The maximum inter cluster distance was observed between cluster VI & IX, followed by cluster IV & IX, cluster III & IX suggesting diversity among lines of these clusters. Cluster IV is characterized by lines having prominent traits like high green fodder yield, high grain yield, tall plants, long and broad leaves.

Yadav *et al.* (2011) observed genetic diversity among thirty six genotypes using Mahalanobis D^2 statistics in oat. These genotypes were grouped in to 11 clusters based on the similarity in the expression of their genetic divergence. Cluster I had the largest number i.e., 9 genotypes followed by cluster II, III and IV which consisted 5 genotypes. Each cluster VII had highest mean values for green fodder yield/plant and plant height VI had highest mean values for days to 50% flowering and plant height, the cluster VII had highest mean values for days to 50 percent flowering and plant height (cm).

Bahadur and Choubey (2009) formed eight clusters based on D^2 values. Clustering pattern was random and independent. The intra-cluster distance varied from 0.0 to 34.5 and 0.0 to 35.4, whereas inter-cluster distance varied from 55.0 to 1014.8 and 40.2 to 998.6 under normal late sown conditions, respectively. Diverse genotypes from varies clusters could be utilized in hybridization programme to create desired variability in forage oat.

Singh and Singh (2011) grouped 70 oat genotypes on the basis of D^2 analysis were into seven clusters and two ungrouped clusters. Cluster I was the largest and contained 16 genotypes.

Mehta *et al.* (2008) studied fifty-seven genotypes of oat evaluated for 11 characters were grouped in eight clusters. The cluster II had 16, while the cluster V had one genotype. The contribution of days to 50% flowering towards genetic divergence was 27.1% followed by tillers per plant (20.3%), leaf stem ratio (14.9%), panicle length (11.2%), crude protein content (7.9%), leaf width (4.2%), dry matter yield (4.1%), green fodder yield (3.9%), plant height (3.1%), leaf length (1.9%), and stem diameter (1.2%).

Kumar *et al.* (2007) studied hierarchical cluster analysis and classified the genotypes into 9 clusters, each containing between one and 20 genotypes.

Mall *et al.* (2006) observed Mahalanobis' D^2 analysis was very useful for study of genetic divergence among elite lines of oat based on 10 characters. The genotypes were grouped into seven clusters. Cluster I was the largest with 37 lines followed by clusters II with six lines. The remaining five clusters consisted of one line and highly diverse from each other. This indicates that there is no parallelism between genetic diversity and geographical origin.

Shekhawat *et al.* (2006) classified 69 genotypes in six clusters according to Mahalanobis D^2 statistic for green fodder yield and 11 related characters. Cluster I was the largest including 39 genotypes followed by cluster IV (12 genotypes), cluster III (10 genotypes), cluster II (five genotypes), cluster V (two genotypes) and cluster VI (one genotype). Days to 50 per cent panicle emergence contributed the highest (21.78%) towards the divergence followed by panicle length (19.39%) and tillers per metre (13.90%).

Kumarmall *et al.* (2006) reported that dry matter yield per plant, number of grains per panicle, grain yield per plant, biological yield per plant and green fodder yield per plant had the greatest contribution towards genetic divergence among lines. Lines from the same geographic region clustered with lines of other geographic region due to selection pressure and genetic drift. This indicates that there is no parallelism between genetic diversity and geographic origin. Hybridization between the lines from different clusters can give good amount of hybrid vigour and good recombinants.

Yanming *et al.* (2006) observed diversity of 35 oat landraces in characters like branch number, spikelet number, ear length, plant height and growth duration. The result of cluster analysis with sum of squares for the five traits showed that 35 oat cultivars could be divided into 6 groups with different characteristics, which could be used in oat breeding.

Kumar *et al.* (2004) evaluated genetic variability of 100 oat germplasm lines representing a wide spectrum of geographical diversity and data were recorded for plant height, number of leaves per plant, flag leaf length, flag leaf width, stem thickness, longest leaf length, longest leaf width, number of nodes on main stem, longest internode length, dry matter yield per plant and green fodder yield per plant.

Choubey *et al.* (2001) studied genetic divergence using D^2 statistic of 300 oat germplasm lines of different eco-geographic origins revealed existence of considerable diversity. The cultivars were grouped into 14 clusters. The cluster III was the largest consisting of 39 genotypes followed by cluster V with 31 genotypes. Clusters X and XIV had nine genotypes each, whereas cluster XII had only two genotypes.

Dubey *et al.* (2000) determined genetic divergence in 90 oat cultivars for 11 developmental characteristics. The 90 cultivars were grouped into 9 clusters on the basis of relative magnitude of D^2 value. Cluster II was the largest with 35 cultivars, followed by cluster IV with 22, cluster III with 13, cluster VII with 10, cluster I with 5, cluster VIII with 2 and clusters V, VI and IX with only one cultivar each. The highest genetic divergence was found between cluster I and VIII. Clusters I, III and IX had promising cultivars for different components.

2.5 Principal component analysis

The idea of principal component analysis was initially floated by Pearson (1901) and later developed by Hotelling (1933) for his work in educational psychology. It was further

described by many workers to solve the complex data matrices by transferring the original set of variables into a smaller set of linear combinations that accounts for most of the variability of the original set (Anderson, 1972; Morrison, 1978; Dillon and Goldstein, 1984).

Krishna *et al.* (2014) studied 50 genotypes of oat using principal component analysis which revealed that the first six most informative components accounted for 84.9% of the variance. Traits were determined on the basis of factor loadings and traits with higher weighting were plant height, panicle length, number of spikelets per panicle, days to flower, dry weight, grain weight, green fodder yield, dry matter yield in PC1; plant height, number of leaves, leaf length, leaf breadth, panicle length, spike length, number of spikelets per panicle in PC2; plant height, number of leaves, stem girth, 1000-seed weight, dry weight, in PC3; plant height, number of leaves, leaf length, leaf breadth, spike length, number of spikelets per panicle, 1000- seed weight, groat yield, days to flower, grain weight, dry matter yield in PC4; plant height, number of leaves, leaf length, 1000- seed weight, groat yield, dry matter yield in PC5; plant height, number of leaves, panicle length, grain weight, dry matter yield in PC6.

Ahmed *et al.* (2011) reported that the first four most informative components accounted for 98.33% of the variance. Traits were determined on the basis of estimated factor loadings. Traits with higher weightage were days to 50% flowering, number of leaves per plant, leaf length, leaf to stem ratio, green fodder yield and grain yield in PC1; days to 50% flowering in PC2, days to 50% flowering; green fodder yield, grain yield in PC3 and green fodder yield in PC4.

Cattivelli *et al.* (2011) determined the genetic diversity by principle component analysis and clustered the 109 genotypes of oat. The most variable traits were seed yield, harvest index, seed weight and seed number per panicle. The lowest was estimated for plant height and days to maturity.

Vaisi *et al.* (2013) reported five factors accounted for 81% of variation. Factor 1 accounted for 27.6% and related significantly with number of seed per panicle, panicle density index and number of florets. Hence, this was introduced as panicle yield improvement factor. Other factors accounted for 19.3, 16.6, 12.3 and 7.3 *per cent* of total variation, respectively.

Kumar *et al.* (2006) analysed the pattern of diversity in 100 germplasm lines of oat using the Principal components method of factor- analysis. The genotypes HFO 604, HFO 566, HFO 305, HFO 644 and HFO 552 were the best for green fodder yield and HFO 717, HFO 244 and HFO 264 were best for seed yield.

CHAPTER-III

MATERIAL AND METHODS

The material used and methods employed for conducting the experiment on “**Evaluation of Oat (*Avena sativa* L.) genotypes for yield and quality characters**” are presented as under:

3.1 Experimental Site and Location

The field experiment was conducted at Forage Research Area of the Department of Genetics & Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar (Haryana) during *Rabi* season of 2015-16. The farm is located about 4 km away from the main campus and situated at about 29°10' latitude, 75° 44' E longitude and at an altitude of 228 m from sea level.

3.2 Climate and Weather conditions

The climate of Hisar is semi-arid and subtropical with hot and dry winds during summer months.

Warm humid in monsoon and cold dry weather in winter are the general features of this region. Both, winter and summer are usually harsh to bear upon. The mean minimum and maximum temperature exhibit wide variations. A maximum temperature zooming 44 to 48°C during summer and temperature dipping as low as to freezing point accompanied with chill frost in winter is of common occurrence.

3.3 Experimental Design and layout plan

Experimental Design	: RBD (Randomized Block Design)
Number of genotype	: 92
Number of Replications	: 3
Plot size	: Three row plot of 3 m each
Spacing	: 45 cm × 10 cm

3.4 Experimental Material

The experimental material comprised of ninety two (92) genotypes of oat (*Avena sativa* L.) including two checks (HJ-8 and OS-403) grown at the farm area of the Foarge Section, Department of Genetics & Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar. In each replication three rows of 3 meter each had grown, one row used for single cut, second row used for multi-cut experiment and third row used for seed purpose. The description of 90 genotypes is given in Table 1.

Table 3.1: List of ninety different genotypes of oat used in the study

S.No.	Name of Genotype	Source	S.No.	Name of Genotype	Source
1	JO-1	JNKVV, JABALPUR	46	HFO-523	CCSHAU,HISAR
2	ALGERIAN	ALGERIA	47	HFO-433	CCSHAU,HISAR
3	HFO-267	CCSHAU,HISAR	48	HFO-885	CCSHAU,HISAR
4	OL-125	PAU, LUDHIANA	49	HFO-896	CCSHAU,HISAR
5	OL-10	PAU, LUDHIANA	50	HFO-839	CCSHAU,HISAR
6	PLP-1	CSKHPAU, PALAMPUR	51	HFO-836	CCSHAU,HISAR
7	JHO-2006-4	IGFRI,JHANSI	52	HFO-863	CCSHAU,HISAR
8	SABZAR	SKAUST,SHRINAGAR	53	HFO-884	CCSHAU,HISAR
9	DUNAV	BULGARIA	54	HFO-841	CCSHAU,HISAR
10	JHO-851	IGFRI,JHANSI	55	HFO-851	CCSHAU,HISAR
11	UPO-94	GBPUAT,PANTNAGAR	56	HFO-880	CCSHAU,HISAR
12	JHO-822	IGFRI,JHANSI	57	HFO-893	CCSHAU,HISAR
13	SKO-90	SKAUST,SHRINAGAR	58	HFO-852	CCSHAU,HISAR
14	JHO-99-1	IGFRI,JHANSI	59	HFO-870	CCSHAU,HISAR
15	FOS-1/29	CCSHAU,HISAR	60	HFO-862	CCSHAU,HISAR
16	DULO	BULGARIA	61	HFO-845	CCSHAU,HISAR
17	UPO-212	GBPUAT,PANTNAGAR	62	HFO-883	CCSHAU,HISAR
18	OS-6	CCSHAU,HISAR	63	HFO-831	CCSHAU,HISAR
19	JHO-2006-2	IGFRI,JHANSI	64	HFO-114	CCSHAU,HISAR
20	KENT	AUSTRALIA	65	HFO-832	CCSHAU,HISAR
21	HFO-505	CCSHAU,HISAR	66	HFO-603	CCSHAU,HISAR
22	HFO-975	CCSHAU,HISAR	67	HFO-605	CCSHAU,HISAR
23	HFO-69	CCSHAU,HISAR	68	HFO-611	CCSHAU,HISAR
24	HFO-876	CCSHAU,HISAR	69	HFO-704	CCSHAU,HISAR
25	HFO-305	CCSHAU,HISAR	70	HFO-715	CCSHAU,HISAR
26	HFO-504	CCSHAU,HISAR	71	HFO-610	CCSHAU,HISAR
27	HFO-864	CCSHAU,HISAR	72	HFO-706	CCSHAU,HISAR
28	HFO-865	CCSHAU,HISAR	73	HFO-703	CCSHAU,HISAR
29	HFO-877	CCSHAU,HISAR	74	HFO-575	CCSHAU,HISAR
30	HFO-879	CCSHAU,HISAR	75	HFO-614	CCSHAU,HISAR
31	HFO-502	CCSHAU,HISAR	76	HFO-707	CCSHAU,HISAR
32	HFO-58	CCSHAU,HISAR	77	HFO-905	CCSHAU,HISAR
33	HFO-78	CCSHAU,HISAR	78	HFO-908	CCSHAU,HISAR
34	HFO-60	CCSHAU,HISAR	79	HFO-914	CCSHAU,HISAR
35	HFO-603	CCSHAU,HISAR	80	HFO-909	CCSHAU,HISAR
36	HFO-878	CCSHAU,HISAR	81	HFO-904	CCSHAU,HISAR
37	HFO-874	CCSHAU,HISAR	82	HFO-910	CCSHAU,HISAR
38	HFO-875	CCSHAU,HISAR	83	HFO-913	CCSHAU,HISAR
39	HFO-872	CCSHAU,HISAR	84	HFO-921	CCSHAU,HISAR
40	HFO-498	CCSHAU,HISAR	85	HFO-924	CCSHAU,HISAR
41	HFO-867	CCSHAU,HISAR	86	HFO-919	CCSHAU,HISAR
42	HFO-508	CCSHAU,HISAR	87	HFO-906	CCSHAU,HISAR
43	KALOJAN	BULGARIA	88	HFO-912	CCSHAU,HISAR
44	HFO-409	CCSHAU,HISAR	89	HFO-902	CCSHAU,HISAR
45	HFO-414	CCSHAU,HISAR	90	HFO-920	CCSHAU,HISAR

3.5 Recording of Experimental Data

The observations were recorded on five randomly selected competitive plants per genotype/replication. These plants were used for recording of data for the following morphological traits as under:

3.5.1 Morphological Characters

Plant height (cm): The plant height recorded for single cut at 50% flowering and for multi-cut observations were taken twice i.e. first cut (65-70 days after sowing) and of the second cut 50% flowering recorded from the ground to the top of the panicle excluding awns.

Days to 50% Flowering: The days to 50% flowering were recorded by tallying the days after sowing to the date at which the genotypes in each replication uncovered half blossoming in single cut and in multi-cut.

Number of Days to Maturity: The days to maturity were recorded by counting the days from date of sowing to the date on which more than 75 percent plants turned out to be physiologically mature.

Flag Leaf Length (cm): Flag leaf length was measured from ligule to the tip of the leaf. It also includes length of the leaf sheath.

Number of Tillers per plant: The total number of tillers per plant was counted from five randomly selected plants and their mean values were recorded.

Internode length (cm): internode length was measured between 3rd & 4th node.

Peduncle Length (cm): Peduncle length was recorded from last node of main culm to the base of the panicle.

Axis Length (cm): Axis length of each genotype was measured from the base of the panicle to the tip of panicle excluding awn at maturity.

No of Spikelets per plant: Number of spikelets / panicle was counted as average of 5 panicles.

Seed yield per meter row length (g): Seed yield per meter row length was recorded.

100 Seed Weight (g)/ seed index: The seeds of five randomly selected plants from each genotype were mixed to draw a representative sample of 100 seeds, which was weighted in gram using electronic balance.

Leaf Length (cm): Leaf length of 3rd leaf from top of the main tiller was measured from ligule to the tip of the leaf. It also includes length of the leaf sheath.

Leaf Width (cm): Leaf width at maximum breadth of 3rd leaf from top of the main tiller was recorded.

Green Fodder per meter row length (kg): The genotypes were harvested for single cut and double cut observations and weighed in grams with the help of electronic balance.

Dry Fodder per meter row length(kg): The plants were dried in shade and dry weights were measured and recorded in grams.

Number of Leaves per plant: The total number of leaves per plant counted at maturity and their mean values are expressed as number of leaves per plant.

3.5.2 Seed Quality Parameters

Laboratory tests were conducted in the laboratory of the Seed Science and Technology section of Department of Genetics and Plant Breeding from the harvested seeds of selected plants on the following seed quality parameters.

Standard germination test (%): Three replications with 100 seeds per replication for each genotype were placed on sufficiently moistened rolled germination papers (between the paper method of standard germination testing), layered with wax paper at 20°C temperature with 90-95% relative humidity in the seed germinator. Final count was recorded on 10th day (ISTA, 2009). At the time of final seedling evaluation, seeds were classified as normal seedling, abnormal seedlings. Normal seedlings were expressed as percent germination.

Shoot length (cm): The thirty seedlings were selected randomly from the normal seedlings in each replication for all genotypes at the time of final count of standard germination and average shoot length of each genotype was measured.

Root length (cm) : The same seedlings, used for calculating shoot length were used for calculating root length in each replication for all the genotypes and average root length was measured.

Seedling length (cm): The same seedlings, used for calculating shoot and root lengths were used for calculating seedling length in each replication for all the genotypes and average seedling length was measured.

$$\text{Seedling length} = \text{Root length} + \text{Shoot length}$$

Seedling dry weight (mg): Thirty normal seedlings taken for measuring the root and shoot length were further kept in hot air oven at 80°C for 24 hours and average dry weight per seedling was recorded in grams.

Seed Vigour index-I: From the observations of standard germination test, the seedling vigour indices were calculated according to the method suggested by Baki and Anderson (1970).

$$\text{Seed Vigour index-I} = \text{Standard Germination (\%)} \times \text{Seedling length (cm)}$$

Seed Vigour Index-II:

$$\text{Seed Vigour index-II} = \text{Standard Germination (\%)} \times \text{Seedling dry weight (g)}$$

Electrical conductivity (mS/cm/seed):

By dipping 50 seeds in 75 ml of distill water and kept for 16hrs in water and the electrical conductivity measured with electrical conductivity meter.

3.5.3 Quality characters Laboratory tests were conducted in the biochemistry laboratory of the forage section of Department of Genetics and Plant Breeding from the harvested seeds and forage of 92 genotypes on the following seed quality parameters.

Forage Crude Protein (%): Calculated using Micro-Kjeldahl method of nitrogen estimation.

Seed Crude Protein (%): Calculated using Micro- Kjeldahl methaod of nitrogen estimation.

Micro- Kjeldahl methaod

Total nitrogen in the samples was estimated by conventional Micro-kjeldahl's method.

Reagents

- i) K_2SO_4 : $CuSO_4$ mixture (9:1)
- ii) Concentrated H_2SO_4
- iii) 40% sodium hydroxide
- iv) N/100 sulphuric acid
- v) Methyl red indicator
- vi) N/100 sodium hydroxide

Procedure

100 mg dried and grinded sample was weighed and transferred to 100 ml Micro-kjeldahl's digestion flask. About one gram of K_2SO_4 : $CuSO_4$ (9:1) mixture was added to it followed by 10 ml of concentrated sulphuric acid. The flasks were then kept in an inclined position on the hot plate in the digestion chamber and heated gently till the solution became transparent giving a bluish green colour. After cooling, the content of the flask was mixed with distilled water, cooled, transferred to 100 ml volumetric flask and volume was made up to the mark with distilled water. Ten ml of the solution, prepared above, was taken for distillation and distilled after adding 10 ml of 40% NaOH. The ammonia was absorbed in 10 ml of N/100 sulphuric acid containing one or two drops of methyl red indicator. The amount of ammonia absorbed by N/100 sulphuric acid was determined by titrating it with N/100 sodium hydroxide. A blank was also digested and distilled in similar way. The percentage of nitrogen was calculated from N/100 H_2SO_4 used, as follows –

1ml of N/100 H_2SO_4 used $\equiv$ 0.00014 g of Nitrogen

Crude protein content was determined by multiplying the Nitrogen content by a factor of 8.162.

3.6 Analysis of variance for design of experiment:

The data were statistically analyzed on the basis of the two way classification model described by Panse and Sukhatme (1967). This model is

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Where,

Y_{ij} = observation in i th treatment and j th block

- μ = General mean
 t_i = i th treatment effects
 b_j = j th block effect
 e_{ij} = Random error associated with the i th treatment and j th block.

The assumptions of the model are:

1. All the observations should be independent.
2. The different effects in the model should be additive.
3. Error involved in the population should be normally and independently

distributed with mean zero and variance (σ^2_e).

Table 3.2: Analysis of variance

Source of Variation	Degree of Freedom	Mean Square	F cal. Value
Replications	($r-1$)	M_R	
Genotypes	($g-1$)	M_G	M_G/M_e
Error	($r-1$)($g-1$)	M_e	

where,

- g = number of genotype
 r = number of replication

The significance of M_R and M_G was tested against M_e by 'F' test at α ($=0.05$) level of significance

3.7 Parameters of variability

i) Mean ($\bar{X}$)

The mean value of each character was worked out by dividing the total sum of values with corresponding number of observations.

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

Where,

- $\bar{X}$ = Sample mean
 X_i = Individual value
 n = Number of observations

ii) Range

The lowest and highest values of each character were recorded.

iii) Standard error of mean (S.E. (m))

Standard error of mean was calculated with the help of error mean squares from the analysis of variance table given as under:

$$S.E. (m) = \frac{\sqrt{MSe}}{r}$$

S.E. = Standard error
MSe = Error mean sum of squares
r = Number of replications

(iv) Critical difference (CD)

For every character, the critical difference as the difference of any two mean values in order to compare the treatment means was calculated using the following formula:

$$\text{S.E. (d)} = \frac{\sqrt{2\text{MSe}}}{r}$$

$$\text{CD at 5 or 1\%} = \frac{\sqrt{2\text{MSe}}}{r} \times 't'$$

Where,

't' is the tabulated value at error degree of freedom at 5 or 1% level of significance as the case may be.

v) Coefficient of variation (C.V.)

The coefficient of variation being a standardized form of variance is useful for comparing the extent of variance between different characters with different scales (Singh and Choudhary, 1977). According to Burton and Devane (1953), genotypic and phenotypic coefficients of variation were estimated based on the estimates of genotypic and phenotypic variances.

$$\text{Coefficient of variation (CV\%)} = \frac{\text{standard deviation}}{\bar{X}} \times 100$$

$$\text{Genotypic coefficient of variability (GCV \%)} = \frac{\sqrt{\sigma^2_g} \times 100}{\bar{X}}$$

$$\text{Phenotypic coefficient of variability (PCV \%)} = \frac{\sqrt{\sigma^2_p} \times 100}{\bar{X}}$$

Where,

$\bar{X}$ = General mean of a particular character

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The genotypic and phenotypic coefficients of variation were categorized as per the method suggested by Shivasubramanian and Menon (1973):

0-10% = Low

10-20% = Moderate

>20% = High

vi) Heritability (broad sense)

Heritability in broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and expressed as percentage (Falconer, 1981).

$$\text{Heritability (h}^2\text{)} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

The calculated heritability was classified into three groups as suggested by Johnson *et al.* (1955):

0-30% = Low

30-60% = Moderate

> 60% = High

vii) Expected genetic advance (GA)

Genetic advance was worked out by adopting the following formula given by Johnson *et al.* (1955):

$$GA = k \times h^2 \times \sqrt{\sigma^2_p}$$

Where,

h^2 = Heritability in broad sense

k = Selection differential, which is equal to 2.06 at 5% intensity of selection (Lush, 1949)

$\sqrt{\sigma^2_p}$ = Phenotypic standard deviation

viii) Genetic advance as per cent of mean (GAM)

Genetic advance as per cent of mean for each character was worked out as suggested by Johnson *et al.* (1955).

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

$\bar{X}$ = General mean

Genetic advance as per cent of mean was categorized as per the formula suggested by Johanson *et al.* (1955).

0-10 % = Low

10-20 % = Moderate

>20 % = High

3.8 Correlation coefficient analysis

Correlation coefficients at phenotypic and genotypic level were calculated using the variances and co-variances as under:

$$\text{Phenotypic correlation} = r_{ij} (P) = \frac{\sigma^2_{p_{ij}}}{\sqrt{\sigma^2_{p_{ii}} \times \sigma^2_{p_{jj}}}}$$

Where,

$\sigma^2_{p_{ij}}$ = Phenotypic co-variance of character x_i and x_j

σ^2_{pii} = Phenotypic variance of character xi

σ^2_{pjj} = Phenotypic variance of character xj

$$\text{Genotypic correlation} = r_{ij}(G) = \frac{\sigma^2_{g_{ij}}}{\sqrt{\sigma^2_{g_{ii}} \times \sigma^2_{g_{jj}}}}$$

Where,

$\sigma^2_{g_{ij}}$ = Genotypic co-variance of character xi and xj

$\sigma^2_{g_{ii}}$ = Genotypic variance of character xi

$\sigma^2_{g_{jj}}$ = Genotypic variance of character xj

Significance of phenotypic correlations was tested at 5 per cent and 1 per cent levels of significance against the expected value from Fisher's table at (n-2) degree of freedom.

3.9 Genetic diversity

a) Mahalanobis D² analysis

Mahalanobis (1936) D² analysis was used for assessing the genetic divergence among the test genotypes involving quantitative characters. The generalized distance between any two populations is given by the formula:

$$D^2 = \sum \sum \lambda_{ij} \sigma_{ai} \sigma_{aj}$$

Where,

D² = Square of generalized distance

λ_{ij} = Reciprocal of the common dispersal matrix

$\sigma_{ai} = (\mu_{i1} - \mu_{i2})$

$\sigma_{aj} = (\mu_{j1} - \mu_{j2})$

μ = General mean

Since, the formula for computation requires inversion of higher order determinant, transformation of the original correlated unstandardized characters (X's) to standardized uncorrelated variables (Y's) was done to simplify the computational procedure. The D² values were obtained as the sum of squares of the differences between pairs of corresponding uncorrelated (s) values of any two uncorrelated genotypes (Rao, 1960).

b) Cluster of D² values

All n (n-1)/2 D² values were clustered using ward minimum method described by Rao (1960).

c) Intra cluster distance-

The intra cluster distances were calculated by the formula given by Singh and Choudhary (1977).

$$\text{Square of the intra cluster distance} = \frac{\sum D^2_i}{n}$$

Where,

$\sum D^2_i$ is the sum of distances between all possible combinations of the genotypes included in a cluster.

n = Number of all possible combinations

d) Inter cluster distance-

The inter-cluster distances were calculated by the formula described by Singh and Choudhary (1977).

$$\text{Square of the inter cluster distance} = \frac{\sum D^2_{ij}}{n_i n_j}$$

Where,

$\sum D^2_{ij}$ is the sum of distances between all possible combinations ($n_i n_j$) of the genotypes included in the clusters under study.

n_i = Number of genotypes in cluster i

n_j = Number of genotypes in cluster j

In brief, the steps involved for the estimation of D^2 values are as follows (Rao, 1952).

1. Pivotal condensation of error variance and co-variance matrix to obtain inverse matrix.
2. Transformation of original correlated data into un-correlated variables.
3. Calculation of mean values of the transformed characters.
4. **Calculation of D^2 values:** For each combination, deviation between the means was computed and the D^2 values were computed and arranged in the form of matrix.
5. **Determination of group constellations:** As such no standard rules are available for making the clusters because cluster is not a well defined term. The only criterion appears to be that any two genotypes belonging to the same cluster should at least on an average, show a smaller D^2 value than those belonging to two different clusters. The D^2 values for all the combinations presented in the matrix form were arranged in increasing order of magnitude and clustering was done according to the method suggested by (Rao, 1952).

At first, the two most closely associated genotypes were chosen and then third genotype was located which had the smaller average D^2 value as compared to the first two genotypes. Following this methodology, the subsequent genotypes were chosen which have smaller average D^2 value from the first three genotypes and change in D^2 value within a cluster due to inclusion of additional genotype was computed and so on. The new genotypes were added so long as the increase in average D^2 value became abruptly high, then this genotype was not included in the former groups. The genotypes of first cluster were omitted and rest were treated similarly for constructing new clusters.

6. Intra and inter cluster distance

The intra cluster D^2 value was calculated as the sum of $n(n-1)/2$ D^2 values among the genotypes within a cluster divided by $n(n-1)/2$. The single genotype always has zero intra cluster D^2 value. For calculating the inter cluster D^2 value, all possible D^2 values between genotypes of two clusters were added and then divided by $n_1 \times n_2$, where n_1 and n_2 represented the number of genotypes in the first and second cluster, respectively. The intra and inter cluster distances were calculated by taking the square root of respective D^2 value between genotypes of a particular cluster and between genotypes belonging to two clusters, respectively.

7. Clusters mean value

The cluster mean of a particular character is the summation of mean values of the genotypes included in a cluster divided by number of genotypes in the same cluster.

3.9 Principal component analysis

It is a multivariate statistical technique to reduce the data with large number of correlated variables into a substantially smaller set of new variables, through linear combination of the variables that accounts most of the variation present in the original variables. Principal component are generally estimated either from correlation matrix or variance-covariance matrix. When the variables are measured in different units, scale effects can influence the composition of derived components. In such situations, it becomes desirable to standardize the variables and the correlation matrix comes to the rescue. In the recent investigation correlation matrix was used to extract the principal components.

Suppose the vector of observations $X = (X_1, X_2, \dots, X_p)$ had correlation matrix R . The eigen values and associated eigen vectors of correlation matrix were determined by solving the determinantal equation:

$$|R - \lambda I| = 0$$

Being $(\lambda_1, v_1), (\lambda_2, v_2), \dots, (\lambda_p, v_p)$ the eigen values and eigen vector pairs of R . With $\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_p$, then the first principal component Y_1 was calculated as

$$Y_1 = v_1'X = v_{11}X_1 + v_{12}X_2 + \dots + v_{1p}X_p$$

Such that the variance of Y_1 was maximized subject to the constraint that the sum of squared weights was equal to one (i.e. $\sum v_{1j}^2 = 1$). The second principal component was calculated as:

$$Y_2 = v_2'X = v_{21}X_1 + v_{22}X_2 + \dots + v_{2p}X_p$$

This was uncorrelated with first principal component and $\sum v_{2j}^2 = 1$

The principal components were uncorrelated with each other and their variances were equal to the eigen values $\lambda_1, \lambda_2, \dots, \lambda_p$, i.e.

$$V(Y_j) = \lambda_j (j = 1, \dots, p)$$

The total variances in P variables was calculated by

$$\sum_{j=1}^p V(Y_j) = \text{tr}(R) = p = \lambda_1 + \lambda_2 + \dots + \lambda_p = \sum_{j=1}^p \lambda_j^p$$

Therefore, the proportion of the total variance explained by j^{th} principal component was estimated as:

$$\lambda_j / p \quad (j = 1, \dots, p)$$

In view of above, the standardized principal components were given by:

$$Y_1^* = Y_1 / \sqrt{\lambda_1}, Y_2^* = Y_2 / \sqrt{\lambda_2}, \dots, Y_p^* = Y_p / \sqrt{\lambda_p}$$

For deciding number of principal components to be retained, Kaiser's (1958) suggestion of dropping those principal components of correlation matrix with eigen roots less than one, was followed.

3.9.1 Principal factor analysis

For further investigation principal factor analysis was carried out as it has many added advantages over principal component analysis. It is closely related to principal component analysis, but differs in that it assumes a definite model where each observed variable is expressed linearly in terms of common factor and unique factor. The common factors account for the correlation among the variables, while each unique factor accounts for the remaining variance (including error) of that variable. Moreover, in principal component analysis total variation contained in a set of variables is considered Whereas, in factor analysis interest centers only on that part of variance, which is shared by the common factors.

The common factor analytical model can be written in the following form:

$$X_j = I_{j1} f_1 + I_{j2} f_2 + \dots + I_{jm} f_m + e_j \dots (i)$$

Where, each of the p observed variable has been described in terms of a common factor and a unique factor.

For a set of p variables, linear model (i) can be written in a slightly expanded form as:

$$\begin{aligned} X_1 &= I_{11} f_1 + I_{12} f_2 + \dots + I_{1m} f_m + e_1 \\ X_2 &= I_{21} f_1 + I_{22} f_2 + \dots + I_{2m} f_m + e_2 \\ &\vdots \quad \quad \quad \vdots \quad \quad \quad \vdots \quad \quad \quad \vdots \quad \quad \vdots \\ X_p &= I_{p1} f_1 + I_{p2} f_2 + \dots + I_{pm} f_m + e_p \quad \dots (ii) \end{aligned}$$

Such a set of equations is called factor pattern. Factor analysis yields not only patterns but also correlation between variables and the factors. A table of correlation is called factor structure. A structure and pattern both are necessary in order to furnish a complete solution.

The factor model in matrix notation can be written as:

$$X = LF + e \quad \dots (iii)$$

Where, $X = (p \times 1)$ vector of observed variables.

$L = (p \times m)$ matrix of unknown constants called factor loading.

$$= \begin{vmatrix} I_{11} & I_{12} & \dots\dots\dots \\ I_{21} & I_{22} & \dots\dots\dots \\ \vdots & \vdots & \\ \vdots & \vdots & \\ I_{p1} & I_{p2} & \dots\dots\dots \end{vmatrix} \begin{vmatrix} I_{1m} \\ I_{2m} \\ \vdots \\ \vdots \\ I_{pm} \end{vmatrix}$$

$F = (m \times 1)$ vector of unobservable variables called common factors.

$F' = (f_1, f_2, \dots, f_m)$ and

$e = (p \times 1)$ vector of unobservable variables called specific factors.

$e' = (e_1, e_2, \dots, e_p)$

It is obvious from each equation in (ii) that the variance of a variable X consists of two parts, viz.,

$$\begin{aligned} V(X) &= h_j^2 + \Phi_j \quad (j = 1 \dots\dots P) \\ &= I_{j1}^2 + I_{j2}^2 + \dots\dots + I_{jm}^2 + \Phi_j \end{aligned}$$

Where, h_j^2 is that portion of the variance of j^{th} variable contributed by m common factors, also called communality and the specific variance (Φ_j) contributed by specific factors. The j^{th} communality is the sum of squares of the loading or common factor coefficients of j^{th} variable.

Principal component and maximum likelihood methods of factor extraction are most commonly used besides other. The advantage of using principal component method is that no distributional assumption is required whereas; maximum likelihood assumes that the general form of population distribution is known and follows multivariate normal distribution. Therefore, principal component method was used in the present study.

As the initial factor loadings were not clearly interpretable, the factor axes were rotated using varimax rotation (Kaiser, 1958) which is the most popular method of rotation. By this the variance of the squared loading across a factor was maximized which corresponded to spreading out of the squares of loading on each factor as much as possible. It made possible to obtain groups of large and negligible coefficients in different columns of the rotated factor loading.

Principal factor scores were determined using Anderson-Rubin method which is a modification of Bartlett's method (scores have mean = 1 and the sum of squares of unique factors over the range of variables is minimized) which ensures orthogonality of estimated factors. The scores produced have mean = 0 and SD = 1 and are uncorrelated. Plotting of different genotypes was done using their individual factor scores taking different principal factors as axes.

The observations recorded with regard to different morphological characters, seed yield and quality characters on 92 genotypes of oat were analysed using appropriate statistical methods. The results have been presented under the following heads:

- 4.1 Analysis of variance
- 4.2 Mean performance and range
- 4.3 Variability and heritability parameters
- 4.4 Correlation coefficient analysis
- 4.5 Path-coefficient analysis
- 4.6 Genetic divergence
- 4.7 Principal component analysis

4.1 Analysis of variance:

The mean sum of squares with respect to dry matter yield and its component characters in single cut, first cut of multi-cut and second cut of multi-cut are arranged in the tables 4.1, 4.2 and 4.3 respectively. A perusal of these tables clearly indicates that mean of squares due to genotypes were highly significant for all the characters, thereby indicating the presence of sufficient genetic variability among the genotypes for all the characters studied.

4.2 Mean performance and range

The mean values of all the 24 characters in single cut, 11 characters in first cut of multi-cut and 20 characters in second cut of multi-cut analysed for 92 genotypes of oat have been given in table 4.4, 4.5 and 4.6 respectively.

4.2.1 Mean performance in single cut

4.2.1.1 Plant height (cm)

The maximum plant height was recorded in the genotype, HFO-864 (150 cm) and minimum in HFO-267 (70 cm). The genotypes namely, JO-1, OL-125, JHO-822, FOS-1/29, DULO, UPO-212, KENT, HFO-603, HFO-409, HFO-605, HFO-611, HFO-614 and HFO-118, were best genotypes recorded with highest plant height.

4.2.1.2 Days to 50% flowering (days)

The maximum HFO 611(100 days) and the minimum HFO 502 and HFO 874 (86 days) number of days to 50% flowering were observed in genotypes. this character was recorded in genotypes, HFO-267, OL 125, OL 10, JHO 851, DULO, UPO 212, OS 6, HFO 505, HFO-975, HFO-876, HFO-877, HFO-and HFO- 904 were best.

Table 4.1: Analysis of variance for dry matter yield and its component characters in single cut oat

Sources of variation	d.f.	Mean squares										
		PH	DF	DM	FLL	IL	TPL	PL	AL	NOS	SY	SI
Replication	2	214.97	32.58	3121.11	0.54	1.21	30.52	6.04	3.27	7394	14410.51	1.92
Genotypes	91	901.13**	21.21**	103.68**	77.92**	41.76**	1.51**	101.65**	56.87**	420.52**	2521.09**	0.772**
Error	182	112.3	2.73	2.94	5.27	1.65	0.25	6.93	6.68	25.72	92.41	0.012

** Significant at 1%, * Significant at 5%.

Sources of variation	d.f.	Mean squares												
		LL	LW	GFY	DMY	NOLS	CP(G)	CP(F)	GP	SL	SDW	SV-1	SV-2	EC
Replication	2	7.53	0.012	0.003	0.027	572.83	0.984	0.067	2835.76	1.4	42.83	3276873	2326.78	0.024
Genotypes	91	105.03**	0.38**	0.279**	0.008**	53.22**	4.323**	1.603**	26.41**	14.03**	11.96**	176467.538**	88064.42**	0.015**
Error	182	13.23	0.021	0.018	0.001	15.26	0.162	0.06	4.99	0.889	0.046	12384.97	745.44	0.001

** Significant at 1%, * Significant at 5%.

Table 4.2: Analysis of variance for dry matter yield and its component characters in Ist cut of multi-cut oat

Sources of variation	d. f.	Mean squares				
		PH	TPL	GFY	DMY	CPM
Replication	2	337.45	1.404	4262.047	582.6	0.431
Genotypes	91	231.494**	1.397**	7213.91**	412.6**	1.51**
Error	182	53.394	0.245	603.76	70.862	0.217

** Significant at 1%

* Significant at 5%.

Table 4.3: Analysis of variance for dry matter yield and its component characters in 2ndcut of multi-cut oat

Sources of variation (SV)	d.f.	Mean squares													
		PH	DF	FLL	IL	TPL	PL	AL	SI	LL	LW	GFY	DMY	NOL	CPMC
Replication	2	167.24	3565.45	0.623	0.406	0.013	8.32	16.63	1.92	7.52	0.206	1804.34	57.89	23.83	0.751
Genotypes	91	371.03**	103.68**	69.74**	38.49**	1.396**	78.44**	45.75	0.772**	105.03**	0.39**	41455.09**	1903.04**	53.22**	3.403**
Error	182	93.19	2.94	5.09	3.39	0.246	6.96	4.66	0.012	13.22	0.021	7526.6	352.82	15.26	0.167

** Significant at 1%,

* Significant at 5%.

4.2.1.3 Days to maturity (days)

The maximum (133.7 days) and the minimum (110.3 days) number of days to maturity were observed in genotypes, HFO-877 and HFO-893, respectively. The days to maturity in genotypes, HFO-975, HFO-504, HFO-884, HFO-502, HFO-885, HFO-880, HFO-852, HFO-862, HFO-883, HFO-603, HFO-614, HFO-924 and HFO-906 attained maturity in less number of days than checks.

4.2.1.4 Flag leaf length (cm)

The maximum flag leaf length was recorded in the genotype, HFO-703 (38 cm) and it was minimum in HFO-836(11cm). The genotypes namely, HFO-305, HFO-879, HFO-603, KALOJAN, HFO-114, HFO-910, HFO-904, and HFO-912 had high flag leaf length.

4.2.1.5 Internode length (cm)

The maximum internode length was recorded in genotype, HFO-69 and DULO (25 cm) and it was minimum in DUNAV (8 cm). The genotypes namely, HFO-851, HFO-893, HFO-852, HFO-862, HFO-114, HFO-610, HFO-706, HFO-703 and HFO 912 had high internode length.

4.2.1.6 Number of tillers/plant

The maximum number of tillers/plant were recorded in genotype, HFO-832 (11.5) and it was minimum in HFO-909 (7.2 cm). The genotypes namely PLP-1, JHO-2006-4, JHO-851, FOS-1/29, OS-6, HFO-874 and HFO-875, had more number of tillers/plant.

4.2.1.7 Peduncle length (cm)

The maximum peduncle length was recorded in the genotype, HFO-851 (38.8 cm) and it was minimum in HFO-872 (12.2 cm). The genotypes namely, HFO-305, HFO-78, HFO-867, HFO-508, HFO-409, HFO-839, HFO-893, HFO-852 and HFO-905, had same value of peduncle length with standard checks.

4.2.1.8 Axis length (cm)

The maximum axis length was recorded in genotype, HFO-703 (30.3 cm) and it was minimum in HFO-267 and HFO-975 (8.7 cm). The genotypes namely, JHO-851, JHO-822, HFO-504, HFO-885, HFO-603 and HFO-704 had highest axis length.

4.2.1.9 Number of spikelets/panicle

The maximum number of spikelets /panicle were recorded in genotype, HFO-878 (107.3) and it was minimum in HFO-610 (47.7). The genotypes namely, FOS-1/29, HFO-305, HFO-864, HFO-877, HFO-879, HFO-78, HFO-60, HFO-614, HFO-707 and HFO-920 had same number of spikelets/panicle with checks.

4.2.1.10 Seed yield per meter row length (g)

The highest mean for seed yield/plant (g) was observed in case of genotype, HFO-912 (174.4 g), likewise, the lowest mean was recorded for genotype, SABZAR (41.3 g). The

genotypes namely, JO-1, ALGERIAN, KENT, HFO-504, HFO-78, HFO-867 and HFO-704, had shown highest yield.

4.2.1.11 100 seed weight (g)

The highest mean value of 100 seed weight (g) was observed in genotype, HFO-878 (4.56 g) and the lowest in SABZAR (2.01 g). The genotypes with higher 100 seed weight value were HFO-879, HFO-433, HFO-883, HFO-610, HFO-706, HFO-703, and HFO-912.

4.2.1.12 Leaf length (cm)

The highest mean value of leaf length was observed in genotype SABZAR (50 cm) and the lowest in HFO-870 (8 cm). The genotypes followed SABZAR with highest leaf length were JHO-851, JHO-822, DULO, KENT, HFO-502, KALOJAN, HFO-433, HFO-851 and HFO-704.

4.2.1.13 Leaf width (cm)

The highest mean value of leaf width was observed in genotype, HFO-831 (2.8 cm) and the lowest in SKO-90 (0.6 cm). The genotypes with highest leaf width JHO-2006-2, HFO-433, HFO-841, HFO-851, HFO-870, HFO-605, HFO-909 and HFO-904.

4.2.1.14 Green fodder yield (Kg)

The highest mean value of green fodder yield was observed in genotype HFO-58 (1.847) and the lowest in HFO-852 (.468 g). The genotypes JO-1, JHO-99-1, DULO, UPO-212, KENT, HFO-864, HFO-879, HFO-58, HFO-878 and HFO-409 found superior than checks for green fodder yield.

4.2.1.15 Dry matter yield (Kg)

The highest mean value of dry matter yield was observed in genotype JO-1 (0.357) and the lowest in HFO-69 (0.107 g). The genotypes showed superior results for dry matter yield were ALGERIAN, SABZAR, JHO-851, JHO-99-1, FOS-1/29, DULO, HFO-876, KENT, HFO-504, HFO-877, HFO-879, HFO-508, HFO-845, HFO-883, HFO-611, HFO-715, HFO-908, HFO-914, HFO-910, HFO-913 and HFO-912.

4.2.1.16 Number of leaves/plant

The maximum number of leaves per plant were recorded in genotype HFO-875 and HFO-831 (50.8) and it was minimum in HFO-909 (31.4). The genotypes JO-1, OL-10, PLP-1, JHO-851, FOS-1/29, HFO-505, HFO-305, HFO-877, HFO-878, HFO-874, KALOJAN, HFO-836, HFO-862, HFO-845 and HFO-832 had highest number of leaves/plant.

4.2.1.17 Crude Protein in grains (%)

The highest mean value of crude protein in grains was observed in genotype, HFO-60 (14.49%) and the lowest in JHO-2006-2 (9.69%). The genotypes with high value crude

protein in grains were HFO-267, OS-6, HFO-864, HFO-498, HFO-896, HFO-851, HFO-862, HFO-883, HFO-905 and HFO-921.

4.2.1.18 Crude Protein in forage (%)

The highest mean value of crude protein in forage was observed in genotype HFO-575 (14.7 %) and the lowest in HFO-877 (11.3 %). The genotypes with highest crude protein in forage were JHO-851, HFO-867, HFO-896, , HFO-851, HFO-880, HFO-852, HFO-862, HFO-909 and HFO-913.

4.2.1.19 Germination (%)

The highest mean value of germination (%) was observed in genotypes HFO-610, HFO-614, HFO-914, HFO-924 (92%) and the lowest in case of HFO-845 (81 %). The genotypes showed highest germination% value were JHO-822, HFO-504, HFO-878, HFO-896, HFO-703, HFO-707 and HFO-906.

4.2.1.20 Seedling length (cm)

The maximum seedling length was recorded in genotype, HFO-896 (38.71 cm) and it was minimum in DUNAV (27.62 cm). The genotypes, JHO-851, JHO-99-1, HFO-914, HFO-909, HFO-913, HFO-919 and HFO-906 had the highest seedling length.

4.2.1.21 Seedling dry weight (g)

The maximum seedling dry weight was recorded in genotype, HFO-908 (15.6 mg) and it was minimum in DULO (7.01 mg). The genotypes namely, HFO-305, HFO-879, HFO-872, HFO-896, HFO-852, HFO-707, HFO-909 and HFO-919 had highest seedling dry weight.

4.2.1.22 Seed vigour index I

The maximum seed vigour index I was recorded in genotype, HFO-896 (3526.3) and it was minimum in DUNAV (2335.3). The genotypes JHO-851, JHO-99-1, HFO-914, HFO-913, HFO-919 and HFO-906 had highest seed vigour index I.

4.2.1.23 Seed vigour index II

The maximum seed vigour index II was recorded in case of genotype, HFO-908 (1368.2) and it was minimum in case of DULO (593.9). The genotypes namely, HFO-305, HFO-879, HFO-872, HFO-867, HFO-896, HFO-845 and HFO-909 had highest seed vigour index II.

4.2.1.24 Electrical conductivity

The maximum seed EC was recorded in case of genotype, HFO-896 (0.173) and it was minimum in case of HFO-836 (0.367). The genotypes namely, HFO-267, OS-6, HFO-975, HFO-603, HFO-867, HFO-852, HFO-614 and HFO-913 had highest seed EC.

Table 4.4: Mean values of dry matter yield and its component characters of 92 genotype of oat in single cut

Genotypes	PH	DF	DM	FLL	IL	TPL	PL	AL	NOS	SY	SI	LL	LW	GFY	DMY	NOL	CPg	CPf	GP	SL	SDW	SVI	SVII	EC
JO-1	135	93	117	22	17	8.97	22.2	21.7	78	164	3.61	35	1.3	1.679	0.357	42	12.31	13.42	87	31.63	8.62	2760	750	0.290
ALGERIAN	118	95	124	25	18	9.30	28.0	23.3	74	159	3.15	35	1.9	1.181	0.304	41	12.98	13.33	89	30.75	7.83	2724	693	0.282
HFO-267	70	92	114	24	17	8.87	19.8	8.7	79	107	3.23	34	1.5	0.689	0.128	38	13.79	13.13	90	33.47	7.93	2997	708	0.201
OL-125	128	92	118	25	13	8.53	20.8	23.7	67	115	3.16	34	1.7	1.155	0.199	42	11.33	13.19	85	29.19	8.92	2478	755	0.353
OL-10	124	92	122	18	13	9.90	22.8	14.7	65	79	2.93	28	1.2	0.812	0.169	48	10.81	12.70	85	29.52	7.05	2517	599	0.340
PLP-1	82	97	125	30	16	10.13	20.7	22.3	52	98	2.23	41	1.9	0.804	0.163	44	11.46	13.18	85	27.82	9.14	2372	779	0.383
JHO-2006-4	115	94	120	28	19	10.23	20.7	21.3	65	109	3.25	40	1.3	1.038	0.210	42	13.17	13.72	89	33.04	7.33	2953	652	0.282
SABZAR	85	94	122	26	21	8.87	28.7	22.0	53	41	2.05	50	1.7	0.870	0.222	44	13.63	13.68	85	31.92	8.11	2704	684	0.434
DUNAV	87	96	130	18	8	9.90	28.8	21.0	51	122	2.25	28	1.3	0.704	0.175	44	10.46	12.56	85	27.62	8.25	2335	696	0.390
JHO-851	126	97	120	24	20	10.20	13.3	28.7	70	103	3.19	44	1.9	1.136	0.228	49	13.26	14.17	89	35.07	8.93	3109	788	0.252
UPO-94	110	93	115	21	11	9.67	22.0	22.7	62	132	3.57	32	1.8	0.822	0.181	44	12.81	13.79	87	31.63	9.25	2739	800	0.360
JHO-822	126	89	115	25	21	8.75	32.2	29.7	69	125	2.70	43	1.9	1.035	0.193	42	13.41	13.12	91	33.26	9.88	3035	899	0.252
SKO-90	112	97	119	19	11	8.67	35.0	17.0	60	89	2.46	26	0.6	0.627	0.128	39	11.68	13.19	87	33.08	9.03	2871	783	0.287
JHO-99-1	121	94	117	26	11	8.70	26.7	15.7	60	98	2.99	33	1.3	1.488	0.228	42	13.17	13.37	91	35.25	7.69	3203	696	0.231
FOS-1/29	142	96	120	24	18	10.20	26.7	18.0	82	105	3.31	39	1.9	1.177	0.240	48	10.43	11.68	83	32.43	8.93	2702	742	0.300
DULO	148	92	119	25	25	9.47	24.7	22.3	69	92	3.08	42	1.8	1.553	0.316	44	12.61	13.45	85	28.84	7.01	2450	594	0.367
UPO-212	148	92	117	30	20	8.47	24.7	24.8	77	86	3.34	41	2.0	1.446	0.263	39	11.23	13.32	85	30.73	8.18	2610	693	0.357
S-6	118	90	118	26	20	10.43	27.8	27.7	81	163	3.50	35	1.7	1.055	0.193	50	13.86	13.70	88	34.48	11.44	3032	1003	0.191
JHO-2006-2	85	97	118	20	15	8.83	22.8	16.0	59	120	2.47	32	2.2	0.825	0.140	42	9.69	13.06	85	31.60	11.01	2676	930	0.350
KENT	135	93	120	22	18	8.60	26.8	24.3	69	158	3.24	42	2.0	1.329	0.187	43	10.25	13.87	88	34.01	11.76	2991	1031	0.223
HFO-505	103	91	114	22	19	8.80	27.3	22.8	74	103	3.62	38	1.8	1.065	0.128	47	12.34	13.57	88	32.73	10.55	2866	924	0.247
HFO-975	79	90	112	20	11	8.67	21.8	8.7	77	49	3.54	30	1.4	0.884	0.187	41	13.37	12.46	84	29.20	10.77	2450	902	0.191
HFO-69	108	93	117	20	25	9.57	20.8	22.0	83	80	3.13	30	1.7	1.080	0.107	45	13.09	11.69	88	32.06	7.58	2823	663	0.211
HFO-876	106	87	131	23	17	9.43	22.7	20.7	76	90	3.62	28	1.5	0.578	0.210	46	12.25	11.80	83	28.38	9.28	2356	769	0.380

HFO-305	117	92	116	34	16	9.97	32.3	24.7	90	155	3.74	37	1.6	1.088	0.205	50	13.49	13.61	90	33.08	14.17	2995	1279	0.221
HFO-504	98	90	113	21	18	8.67	20.7	28.0	77	52	2.91	41	2.4	0.808	0.240	42	13.42	12.59	91	31.61	9.53	2879	867	0.302
HFO-864	150	96	113	21	15	8.77	16.3	20.0	91	68	3.30	26	1.3	1.567	0.187	41	14.15	11.65	89	28.54	9.70	2549	864	0.293
HFO-865	111	96	120	25	17	8.03	22.7	21.3	78	67	3.89	27	1.7	1.096	0.169	40	13.43	12.97	83	30.05	10.45	2504	868	0.323
HFO-877	91	88	133	21	15	10.27	22.0	18.3	81	75	3.52	25	1.4	0.639	0.216	47	13.05	11.31	83	29.03	10.20	2417	850	0.293
HFO-879	109	93	119	24	22	8.93	26.7	24.3	82	123	4.17	42	2.0	1.495	0.287	42	13.91	13.68	89	30.60	13.81	2730	1229	0.243
HFO-502	104	86	113	33	17	8.53	36.8	22.3	69	100	3.60	37	1.6	1.036	0.187	42	12.34	13.38	85	30.25	12.25	2582	1042	0.230
HFO-58	108	92	115	16	13	9.53	16.7	20.0	75	53	3.55	38	1.6	1.847	0.163	46	11.74	13.54	86	32.76	11.12	2824	957	0.243
HFO-78	120	92	116	21	11	8.77	36.8	23.7	92	163	3.73	35	1.2	0.733	0.123	41	10.75	13.31	84	29.33	10.55	2468	887	0.241
HFO-60	115	94	119	18	15	8.90	20.5	20.0	92	113	3.02	37	1.6	0.876	0.193	41	14.49	13.74	88	32.08	11.55	2838	1016	0.217
HFO-603	132	91	120	30	16	8.27	33.3	24.7	79	136	3.49	34	1.8	0.872	0.185	38	13.19	13.95	85	28.78	10.73	2456	912	0.191
HFO-878	101	92	132	25	16	9.43	30.3	23.7	107	126	4.56	38	2.1	1.474	0.152	49	13.75	12.51	91	31.43	8.64	2875	786	0.241
HFO-874	107	86	132	21	16	10.23	23.0	20.7	82	86	3.59	31	1.8	0.604	0.122	46	12.57	12.41	83	31.70	11.01	2638	915	0.260
HFO-875	98	95	134	20	17	10.20	25.3	20.5	74	82	3.48	33	2.0	0.661	0.105	51	13.21	13.40	82	33.57	11.44	2763	939	0.273
HFO-872	108	97	129	14	12	9.27	23.0	13.0	84	71	3.23	21	1.3	0.501	0.108	44	13.40	13.36	84	33.53	14.10	2829	1185	0.200
HFO-498	105	91	121	18	19	9.20	31.7	17.2	49	92	3.41	26	1.6	0.548	0.146	42	13.98	13.10	86	30.19	10.24	2607	880	0.230
HFO-867	83	91	130	20	17	8.80	35.5	23.7	72	142	3.71	41	1.8	0.506	0.181	40	12.83	14.12	89	34.19	13.10	3049	1166	0.191
HFO-508	111	92	120	20	21	8.73	31.8	24.0	67	120	3.41	43	1.7	1.000	0.210	43	12.37	13.39	88	28.45	11.12	2511	979	0.333
KALOJAN	89	97	130	36	10	9.40	20.8	24.8	60	97	2.52	37	2.0	0.912	0.195	47	11.74	13.28	85	30.92	10.48	2639	891	0.343
HFO-409	147	96	128	26	15	9.50	31.8	15.2	58	94	3.13	38	2.6	1.228	0.158	44	10.97	13.27	84	28.58	11.30	2408	949	0.290
HFO-414	116	97	125	26	11	8.40	12.2	10.3	57	106	2.95	39	1.5	0.795	0.140	39	12.07	13.47	83	28.18	9.90	2347	820	0.307
HFO-523	124	95	122	27	13	8.67	19.3	20.7	53	93	3.33	30	2.0	0.941	0.144	42	13.66	12.31	86	28.08	10.52	2421	905	0.303
HFO-433	100	97	122	17	15	8.77	22.0	21.3	62	98	3.92	42	2.5	1.051	0.160	43	12.75	13.36	84	30.33	10.38	2536	866	0.323
HFO-885	109	94	113	29	19	9.23	31.7	29.0	55	120	3.33	31	1.6	0.959	0.142	44	13.59	13.67	87	31.92	7.33	2787	638	0.231
HFO-896	93	93	117	26	15	8.70	29.7	23.3	64	54	3.45	38	1.6	0.797	0.171	38	14.37	14.23	91	38.71	13.21	3526	1200	0.173
HFO-839	76	93	117	19	18	9.17	33.3	25.0	71	82	3.46	33	1.4	0.756	0.105	39	13.06	14.07	85	32.14	11.26	2739	956	0.217

HFO-836	76	95	119	11	15	9.53	19.3	17.0	74	87	3.45	21	1.9	0.665	0.121	46	11.39	12.69	83	29.22	10.48	2435	871	0.373
HFO-863	86	96	127	17	17	8.87	26.0	27.7	60	93	3.14	29	2.0	0.721	0.125	39	12.54	12.45	82	31.04	11.29	2553	925	0.340
HFO-884	83	93	129	19	16	9.20	22.0	19.8	70	89	3.24	36	1.4	0.707	0.137	40	12.58	13.45	83	30.47	10.95	2535	909	0.250
HFO-841	97	92	123	20	14	9.20	21.7	25.3	57	71	2.29	38	2.5	0.771	0.122	40	13.42	13.73	84	29.41	10.91	2477	917	0.330
HFO-851	73	91	115	27	23	8.90	38.8	24.5	64	67	2.85	41	2.3	0.580	0.156	43	13.96	14.07	86	33.42	12.59	2882	1081	0.230
HFO-880	99	95	112	21	11	8.57	25.8	25.2	71	111	3.67	31	1.9	0.605	0.122	40	12.75	14.31	82	33.02	11.52	2716	945	0.606
HFO-893	97	93	110	21	22	8.27	34.5	26.3	58	77	3.29	29	2.2	0.472	0.121	43	10.47	13.15	85	31.68	11.78	2700	1000	0.207
HFO-852	112	92	111	26	22	7.47	34.2	25.3	51	120	3.33	35	1.8	0.468	0.110	36	13.74	14.29	86	34.90	13.18	3011	1133	0.187
HFO-870	99	97	114	13	11	8.00	22.5	22.5	79	103	3.18	9	2.5	0.594	0.140	40	13.78	13.17	91	32.17	7.15	2937	651	0.424
HFO-862	105	91	112	20	23	8.67	37.7	22.0	62	134	3.80	30	1.9	0.500	0.130	46	14.01	14.15	84	34.46	8.50	2902	715	0.201
HFO-845	112	93	115	21	17	8.57	28.7	23.7	71	72	3.40	36	2.0	0.793	0.213	44	12.70	12.51	81	32.20	13.55	2609	1093	0.221
HFO-883	107	94	113	22	17	8.60	31.7	26.7	61	121	4.05	39	2.1	1.241	0.218	41	13.57	13.10	91	34.68	8.18	3164	744	0.252
HFO-831	93	98	117	19	15	10.13	29.8	16.3	54	81	3.48	35	2.8	1.084	0.154	51	11.21	12.67	85	32.39	12.26	2738	1033	0.220
HFO-114	107	93	129	32	22	9.27	24.3	25.3	60	76	3.50	31	2.1	1.003	0.193	40	10.35	12.42	87	30.39	11.26	2649	979	0.313
HFO-832	101	97	120	16	17	11.53	20.3	19.0	58	131	3.80	32	1.7	0.868	0.204	49	12.27	13.66	90	33.57	8.50	3032	764	0.292
HFO-603	123	97	113	22	13	8.87	23.0	28.0	73	103	3.17	34	2.0	1.257	0.256	40	13.45	12.73	87	31.28	11.51	2729	1002	0.250
HFO-605	125	98	129	24	19	9.80	22.3	25.7	57	98	2.55	32	2.2	1.048	0.195	31	13.71	13.49	88	32.15	12.25	2836	1078	0.230
HFO-611	126	100	126	24	17	9.07	19.7	24.3	74	82	2.31	31	2.0	1.145	0.253	40	12.05	12.48	85	31.73	11.76	2705	998	0.303
HFO-704	112	94	114	32	20	9.40	30.3	28.0	71	147	3.09	41	2.0	1.099	0.145	38	9.84	13.36	84	31.31	12.08	2618	1007	0.260
HFO-715	112	94	116	24	18	8.33	28.3	20.5	51	99	2.11	33	1.7	1.217	0.238	40	13.16	13.10	84	31.60	11.65	2666	979	0.303
HFO-610	112	94	115	25	24	8.80	26.3	23.3	48	110	3.96	31	1.7	0.729	0.181	38	12.43	12.50	87	31.52	13.18	2747	1146	0.231
HFO-706	110	94	119	15	23	9.07	23.0	26.0	58	61	4.09	29	2.0	0.692	0.179	37	13.18	11.32	92	30.68	10.59	2839	974	0.252
HFO-703	120	95	120	38	22	8.67	26.0	30.3	54	83	3.96	33	1.8	1.126	0.158	37	13.59	11.68	91	30.06	10.85	2741	987	0.211
HFO-575	117	92	116	17	12	7.80	16.2	16.0	58	84	3.99	32	1.3	0.646	0.153	37	13.90	14.69	90	34.34	9.31	3097	838	0.252
HFO-614	128	93	111	18	13	9.00	24.7	20.3	82	93	4.18	26	1.8	0.755	0.200	39	11.04	14.33	92	33.46	8.50	3088	781	0.201
HFO-707	114	93	114	25	12	8.40	19.0	24.0	89	103	3.71	36	1.9	0.855	0.168	35	12.61	11.58	91	31.08	13.03	2834	1186	0.247

HFO-905	110	94	115	25	22	9.27	38.0	29.7	53	124	3.45	38	2.0	0.924	0.175	33	14.12	13.40	87	31.05	12.36	2708	1075	0.220
HFO-908	104	93	120	22	21	9.40	24.7	26.7	64	65	3.97	34	1.7	0.905	0.213	37	13.95	13.45	88	31.78	15.58	2796	1368	0.231
HFO-914	112	94	118	25	18	8.27	34.3	23.7	66	94	3.91	35	1.8	0.790	0.218	40	13.76	13.29	92	35.94	8.08	3316	743	0.292
HFO-909	113	96	116	26	18	7.27	18.7	26.7	71	98	3.59	38	2.3	1.119	0.206	31	12.08	14.00	81	35.03	15.03	2850	1219	0.200
HFO-904	111	91	120	28	16	8.60	23.3	23.3	75	89	3.54	32	2.3	0.918	0.204	39	13.48	13.74	84	32.49	12.47	2741	1048	0.213
HFO-910	98	93	114	32	17	9.33	32.5	27.3	64	111	3.35	32	1.7	1.230	0.249	41	12.57	13.47	85	32.65	12.22	2775	1035	0.213
HFO-913	107	92	115	27	18	8.73	26.2	23.0	74	103	3.96	32	1.5	1.041	0.227	39	13.21	14.30	90	36.58	8.89	3300	800	0.191
HFO-921	108	92	114	20	16	8.87	22.2	18.3	60	136	3.58	36	1.3	0.631	0.115	38	13.57	13.67	90	32.06	11.09	2885	995	0.292
HFO-924	109	96	112	26	12	7.20	25.3	22.0	58	87	3.29	35	1.7	1.506	0.258	33	10.53	12.51	92	32.84	12.11	3030	1114	0.302
HFO-919	122	92	114	20	15	9.47	27.5	23.3	51	112	2.50	27	1.4	1.063	0.200	38	12.30	13.72	89	34.77	13.92	3100	1239	0.221
HFO-906	107	92	113	28	18	9.27	32.0	23.2	65	60	3.17	36	1.8	0.709	0.154	37	11.96	13.14	91	34.58	9.17	3160	834	0.201
HFO-912	110	93	115	32	23	8.73	21.0	26.5	55	174	3.87	27	1.5	1.612	0.303	39	9.91	13.71	88	31.24	8.00	2758	704	0.231
HFO-902	111	94	118	30	16	8.33	22.3	22.7	69	113	3.63	33	2.4	0.740	0.194	37	10.08	13.36	85	32.05	11.90	2723	1010	0.213
HFO-920	110	95	118	23	15	9.40	18.0	20.7	87	98	3.98	34	1.7	0.946	0.200	37	12.42	13.56	85	34.41	12.82	2938	1090	0.210
HJ 8	141	96	124	26	17	8.58	24.2	22.7	77	147	4.11	34	2.0	1.157	0.247	40	13.23	14.07	89	34.13	12.93	3040	1148	0.190
OS 403	142	94	124	24	17	8.38	29.2	22.8	68	153	3.46	33	1.6	1.391	0.296	41	13.17	14.07	87	33.62	13.10	2936	1141	0.200
Mean	110	93	119	23	17	9.03	25.8	22.3	68	102	3.36	34	1.8	0.958	0.186	42	12.61	13.23	87	31.88	10.64	2,771	920	0.268
C.D. (5%)	17.1	2.7	2.77	3.7	2.1	0.81	4.25	4.17	8.18	15.5	0.17	5.7	0.23	0.22	0.054	6.3	0.649	0.395	3.60	1.52	0.346	179.4	44.02	0.040
C.V. (%)	9.66	1.8	1.44	9.8	7.6	5.58	10.2	11.6	7.42	9.39	3.2	10.7	8.01	13.92	17.89	9.4	3.19	1.85	2.57	2.96	2.01	4.02	2.97	9.31

PH- Plant height (cm), DF - NO. of days to 50% flowering, DM- Number of days to maturity, FLL- Flag leaf length (cm), IL- Internode length (cm), TPL-Number of tillers per plant, PL- Peduncle length (cm), AL- Axis length (cm), NOS- Number of spikelets per panicle, SY- Seed yield(g), SI-100 seed weight(g), LL- Leaf length(cm), LW- Leaf width(cm), GFY- Green fodder yield(kg), DMY- Dry matter yield(kg), NOLS- Number of leaves per plant, CPg- Crude protein in grain (%), CPf- Crude protein in forage (%) GP- Germination %, SL- Seedling length(cm), SDW- Seedling dry weight(mg), SVI- Seed vigour index-1, SVII- Seed vigour index-2, EC- Electrical conductivity(mS/cm/seed)

4.2.2 Mean performance in 1st cut of multi-cut

4.2.2.1 Plant height (cm)

The maximum plant height was recorded in the genotype, UPO-212 (68 cm) and minimum in HFO-875 (27 cm). The genotypes namely, JO-1, OL-1, JHO-99-1, DULO, OL-10, KENT, HFO-502, HFO-839, HFO-603, HFO-704 and HFO-912 had recorded highest plant height.

4.2.2. Number of tillers/plant

The maximum numbers of tillers per plant were recorded in genotype, HFO-603 (10.5) and found minimum in HFO-919 and HFO-904 (7.1 cm). The genotypes namely UPO-94, PLP-1, SABZAR, HFO-504, HFO-875, HFO-872, HFO-114, HFO-851, HFO-498, HFO-879, HFO-504, HFO-305, DULO, JHO-822 and HFO-267 had more tillers /plant.

4.2.2.3 Green fodder yield (kg)

The highest mean value of green fodder yield was observed in genotype, UPO-121 (0.372Kg) and the lowest in HFO-872 (.087 Kg). The genotypes with highest value of green fodder yield were OL-125, SABZAR, JHO99-1, FOS-1/29, HFO-505, HFO-879, HFO-502, HFO-58, HFO-78, HFO-409, HFO-839, HFO-836, HFO-884, HFO-845, HFO-883, HFO-610, HFO-706, HFO-908, HFO-924 and HFO-912.

4.2.2.4 Dry matter yield (kg)

The highest mean value of dry matter yield was observed in genotype, UPO-212 (0.082Kg) and the lowest in HFO-872 (0.030 g). The genotypes with highest value of dry matter yield were ALGERIAN, OL-125, JHO-99-1, HFO-879, HFO-502, HFO-58, HFO-876, HFO-409, HFO-839, HFO-836, HFO-884, HFO-852, HFO-845, HFO-883, HFO-610, HFO-706, HFO-904, HFO-924 and HFO-912.

4.2.2.5 Crude Protein in forage (%)

The highest mean value of crude protein in forage was observed in genotype, HFO-896(15.60%) and the lowest in HFO-877 (12.1 %). The genotypes with highest crude protein in forage HFO-267, JHO-851, JHO-2006-2, KENT, HFO-504, HFO-877, HFO-867, KALOJAN, HFO-433, HFO-839, HFO-841, HFO-852, HFO-715, HFO-614, HFO-914 and HFO-913.

Table 4.5: Mean values of dry matter yield and its component characters of 92 genotype of oat in Ist cut of multi-cut oat

Genotype	PH	TPL	GFY	DMY	CP	GP	SL	SDW	SVI	SVII	EC
JO-1	62	8.30	223	55	14.18	87	31.63	8.62	2760	750	0.290
ALGERIAN	56	9.00	199	57	13.89	89	30.75	7.83	2724	693	0.282
HFO-267	52	8.13	175	45	15.21	90	33.47	7.93	2997	708	0.201
OL-125	64	8.17	267	63	13.81	85	29.19	8.92	2478	755	0.353
OL-10	64	9.53	201	47	13.54	85	29.52	7.05	2517	599	0.340
PLP-1	41	9.20	125	35	13.81	85	27.82	9.14	2372	779	0.383
JHO-2006-4	56	9.93	242	53	13.81	89	33.04	7.33	2953	652	0.282
SABZAR	58	8.43	255	55	13.81	85	31.92	8.11	2704	684	0.434
DUNAV	33	9.17	202	42	13.81	85	27.62	8.25	2335	696	0.390
JHO-851	48	9.63	210	48	13.81	89	35.07	8.93	3109	788	0.252
UPO-94	47	9.23	195	45	13.81	87	31.63	9.25	2739	800	0.360
JHO-822	58	8.37	224	54	13.81	91	33.26	9.88	3035	899	0.252
SKO-90	48	8.03	207	48	13.81	87	33.08	9.03	2871	783	0.287
JHO-99-1	65	8.10	330	72	13.81	91	35.25	7.69	3203	696	0.231
FOS-1/29	63	9.33	315	68	13.81	83	32.43	8.93	2702	742	0.300
DULO	65	8.37	205	49	13.81	85	28.84	7.01	2450	594	0.367
UPO-212	68	7.83	372	82	13.81	85	30.73	8.18	2610	693	0.357
OS-6	59	9.20	243	27	13.81	88	34.48	11.44	3032	1003	0.191
JHO-2006-2	35	8.10	140	38	13.81	85	31.60	11.01	2676	930	0.350
KENT	62	7.70	179	46	13.81	88	34.01	11.76	2991	1031	0.223
HFO-505	59	8.60	242	55	13.81	88	32.73	10.55	2866	924	0.247
HFO-975	53	8.23	227	54	13.81	84	29.20	10.77	2450	902	0.191
HFO-69	59	9.13	196	50	13.81	88	32.06	7.58	2823	663	0.211
HFO-876	28	9.20	232	58	13.81	83	28.38	9.28	2356	769	0.380
HFO-305	55	9.43	202	48	13.81	90	33.08	14.17	2995	1279	0.221
HFO-504	55	8.23	214	52	13.81	91	31.61	9.53	2879	867	0.302

HFO-864	52	8.63	244	37	13.81	89	28.54	9.70	2549	864	0.293
HFO-865	50	7.70	218	53	13.81	83	30.05	10.45	2504	868	0.323
HFO-877	29	9.10	212	52	13.81	83	29.03	10.20	2417	850	0.293
HFO-879	56	8.23	253	63	13.81	89	30.60	13.81	2730	1229	0.243
HFO-502	63	8.30	324	75	13.81	85	30.25	12.25	2582	1042	0.230
HFO-58	62	8.77	337	80	13.81	86	32.76	11.12	2824	957	0.243
HFO-78	59	8.30	246	27	13.81	84	29.33	10.55	2468	887	0.241
HFO-60	58	8.43	223	55	13.81	88	32.08	11.55	2838	1016	0.217
HFO-603	57	8.00	207	53	13.81	85	28.78	10.73	2456	912	0.191
HFO-878	59	9.10	235	57	13.81	91	31.43	8.64	2875	786	0.241
HFO-874	52	9.53	228	55	13.81	83	31.70	11.01	2638	915	0.260
HFO-875	27	9.30	227	53	13.81	82	33.57	11.44	2763	939	0.273
HFO-872	47	8.97	87	30	13.81	84	33.53	14.10	2829	1185	0.200
HFO-498	53	8.37	225	53	13.81	86	30.19	10.24	2607	880	0.230
HFO-867	48	8.37	160	24	13.81	89	34.19	13.10	3049	1166	0.191
HFO-508	54	8.30	110	30	13.81	88	28.45	11.12	2511	979	0.333
KALOJAN	29	8.40	150	35	13.81	85	30.92	10.48	2639	891	0.343
HFO-409	56	8.83	242	58	13.81	84	28.58	11.30	2408	949	0.290
HFO-414	56	8.10	175	40	13.81	83	28.18	9.90	2347	820	0.307
HFO-523	60	8.17	208	50	13.81	86	28.08	10.52	2421	905	0.303
HFO-433	57	8.37	205	44	13.81	84	30.33	10.38	2536	866	0.323
HFO-885	55	8.90	222	53	13.81	87	31.92	7.33	2787	638	0.231
HFO-896	54	8.23	171	41	13.81	91	38.71	13.21	3526	1200	0.173
HFO-839	64	7.67	282	74	13.81	85	32.14	11.26	2739	956	0.217
HFO-836	45	8.33	273	70	13.81	83	29.22	10.48	2435	871	0.373
HFO-863	48	8.83	154	39	13.81	82	31.04	11.29	2553	925	0.340
HFO-884	42	8.30	262	66	13.81	83	30.47	10.95	2535	909	0.250
HFO-841	60	8.97	220	48	13.81	84	29.41	10.91	2477	917	0.330
HFO-851	49	8.10	173	40	13.81	86	33.42	12.59	2882	1081	0.230

HFO-880	53	7.97	179	44	13.81	82	33.02	11.52	2716	945	0.606
HFO-893	55	7.63	223	54	13.81	85	31.68	11.78	2700	1000	0.207
HFO-852	52	6.90	231	57	13.81	86	34.90	13.18	3011	1133	0.187
HFO-870	53	7.43	158	40	13.81	91	32.17	7.15	2937	651	0.424
HFO-862	56	8.00	236	57	13.81	84	34.46	8.50	2902	715	0.201
HFO-845	57	8.50	307	73	13.81	81	32.20	13.55	2609	1093	0.221
HFO-883	57	8.10	252	63	13.81	91	34.68	8.18	3164	744	0.252
HFO-831	44	9.70	173	42	13.81	85	32.39	12.26	2738	1033	0.220
HFO-114	56	8.77	175	43	13.81	87	30.39	11.26	2649	979	0.313
HFO-832	32	10.03	150	35	13.81	90	33.57	8.50	3032	764	0.292
HFO-603	66	7.83	174	42	13.81	87	31.28	11.51	2729	1002	0.250
HFO-605	58	7.90	200	47	13.81	88	32.15	12.25	2836	1078	0.230
HFO-611	60	8.37	217	52	13.81	85	31.73	11.76	2705	998	0.303
HFO-704	61	8.10	222	53	13.81	84	31.31	12.08	2618	1007	0.260
HFO-715	59	7.77	204	49	13.81	84	31.60	11.65	2666	979	0.303
HFO-610	58	7.70	247	57	13.81	87	31.52	13.18	2747	1146	0.231
HFO-706	56	8.10	250	60	13.81	92	30.68	10.59	2839	974	0.252
HFO-703	57	7.50	163	39	13.81	91	30.06	10.85	2741	987	0.211
HFO-575	58	6.93	238	57	13.81	90	34.34	9.31	3097	838	0.252
HFO-614	57	8.23	225	53	13.81	92	33.46	8.50	3088	781	0.201
HFO-707	57	7.23	213	47	13.81	91	31.08	13.03	2834	1186	0.247
HFO-905	60	7.70	175	40	13.81	87	31.05	12.36	2708	1075	0.220
HFO-908	58	8.10	241	55	13.81	88	31.78	15.58	2796	1368	0.231
HFO-914	57	8.03	143	34	13.81	92	35.94	8.08	3316	743	0.292
HFO-909	52	6.63	172	40	13.81	81	35.03	15.03	2850	1219	0.200
HFO-904	49	7.93	236	57	13.81	84	32.49	12.47	2741	1048	0.213
HFO-910	53	8.63	208	48	13.81	85	32.65	12.22	2775	1035	0.213
HFO-913	53	8.20	137	31	13.81	90	36.58	8.89	3300	800	0.191
HFO-921	60	7.77	203	45	13.81	90	32.06	11.09	2885	995	0.292

HFO-924	58	6.63	240	57	13.81	92	32.84	12.11	3030	1114	0.302
HFO-919	57	8.03	194	46	13.81	89	34.77	13.92	3100	1239	0.221
HFO-906	58	7.97	182	44	13.81	91	34.58	9.17	3160	834	0.201
HFO-912	62	7.93	319	73	13.81	88	31.24	8.00	2758	704	0.231
HFO-902	55	7.57	214	53	13.81	85	32.05	11.90	2723	1010	0.213
HFO-920	61	8.17	219	53	13.81	85	34.41	12.82	2938	1090	0.210
HJ 8	64	7.97	230	53	13.81	89	34.13	12.93	3040	1148	0.190
OS 403	64	7.90	240	57	13.81	87	33.62	13.10	2936	1141	0.200
Mean	54	8.34	216	51	13.83	87	31.88	10.64	2,771	920	0.268
C. D	11.78	0.80	39.62	13.57	0.751	3.60	1.52	0.346	179.4	44.02	0.040
CV(%)	13.45	5.94	11.37	16.64	3.33	2.57	2.96	2.01	4.02	2.97	9.31

PH- Plant height (cm), TPL-Number of tillers per plant, GFY- Green fodder yield(kg), DMY- Dry matter yield(kg), NOLS- Number of leaves per plant, CPf- Crude protein in forage (%) GP- Germination %, SL- Seedling length(cm), SDW- Seedling dry weight(mg), SVI- Seed vigour index-1, SVII- Seed vigour index-2, EC- Electrical conductivity(mS/cm/seed)

4.2.3 Mean performance in 2nd cut of multi-cut

4.2.3.1 Plant height (cm)

The maximum plant height was recorded in the genotype, HFO-878 (98cm) and minimum in KALOJAN (43cm). The genotypes namely, JHO-822, DULO, UPO-212, OS-6 , HFO-504, HFO-603, HFO-863, HFO-862, HFO-603, HFO-611, HFO-914, and HFO-610, had maximum plant height.

4.2.3.2 Days to 50% flowering (days)

The maximum HFO 875 (134 days) and the minimum HFO 893 (111 days) number of days to 50% flowering were observed in genotypes. The genotypes, HFO-975, HFO-504, HFO-864, HFO 880, HFO-852, HFO-862, HFO-614 and HFO 924 were best for the days to 50% flowering.

4.2.3.3 Flag leaf length (cm)

The maximum flag leaf length was recorded in the genotype, HFO-703 (34 cm) and it was minimum in HFO-870 (12cm). The genotypes namely PLP-1, UPO-212, HFO-305, HFO-502, HFO-603, KALOJAN, HFO-885, HFO-114, HFO-704, HFO-910, HFO-902 and HFO-912 had recorded higher flag leaf length.

4.2.3.4 Internode length (cm)

The maximum internode length was recorded in the genotypes, HFO-69 and HFO-610 (24 cm) and it was minimum in DUNAV (8cm). The genotypes namely, HFO-851, HFO-893, HFO-706, HFO-862, HFO-703, HFO-905 and HFO-912 had large internode length.

4.2.3.5 Number of tillers/plant

The maximum number of tillers /plant were recorded in genotype, HFO-832 (10.7) and it was minimum in HFO-909 and HFO-924 (7 cm). The genotypes namely OL-10, PLP-1, JHO-2006-4, DUNAV, JHO-851, UPO-94, OS-6, HFO-69, HFO-879, HFO-305, HFO-841, HFO-831 and HFO-874, had higher number of tillers /plant.

4.2.3.6 Peduncle length (cm)

The maximum peduncle length was recorded in the genotype, HFO-905 (38cm) and it was minimum in HFO-414 (12.2 cm). The genotypes namely, SKO-90, HFO-502, HFO-78, HFO-603, HFO-867, HFO-893, HFO-611, HFO-914 and HFO-910 had highest peduncle length.

4.2.3.7 Leaf length (cm)

The highest mean value of leaf length was observed in genotype, SABZAR (50 cm) and the lowest in HFO-870 (9 cm). The genotypes with highest leaf length value were PLP-1, JHO-851, UPO-212, DULO, KENT, HFO-504, HFO-879, HFO-433, HFO-851, HFO-867, HFO-508 and HFO-704.

4.2.3.8 Leaf width (cm)

The highest mean value of leaf width was observed in genotype, HFO-831 (2.8 cm) and the lowest in SKO-90 (0.6 cm). The genotypes with highest leaf width, HFO-504, HFO-409, HFO-433, HFO-841, HFO-851, HFO-893, HFO-870, HFO-831, HFO-605, HFO-909, HFO-902 and HFO-904.

4.2.3.9 Green fodder yield (kg)

The highest mean value of green fodder yield was observed in genotype, HFO-114 (0.857 kg) and the lowest in HFO-852 (0.222 kg). The genotypes with highest value of green fodder yield were ALGERIAN, PLP-1, JHO-2006-2, HFO-69, HFO-865, HFO-58, HFO-78 HFO-60, HFO-508, HFO-414, HFO-433, HFO-896, HFO-863, HFO-831, HFO-603, HFO-904, HFO-912 and HFO-902.

4.2.3.10 Dry matter yield (kg)

The highest mean value of dry matter yield was observed in genotype, HFO-414 (0.193Kg) and the lowest in HFO-852 (0.075 Kg). The genotypes with highest value of dry matter yield were HFO-267, PLP-1, JHO-822, OS-6, HFO-69, HFO-864, HFO-865, HFO-58, HFO-78, HFO-60, HFO-508, HFO-433, HFO-885, HFO-896, HFO-863, HFO-831, HFO-114, HFO-603, HFO-605, HFO-904, HFO-912 and HFO-902.

4.2.3.11 Number of leaves/plant

The maximum number of leaves/plant were recorded in the genotypes, HFO-875 and HFO-831 (50) and it was minimum in HFO-909 (30). The genotypes namely OS-6, OL-10, HFO-876, HFO-305, HFO-877, HFO-58, HFO-878, HFO-874, HFO-875, KALOJAN, HFO-832, HFO-831, HFO-862 and HFO-836 had highest leaves /plant.

4.2.3.12 Crude Protein in forage (%)

The highest mean value of crude protein in forage was observed in genotype, HFO-896 (13.57 %) and the lowest in HFO-706 (9.63 %). The genotypes with highest crude protein in forage HFO-851, HFO-862, HFO-575, HFO-909, HFO-913, JO-1, KENT, OS-6, HFO-603, HFO-875, HFO-867 and HFO-885

Table 4.6: Mean values of dry matter yield and its component characters of 92 genotype of oat in 2nd cut of multicut oat

Genotype	PH	DM	FLL	IL	TPL	PL	AL	SI	LL	LW	GFY	DMY	NOL	CPMC	G	SL	SDW	SVI	SVII	EC
JO-1	74	117	21	17	8.73	21.5	20.7	3.61	35	1.3	443	116	41	12.93	87	31.63	8.62	2760	750	0.290
ALGERIAN	68	125	24	18	9.43	27.0	21.7	3.15	35	1.9	660	120	40	11.68	89	30.75	7.83	2724	693	0.282
HFO-267	60	115	22	17	8.57	19.0	8.7	3.23	34	1.4	524	133	37	13.56	90	33.47	7.93	2997	708	0.201
OL-125	70	119	23	13	8.60	20.0	20.3	3.16	34	1.7	407	98	41	11.92	85	29.19	8.92	2478	755	0.353
OL-10	72	123	17	12	9.97	22.0	14.7	2.93	28	1.2	353	95	47	10.97	85	29.52	7.05	2517	599	0.340
PLP-1	67	126	28	16	9.63	23.3	20.3	2.23	41	1.9	610	148	43	10.17	85	27.82	9.14	2372	779	0.383
JHO-2006-4	74	120	27	19	10.37	20.0	20.3	3.25	40	1.3	412	102	41	12.15	89	33.04	7.33	2953	652	0.282
SABZAR	72	122	24	21	8.87	28.0	22.0	2.05	50	1.7	410	113	43	11.33	85	31.92	8.11	2704	684	0.434
DUNAV	45	131	17	8	9.60	27.7	21.0	2.25	28	1.3	512	129	43	10.70	85	27.62	8.25	2335	696	0.390
JHO-851	82	120	23	20	10.07	13.0	26.0	3.19	44	1.9	408	105	48	12.95	89	35.07	8.93	3109	788	0.252
UPO-94	66	116	19	11	9.67	21.3	21.0	3.57	32	1.8	505	132	43	12.88	87	31.63	9.25	2739	800	0.360
JHO-822	87	116	23	21	8.80	31.0	28.0	2.70	43	1.9	507	133	41	12.46	91	33.26	9.88	3035	899	0.252
SKO-90	59	119	18	11	8.47	33.0	16.0	2.46	26	0.6	407	107	38	11.85	87	33.08	9.03	2871	783	0.287
JHO-99-1	71	117	24	11	8.53	25.7	15.0	2.99	33	1.3	285	78	41	12.85	91	35.25	7.69	3203	696	0.231
FOS-1/29	72	121	23	17	9.77	25.7	17.7	3.31	39	1.9	463	118	47	9.88	83	32.43	8.93	2702	742	0.300
DULO	97	120	24	21	8.80	23.7	22.3	3.08	42	1.8	463	123	43	12.19	85	28.84	7.01	2450	594	0.367
UPO-212	88	117	29	20	8.27	24.0	23.0	3.34	41	2.0	365	97	38	11.77	85	30.73	8.18	2610	693	0.357
OS-6	95	118	24	20	9.63	26.7	26.3	3.50	35	1.7	503	132	49	13.12	88	34.48	11.44	3032	1003	0.191
JHO-2006-2	65	119	19	15	8.53	22.0	15.0	2.47	32	2.1	527	135	41	11.48	85	31.60	11.01	2676	930	0.350
KENT	73	120	21	18	8.13	26.0	23.3	3.24	42	2.0	393	100	42	12.44	88	34.01	11.76	2991	1031	0.223
HFO-505	64	114	21	19	9.03	25.7	22.0	3.62	38	1.8	477	125	46	12.33	88	32.73	10.55	2866	924	0.247
HFO-975	66	113	18	11	8.67	20.8	8.3	3.54	30	1.4	424	112	40	10.96	84	29.20	10.77	2450	902	0.191
HFO-69	75	117	19	24	9.57	19.7	21.0	3.13	30	1.7	562	143	44	9.99	88	32.06	7.58	2823	663	0.211
HFO-876	65	131	23	17	9.63	21.0	20.7	3.62	28	1.5	448	115	45	11.31	83	28.38	9.28	2356	769	0.380
HFO-305	68	116	31	16	9.87	30.7	23.0	3.74	37	1.6	417	108	49	12.53	90	33.08	14.17	2995	1279	0.221
HFO-504	91	113	20	18	8.67	19.7	26.7	2.91	41	2.4	300	86	41	11.75	91	31.61	9.53	2879	867	0.302

HFO-864	75	113	21	15	9.07	15.7	19.3	3.30	26	1.3	523	137	40	10.35	89	28.54	9.70	2549	864	0.293
HFO-865	72	120	25	17	8.13	21.7	21.3	3.89	27	1.6	577	145	39	10.34	83	30.05	10.45	2504	868	0.323
HFO-877	52	134	20	14	9.53	20.7	18.3	3.52	25	1.4	485	123	46	10.05	83	29.03	10.20	2417	850	0.293
HFO-879	74	119	23	22	8.67	26.0	22.7	4.17	42	2.0	537	137	41	12.59	89	30.60	13.81	2730	1229	0.243
HFO-502	80	114	32	17	8.73	34.8	21.7	3.60	37	1.6	389	98	41	12.19	85	30.25	12.25	2582	1042	0.230
HFO-58	79	115	15	13	9.20	16.0	20.3	3.55	38	1.6	690	163	45	11.59	86	32.76	11.12	2824	957	0.243
HFO-78	79	116	20	11	8.73	35.0	22.0	3.73	35	1.2	548	138	40	12.79	84	29.33	10.55	2468	887	0.241
HFO-60	81	119	17	15	8.87	20.5	20.0	3.02	37	1.6	713	173	40	11.43	88	32.08	11.55	2838	1016	0.217
HFO-603	96	120	29	16	8.43	33.3	23.0	3.49	34	1.8	427	103	37	13.31	85	28.78	10.73	2456	912	0.191
HFO-878	98	133	24	16	9.53	29.7	23.7	4.56	38	2.1	435	115	48	11.31	91	31.43	8.64	2875	786	0.241
HFO-874	72	132	20	16	9.97	22.3	20.0	3.59	31	1.8	347	92	45	11.85	83	31.70	11.01	2638	915	0.260
HFO-875	62	134	19	17	9.73	23.0	19.7	3.48	33	2.0	317	92	50	13.05	82	33.57	11.44	2763	939	0.273
HFO-872	68	130	13	12	9.40	22.3	12.3	3.23	21	1.3	473	123	43	12.10	84	33.53	14.10	2829	1185	0.200
HFO-498	81	121	17	19	8.80	30.0	17.0	3.41	26	1.6	376	95	41	11.72	86	30.19	10.24	2607	880	0.230
HFO-867	73	130	19	17	8.80	32.0	22.7	3.71	41	1.8	387	103	39	13.20	89	34.19	13.10	3049	1166	0.191
HFO-508	79	121	19	21	8.73	29.3	22.7	3.41	43	1.7	572	148	42	12.45	88	28.45	11.12	2511	979	0.333
KALOJAN	43	130	33	10	8.83	20.0	18.3	2.52	37	2.0	470	123	46	12.07	85	30.92	10.48	2639	891	0.343
HFO-409	71	128	25	15	9.27	29.0	15.2	3.13	38	2.6	450	117	43	10.50	84	28.58	11.30	2408	949	0.290
HFO-414	73	126	25	11	8.53	12.2	11.0	2.95	39	1.4	828	193	38	12.08	83	28.18	9.90	2347	820	0.307
HFO-523	71	123	25	13	8.60	18.7	20.3	3.33	30	2.0	395	108	41	10.33	86	28.08	10.52	2421	905	0.303
HFO-433	80	123	16	15	8.80	21.3	20.7	3.92	42	2.5	608	143	42	12.42	84	30.33	10.38	2536	866	0.323
HFO-885	76	114	28	19	9.33	29.7	26.7	3.33	31	1.6	520	135	43	13.01	87	31.92	7.33	2787	638	0.231
HFO-896	67	117	25	15	8.67	26.3	22.0	3.45	38	1.6	648	162	37	13.57	91	38.71	13.21	3526	1200	0.173
HFO-839	65	118	19	18	8.10	27.3	23.0	3.46	33	1.4	457	118	38	12.86	85	32.14	11.26	2739	956	0.217
HFO-836	68	120	10	15	8.77	18.7	16.0	3.45	21	1.9	443	113	45	10.24	83	29.22	10.48	2435	871	0.373
HFO-863	94	128	17	17	9.27	24.3	26.7	3.14	29	2.0	640	157	38	9.67	82	31.04	11.29	2553	925	0.340
HFO-884	76	130	18	16	8.73	21.0	19.0	3.24	36	1.3	420	111	39	11.08	83	30.47	10.95	2535	909	0.250
HFO-841	84	124	19	14	9.40	20.3	24.3	2.29	38	2.5	437	113	39	11.10	84	29.41	10.91	2477	917	0.330
HFO-851	65	116	26	23	8.53	22.7	24.0	2.85	41	2.3	433	117	42	13.08	86	33.42	12.59	2882	1081	0.230

HFO-880	62	113	20	11	8.40	24.2	23.3	3.67	31	1.9	433	113	39	12.38	82	33.02	11.52	2716	945	0.606
HFO-893	60	111	20	22	8.07	32.3	21.3	3.29	29	2.2	493	128	42	12.40	85	31.68	11.78	2700	1000	0.207
HFO-852	68	112	25	21	7.33	27.7	24.0	3.33	35	1.8	222	75	35	13.43	86	34.90	13.18	3011	1133	0.187
HFO-870	45	115	12	11	7.87	20.7	20.3	3.18	9	2.5	377	98	39	12.37	91	32.17	7.15	2937	651	0.424
HFO-862	88	113	19	23	8.43	31.0	21.0	3.80	30	1.9	273	80	45	13.18	84	34.46	8.50	2902	715	0.201
HFO-845	75	116	20	17	8.93	25.7	21.7	3.40	36	2.0	457	117	43	10.58	81	32.20	13.55	2609	1093	0.221
HFO-883	73	114	21	17	8.53	27.3	25.0	4.05	39	2.0	437	118	40	12.37	91	34.68	8.18	3164	744	0.252
HFO-831	62	118	18	15	10.13	27.3	16.7	3.48	35	2.8	602	150	50	10.95	85	32.39	12.26	2738	1033	0.220
HFO-114	77	130	31	21	9.20	22.3	24.0	3.50	31	2.1	857	187	39	10.15	87	30.39	11.26	2649	979	0.313
HFO-832	68	121	15	17	10.47	19.7	19.3	3.80	32	1.6	443	113	48	12.06	90	33.57	8.50	3032	764	0.292
HFO-603	90	114	21	13	8.27	23.0	27.0	3.17	34	2.0	637	158	39	10.23	87	31.28	11.51	2729	1002	0.250
HFO-605	82	130	23	19	8.33	22.3	25.0	2.55	32	2.2	517	135	30	12.30	88	32.15	12.25	2836	1078	0.230
HFO-611	96	127	23	17	8.80	19.7	23.7	2.31	31	2.0	297	83	39	10.43	85	31.73	11.76	2705	998	0.303
HFO-704	80	114	31	20	8.53	30.3	24.0	3.09	41	2.0	440	117	37	12.35	84	31.31	12.08	2618	1007	0.260
HFO-715	76	116	23	18	8.20	28.3	20.3	2.11	33	1.7	413	105	39	11.13	84	31.60	11.65	2666	979	0.303
HFO-610	87	116	24	24	8.13	26.3	21.7	3.96	31	1.7	457	117	37	10.67	87	31.52	13.18	2747	1146	0.231
HFO-706	85	120	14	23	8.53	23.0	25.7	4.09	29	1.9	340	96	36	9.63	92	30.68	10.59	2839	974	0.252
HFO-703	82	121	34	22	7.93	26.0	27.0	3.96	33	1.8	410	106	36	10.63	91	30.06	10.85	2741	987	0.211
HFO-575	74	117	15	12	7.37	16.2	16.0	3.99	32	1.3	317	72	36	13.57	90	34.34	9.31	3097	838	0.252
HFO-614	68	112	18	13	8.67	24.7	20.7	4.18	26	1.8	487	128	38	12.52	92	33.46	8.50	3088	781	0.201
HFO-707	63	115	23	12	7.67	19.0	23.0	3.71	36	1.9	460	119	34	10.42	91	31.08	13.03	2834	1186	0.247
HFO-905	80	116	23	22	8.13	38.0	28.7	3.45	38	1.9	353	91	32	12.75	87	31.05	12.36	2708	1075	0.220
HFO-908	81	121	20	21	8.53	24.7	25.3	3.97	34	1.7	438	113	36	12.75	88	31.78	15.58	2796	1368	0.231
HFO-914	87	118	24	17	8.47	34.3	23.0	3.91	35	1.8	310	90	39	10.85	92	35.94	8.08	3316	743	0.292
HFO-909	75	117	25	18	7.07	18.7	25.3	3.59	38	2.3	368	92	30	13.07	81	35.03	15.03	2850	1219	0.200
HFO-904	71	121	27	16	8.37	23.3	22.7	3.54	32	2.3	563	147	38	12.28	84	32.49	12.47	2741	1048	0.213
HFO-910	86	115	31	17	9.07	32.5	26.7	3.35	32	1.7	467	120	40	11.78	85	32.65	12.22	2775	1035	0.213
HFO-913	74	116	25	18	8.63	26.2	21.3	3.96	32	1.5	327	85	38	12.94	90	36.58	8.89	3300	800	0.191
HFO-921	66	114	19	16	8.20	22.2	18.3	3.58	36	1.3	367	95	37	12.62	90	32.06	11.09	2885	995	0.292

HFO-924	74	112	25	12	7.07	25.3	20.3	3.29	35	1.7	460	117	32	10.80	92	32.84	12.11	3030	1114	0.302
HFO-919	63	115	19	15	8.47	27.5	22.3	2.50	27	1.3	440	109	37	12.10	89	34.77	13.92	3100	1239	0.221
HFO-906	73	114	27	18	8.40	32.0	23.0	3.17	36	1.8	427	112	36	12.34	91	34.58	9.17	3160	834	0.201
HFO-912	79	116	31	23	8.37	20.0	26.0	3.87	27	1.5	443	112	38	12.11	88	31.24	8.00	2758	704	0.231
HFO-902	82	119	29	16	8.00	20.3	22.0	3.63	33	2.4	667	168	36	12.09	85	32.05	11.90	2723	1010	0.213
HFO-920	65	118	22	15	8.60	17.7	20.0	3.98	34	1.7	680	162	36	11.77	85	34.41	12.82	2938	1090	0.210
HJ 8	90	125	25	16	8.40	22.5	21.7	4.11	34	1.9	713	176	39	13.76	89	34.13	12.93	3040	1148	0.190
OS 403	82	124	22	16	8.33	25.3	21.3	3.46	33	1.5	564	148	40	13.41	87	33.62	13.10	2936	1141	0.200
Mean	74	120	22	17	8.77	24.4	21.3	3.36	31	1.8	470	120	41	11.87	87	31.88	10.64	2,771	920	0.268
C. D	16	2.77	3.7	3	0.799	4.25	3.48	0.17	5.8	0.2	139.8	30.3	6.30	0.659	3.6	1.52	0.346	179.4	44.02	0.040
C.V. (%)	13	1.43	10	11	5.65	10.8	10.2	3.20	11	8.2	18.44	15.64	9.63	3.45	2.6	2.96	2.01	4.02	2.97	9.31

PH- Plant height (cm), DF - NO. of days to 50% flowering, FLL- Flag leaf length (cm), IL- Internode length (cm), TPL-Number of tillers per plant, PL- Peduncle length (cm), AL- Axis length (cm), SI-100 seed weight(g), LL- Leaf length(cm), LW- Leaf width(cm), GFY- Green fodder yield(kg), DMY- Dry matter yield(kg), NOLS- Number of leaves per plant, CPf- Crude protein in forage (%) GP- Germination %, SL- Seedling length(cm), SDW- Seedling dry weight(mg), SVI- Seed vigour index-1, SVII- Seed vigour index-2, EC- Electrical conductivity(mS/cm/seed)

4.3 Variability and heritability parameters

4.3.1 Variability and heritability parameters in single cut

From the experimental results of mean, range, GCV, PCV, heritability (broad sense) and expected genetic advance as percent of mean are given in Table 4.7. It is clearly evident that considerable amount of variation was present among genotypes for each character. Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) which indicates the role of environmental factors on the expression of various traits studied in the present investigation. The character wise interpretation is as under

4.3.1.1 Plant height (cm)- The moderate GCV (14.776%) and PCV (17.652%) values were recorded for this character. This character exhibited high heritability of (70.07%) and high genetic advance value of (25.48%).

4.3.1.2 Days to 50% flowering (days)- The character showed low GCV (2.67%) and PCV (3.19%). High values of heritability (69.31%) and low genetic advance (4.55%) were observed for this character.

4.3.1.3 Days to maturity (days)- The low GCV value of (4.86%) and PCV value of (5.07%) were recorded for days to maturity. This character exhibited high heritability value of (91.95%) and low genetic advance value (9.60%).

4.3.1.4 Flag leaf length (cm)-The high GCV (20.95%) and PCV (23.11%) values were recorded for flag leaf length. This character exhibited high heritability (82.13%) and high value of genetic advance (39.11%).

4.3.1.5 Internode length (cm)- This character showed high values of GCV (21.70%) and PCV (23.01%). High heritability (88.99%) and high genetic advance (42.18%) were observed for this character.

4.3.1.6. Number of tillers/plant– Low GCV (7.16%) and PCV (9.08%) values were recorded for this character. This character exhibited high heritability value of (62.20%) and moderate genetic advance value of (11.63%).

4.3.1.7. Peduncle length (cm)- This character exhibited higher values of GCV (21.81%) and PCV (24.09%). High heritability (81.99%) and high value of genetic advance (40.69%) were observed for this character.

4.3.1.8 Axis length (cm)- The character axis length showed moderate value of GCV (18.31%) and high PCV (21.66%). High values of heritability (71.47%) and high genetic advance (31.89%) were observed for this character.

4.3.1.9 Number of spikelets/panicle- This character exhibited moderate values of GCV (16.79%) and PCV (18.35%). High heritability (83.65%) and high genetic advance (31.63%) values were observed for this character.

4.3.1.10 Seed Yield (g)- The character seed yield showed higher values of GCV (27.79%) and PCV (29.34%). High values of heritability (89.75%) and high genetic advance (54.24%) were observed for this character.

4.3.1.11 100 seed weight (g)- The character 100 seed weight showed moderate values of GCV (14.99) and PCV (15.33%). High values of heritability (95.64%) and high genetic advance (30.20%) were observed for this character.

4.3.1.12 Leaf length (cm)- This character exhibited moderate values of GCV (16.27%) and PCV (19.48%). High heritability (69.83%) and high genetic advance (28.01%) were observed for this character.

4.3.1.13 Leaf width (cm)- This character exhibited moderate value of GCV (19.55%) and high value of PCV (21.13%). High heritability (85.62%) and high genetic advance (37.27%) were observed for this character.

4.3.1.14 Green fodder yield (Kg)- This character exhibited higher values of GCV (30.79%) and PCV (33.79%). High heritability (83.03%) and high genetic advance (57.80%) were observed for this character.

4.3.1.15 Dry matter yield (kg)- This character exhibited high values of GCV (26.33%) and PCV (31.83%). High heritability (68.43%) and high genetic advance (44.88%) were observed for this character.

4.3.1.16 Number of leaves per plant)- This character exhibited moderate values of GCV (8.56. %) and PCV (12.71%). moderate heritability (45.32%) and moderate genetic advance (11.87%) were observed for this character.

4.3.1.17 Crude protein grain (%)- This character exhibited lower values of GCV (9.34%) and PCV (9.87%). High heritability (89.54%) and moderate genetic advance (18.21%) were observed for this character.

4.3.1.18 Crude protein forage (%)- This character exhibited low values of GCV (5.42%) and PCV (5.73%). High heritability (89.58%) and moderate genetic advance (10.57%) were observed for this character.

4.3.1.19 Germination(%)-This character exhibited low values of GCV (3.08%) and PCV (4.01%). Moderate heritability (58.86%) and low genetic advance (4.86%) were observed for this character.

4.3.1.20 Seedling length (cm)- Seedling length showed low values of GCV (6.57%) and PCV (7.20%). This character exhibited high heritability (83.14%) and moderate value of genetic advance (12.33%).

4.3.1.21 Seedling dry weight (g)- This character exhibited moderate values of GCV (18.75%) and PCV (18.85%). High heritability (98.86%) with high genetic advance (38.39%) were observed for this character.

4.3.1.22 Seed vigour index-I -This character exhibited lower values of GCV (8.44%) and PCV (9.35%). High value of heritability (81.54%) and moderate value of genetic advance (15.70%).

4.3.1.23 Seed vigour index-II -This character exhibited moderate values of GCV (18.54%) and PCV (18.77%). High value of heritability (97.50%) and value of genetic advance (37.70%).

4.3.1.24 Electrical conductivity- This parameter showed higher value of GCV (25.57)% and PCV (27.21%). High heritability (88.34%) and high genetic advance (49.4%).

Table 4.7: Mean, range, co-efficient of variation(GCV & PCV), heritability and genetic advance as % of mean for various traits in 92 genotypes of single cut oat

Characters	Mean	Range		Coefficient of variation(%)		Heritability %	Genetic advance as percent of mean
		Min.	Max.	Genotypic	Phenotypic	(Broad sense)	
Plant Height (cm)	109.7	70.30	150.3	14.8	17.7	70.1	25.5
Days to 50% Flowering	93.5	86.00	100.0	2.7	3.2	69.3	4.6
Days to Maturity	119.3	110.30	133.7	4.9	5.1	92.0	9.6
Flag Leaf Length (cm)	23.5	11.00	38.0	21.0	23.1	82.1	39.1
Internode length (cm)	16.9	8.00	25.0	21.7	23.0	89.0	42.2
Tillers per plant	9.1	7.20	11.5	7.2	9.1	62.2	11.6
Peduncle length (cm)	25.8	12.20	38.8	21.8	24.1	82.0	40.7
Axis length (cm)	22.4	8.70	30.3	18.3	21.7	71.5	31.9
No. of spikelets	68.3	47.70	107.3	16.8	18.4	83.7	31.6
Seed Yield (g)	102.4	41.30	174.4	27.8	29.3	89.8	54.2
Seed index (g)	3.4	2.00	4.6	15.0	15.3	95.6	30.2
Leaf length (cm)	34.0	8.70	50.0	16.3	19.5	69.8	28.0
Leaf width (cm)	1.8	0.60	2.8	19.6	21.1	85.6	37.3
Green fodder yield (kg)	0.96	0.50	1.8	30.8	33.8	83.0	57.8
Dry matter yield (kg)	0.19	0.10	0.4	26.3	31.8	68.4	44.9
No. of leaves/plant	41.6	31.40	50.8	8.6	12.7	45.3	11.9
Crude protein grain (%)	12.6	9.70	14.5	9.3	9.9	89.5	18.2
Crude protein forage (%)	13.2	11.30	14.7	5.4	5.7	89.6	10.6
Germination%	86.9	81.00	92.2	3.1	4.0	58.9	4.9
Seedling length (cm)	31.9	27.60	38.7	6.6	7.2	83.1	12.3
Seedling dry weight	10.6	7.00	15.6	18.8	18.9	98.9	38.4
Seed vigourI	2,771.3	2335.30	3526.3	8.4	9.3	81.5	15.7
Seed vigourII	920.5	593.90	1368.2	18.5	18.8	97.5	37.7
Electricalconductivity(dS/m/seed)	0.268	0.10	0.4	25.6	27.2	88.3	49.5

4.3.2 Variability and heritability parameters in Ist cut of multi-cut

4.3.2.1 Plant height (cm)- Moderate GCV (14.18%) and PCV (19.55%) values were recorded for this character. This character exhibited moderate heritability of (52.65%) and high genetic advance value of (21.20%).

4.3.2.2 Number of tillers/plant– Low GCV (7.43%) and PCV (9.51%) values were recorded for this character. This character exhibited high heritability value of (60.98%) and moderate genetic advance value of (11.95%).

4.3.2.3 Green fodder yield (Kg)- This character exhibited high values of GCV (21.72%) and PCV (24.51%). High heritability (78.49%) and high genetic advance (39.64%) were observed for this character.

4.3.2.4 Dry matter yield (Kg)- This character exhibited higher values of GCV (21.10%) and PCV (26.87%). High heritability (61.65%) and high genetic advance (34.13%) were observed for this character.

4.3.2.5 Crude protein forage (%)- This character exhibited lower values of GCV (4.69%) and PCV (5.75%). High heritability (66.50%) and low genetic advance (7.87%) were observed for this character.

Table 4.8: Mean, range, co-efficient of variation (GCV & PCV), heritability and genetic advance as % of mean for various traits in 92 genotypes of Ist cut of multi-cut oat

Characters	Mean	Range		Coefficient of variation (%)		Heritability %	Genetic advance as percent of mean
		Min.	Max.	Genotypic	Phenotypic	(Broad sense)	
Plant Height (cm)	54	27	68	14.183	19.547	52.648	21.199
Tillers per plant	8.34	6.6	10	7.429	9.513	60.977	11.95
Green fodder yield (kg)	216	0.087	0.372	21.718	24.513	78.492	39.636
Dry matter yield (kg)	51	0.03	0.082	21.098	26.871	61.65	34.126
Crude protein forage (%)	14	12.1	15.6	4.687	5.747	66.502	7.874

4.3.3 Variability and heritability parameters in 1st cut of multi-cut

4.3.3.1 Plant height (cm)- Moderate GCV (12.96%) and PCV (18.35%) values were recorded for this character. This character exhibited moderate heritability of (49.84%) and moderate genetic advance value of (18.84%).

4.3.3.2 Days to 50% flowering (days)- The character showed low values of GCV (4.84%) and PCV (5.05%). High values of heritability (91.95%) and low genetic advance (9.57%) were observed for this character.

4.3.3.3 Flag leaf length (cm)-High values of GCV (20.83%) and PCV (23.16%). This character exhibited high heritability (80.89%) and high value of genetic advance (38.59%).

4.3.3.4. Internode length (cm)- This character showed higher values of GCV (20.69%) and PCV (23.49%). High heritability (77.53%) with high genetic advance (37.52%) were observed for this character.

4.3.3.5 Number of tillers/plant– Low GCV (7.06%) and PCV (9.04%) values were recorded for this character. This character exhibited high heritability value of (60.98%) with moderate genetic advance value of (11.36%).

4.3.3.6 Peduncle length (cm)- This character exhibited moderate value of GCV (19.97%) and high value of PCV (22.69%). High heritability (77.40%) and high value of genetic advance (36.18%) were observed for this character.

4.3.3.7 Axis length (cm)- The character axis length showed moderate values of GCV (17.39%) and PCV (20.14%). High values of heritability (74.61%) and high genetic advance (30.95%) were observed for this character.

4.3.3.8 Leaf length (cm)- This character exhibited moderate values of GCV (14.07%) and PCV (15.96%). High heritability (77.68%) and high genetic advance (25.54%) were observed for this character.

4.3.3.9 Leaf width (cm)- This character exhibited moderate value of GCV (19.93%) and high value of PCV (21.53%). High heritability (85.62%) and high genetic advance (37.98%) were observed for this character.

4.3.3.10 Green fodder yield (Kg)- This character exhibited higher values of GCV (22.60%) and PCV (29.17%). High heritability (60.04%) and high genetic advance (36.08%) were observed for this character.

4.3.3.11 Dry matter yield (Kg)- This character exhibited moderate value of GCV (18.92%) and high value of PCV (24.55%). Moderate heritability (59.43%) and high genetic advance (30.05%) were observed for this character.

4.3.3.12 Number of leaves per plant)- This character exhibited low value of GCV (8.77 %) and moderate value of PCV (13.03%). Moderate heritability (45.32%) and moderate genetic advance (12.16%) were observed for this character.

4.3.3.13 Crude protein forage (%)- This character exhibited lower values of GCV (8.75%) and PCV (9.41%). High heritability (86.59%) and moderate genetic advance (16.78%) were observed for this character.

Table 4.9: Mean, range, co-efficient of variation (GCV & PCV), heritability and genetic advance as % of mean for various traits in 92 genotypes of 2nd cut of multi-cut oat

Characters	Mean	Range		Coefficient of variation (%)		Heritability % (Broad sense)	Genetic advance as % of mean
		Min.	Max.	Genotypic	Phenotypic		
Plant Height (cm)	74.28	43.00	98.00	12.96	18.35	49.84	18.84
Days to 50% Flowering	119.62	111.00	134.00	4.84	5.05	91.95	9.57
Flag Leaf Length (cm)	22.29	12.00	33.00	20.83	23.16	80.89	38.59
Internode length (cm)	16.54	8.00	24.00	20.69	23.49	77.53	37.52
Tillers per plant (cm)	8.77	7.10	10.50	7.06	9.04	60.98	11.36
Peduncle length (cm)	24.45	12.00	38.00	19.97	22.69	77.40	36.18
Axis length (cm)	21.28	8.30	28.70	17.39	20.14	74.61	30.95
Seed index (g)	3.36	2.00	4.60	14.99	15.33	95.64	30.20
Leaf length (cm)	30.75	9.00	50.00	14.07	15.96	77.68	25.54
Leaf width(cm)	1.76	0.60	2.80	19.93	21.53	85.63	37.98
Green fodder yield (kg)	0.47	0.22	0.86	22.60	29.17	60.04	36.08
Dry matter yield (kg)	0.12	0.08	0.19	18.92	24.55	59.43	30.05
No. of leaves/plant	40.56	30.00	50.00	8.77	13.03	45.32	12.16
Crude protein forage (%)	11.87	9.63	13.57	8.75	9.41	86.59	16.78

4.4 Correlation coefficient analysis

4.4.1 Correlation coefficient analysis in single cut variety

The results of correlation studies among different characters have been presented in Table 4.10. The correlation coefficients at genotypic level have shown higher magnitude than their corresponding correlation coefficients at phenotypic level thereby, revealing a good amount of strong inherent association between different attributes.

4.4.1.1 Plant height exhibited positive and significant correlation with green fodder yield (0.573), dry matter yield (0.497), seed yield per meter row length (0.323), flag leaf length (0.209) and germination percentage (0.197) while positive and non-significant correlation with seed index (0.106) and internode length (0.09). This character showed negative and non significant correlation with peduncle length (-0.101) and days to maturity (-0.098).

4.4.1.2 Days to 50% flowering exhibited positive and significant correlation with electrical conductivity (0.223), leaf width (0.221), green fodder yield (0.151) and days to maturity (0.124) while positive and non-significant correlation with tillers per plant (0.037), seedling length (0.021), seedling dry weight (0.013) and dry matter yield (0.007). this character showed negative and significant correlation with peduncle length (-0.323), seed index (-0.272), and number of spikelets per panicle (-0.243).

4.4.1.3 Days to maturity exhibited positive and significant correlation with tillers per plant (0.462), number of leaves per plant (0.345) and electrical conductivity (0.194), while positive and non correlated response with number of spikelets (0.064), leaf width (0.05) and seedling dry weight (0.007). This character showed negative and non correlated response with dry matter yield (-0.054), seed vigour index-II (-0.045), flag leaf length (-0.035), and negative and significant correlation has been observed in remaining characters.

4.4.1.4 Flag leaf length exhibited positive and significant correlation with leaf length (0.414), axis length (0.407), dry matter yield (0.338), green fodder yield (0.321), internode length (0.274), seed yield (0.207) and plant height (0.181). Negative and significant correlation showed by number of leaves per plant (0.181), electrical conductivity (-0.169) while negative and non significant correlation observed in tillers per plant (-0.113), crude protein in grains (-0.089), days to 50% flowering (-0.079) and days to maturity (-0.042), remaining character showed positive and non- significant correlation with flag leaf length.

4.4.1.5 Internode length exhibited positive and significant correlation with axis length (0.498), leaf length (0.312), peduncle length (0.305), flag leaf length (0.216), leaf width (0.211), dry matter yield (0.188), crude protein grain (0.159), seed index (0.156), germination % (0.125), seed vigour index-I (0.124) while negative and significant correlation was observed for electrical conductivity (-0.277), days to 50% flowering (-0.162), number of spikelets per panicle (-0.154) and days to maturity (-0.121). This character showed positive and non-significant correlation with remaining characters.

4.4.1.6 Number of tillers/plant exhibited positive and significant correlation with number of leaves per plant (0.738), days to maturity (0.340) while positive and non significant correlation observed for number of electrical conductivity (0.086), spikelets per panicle (0.082), internode length (0.050), seed yield (0.044), leaf length (0.028), days to 50% flowering (0.023), green fodder yield (0.01), dry matter yield (0.038) and the negative and non significant correlation was found with plant height (-0.081), flag leaf length (-0.091), axis length (-0.090), seed index (-0.111), leaf width (-0.058), crude protein grain (-0.088), germination % (-0.105) and remaining character had shown negative and significant correlation.

4.4.1.7 Peduncle length exhibited positive and significant correlation with flag leaf length (0.176), internode length (0.242), axis length (0.322), seed yield (0.227), leaf length (0.150), crude protein forage (0.206), seedling length (0.192), seedling dry weight (0.148), seed vigour index-I (0.165), seed vigour index-II (0.158) . It has negative and significant correlation with days to 50% flowering (-0.272), days to maturity (-0.155), number of spikelets/panicle (-0.157) and electrical conductivity (-0.0254). This character showed negative and non-significant correlation number of tillers/plant (-0.090), number of leaves per plant (-0.009) and it showed positive and non-significant correlation with remaining characters.

4.4.1.8 Axis length exhibited positive and significant correlation with flag leaf length (0.327), internode length (0.393), peduncle length (0.256), seed yield (0.229), leaf length (0.303), leaf width (0.359), green fodder yield (0.192), dry matter yield (0.272), germination % (0.238), seedling length (0.155), seedling dry weight (0.204), seed vigour index I (0.201) and seed vigour index II (0.247) whereas positive and non-significant correlation with plant height (0.079), seed index (0.094), crude protein forage (0.105), crude protein grain (0.105). This character showed negative and significant correlation with days to maturity (-0.145), number of leaves per plant (-0.246), and with remaining character it showed negative and non-significant correlation.

4.4.1.9 Number of spikelets/panicle exhibited positive and significant correlation with plant height (0.129), seed index (0.378), green fodder yield (0.172), number of leaves per plant (0.277), crude protein grain (0.144), and positive and non-significant correlation with days to maturity (0.045), flag leaf length (0.08), axis length (0.059), seed yield (0.099), dry matter yield (0.08), germination % (0.062), seedling length (0.037), seedling dry weight (0.014), seed vigour index-I (0.051), seed vigour index-II (0.023). It showed negative and significant correlation with days to 50% flowering (-0.175), internode length (-0.136), peduncle length (-0.130) while remaining characters showed negative and non-significant correlation with this character.

4.4.1.10 Seed yield was positively and significantly correlated with plant height (0.227), flag leaf length (0.186), tillers per plant (0.204), axis length (0.191), seed index (0.196), green

fodder yield (0.221), dry matter yield (0.273), crude protein forage (0.350), germination % (0.141) while negatively and significant correlation was observed with crude protein grain (-0.152), electrical conductivity (-0.127) and negative and non-significant for days to 50% flowering (-0.014), days to maturity (-0.049), leaf width (-0.099) and seedling dry weight (-0.028). The remaining characters had positive and non-significant correlation.

4.4.1.11 100 seed weight showed positive and significant correlation with number of spikelets per panicle (0.338), seed yield (0.179), germination % (0.284), seedling length (0.201), seedling dry weight (0.121), seed vigour index-I (0.260), seed vigour index-II (0.167) while negative and significant correlation was found with days to 50% flowering (-0.227), days to maturity (-0.133) and electrical conductivity (-0.344) and negative and non-significant correlation with leaf length (-0.098), number of leaves per plant (-0.023). this character showed positive and non-significant correlation with remaining characters.

4.4.1.12 Leaf length had positive and significant with flag leaf length (0.317), internode length (0.250), axis length (0.203), leaf width (0.208), green fodder yield (0.340), dry matter yield (0.291) whereas it showed negative and non-significant correlation with days to 50% flowering (-0.08), days to maturity (-0.029), number of spikelets per panicle (-0.028), seed index (-0.077), electrical conductivity(-0.076) and had positive and non-significant correlation with remaining characters.

4.4.1.13 Leaf width had positive and significant correlation with days to 50% flowering (0.137), internode length (0.202), axis length (0.283), leaf length (0.176), seedling dry weight (0.215), seed vigour index-II (0.192) while positive and non-significant correlation was observed for days to maturity (0.034), flag leaf length (0.077), peduncle length (0.018), seed yield (0.09), seed index (0.021), green fodder yield (0.0027), dry matter yield (0.014), number of leaves per plant (0.018) and electrical conductivity (0.074) whereas it showed negative and non-significant correlation with remaining characters.

4.4.1.14 Green fodder yield exhibited positive and significant with plant height (0.452), days to 50% flowering (0.137), flag leaf length (0.274), axis length (0.126), number of spikelets per panicle (0.152), seed yield (0.189), leaf length (0.247), dry matter yield (0.641), germination % (0.213) and it was correlated positively and non-significantly with internode length (0.094), seed index (0.065), leaf width (0.009), number of leaves per plant (0.055), seedling length (0.033), seedling dry weight (0.094), seed vigour index-I (0.05) and seed vigour index-II (0.058) while it exhibited negative and non-significant correlation with remaining characters.

4.4.1.15 Dry matter yield exhibited positive and significant with plant height (0.391), , flag leaf length (0.254), internode length (0.140), axis length (0.126), seed yield (0.211), leaf length (0.181), green fodder yield (0.654), germination % (0.236), and it correlated positively and non-significant with days to 50% flowering (0.44), number of spikelets per panicle

(0.085), seed index (0.027), crude protein forage (0.034), seedling length (0.04), seedling dry weight (0.085), seed vigour index-I (0.117) and seed vigour index-II (0.045) while it showed negative and non-significant with remaining characters.

4.4.1.16 Number of leaves per plant correlated positively and significantly with days to maturity (0.223), tillers per plant (0.504), number of spikelets per panicle (0.164) and electrical conductivity (0.216) while positive and non-significant correlation found with peduncle length (0.035), seed yield (0.041), leaf length (0.012), leaf width (0.33), green fodder yield (0.022) and dry matter yield (0.023). This character showed negative and non-significant correlation with plant height (-0.078), days to 50% flowering (-0.116), internode length (-0.025), seed index (-0.025) and crude protein grain (-0.097) whereas remaining characters were negatively and significantly correlated with number of leaves per plant.

4.4.1.17 Grain crude protein showed positive and significant correlation with internode length (0.162), seed index (0.153), crude protein forage (0.149), germination % (0.328), seedling length (0.256), seed vigour index-I (0.320) and seed vigour index-II (0.126) and it was correlated positively and non-significantly with peduncle length (0.044) and leaf length (0.03). The negative and significant correlation was observed with days to 50% flowering (-0.129), seed yield (-0.138), and electrical conductivity (-0.229) while remaining character had shown negative and non-significant correlation.

4.4.1.18 Forage crude protein showed positive and significant correlation with peduncle length (0.189), seed yield (0.309), leaf length (0.233), crude protein grain (0.138), germination % (0.), seedling length (0.520), seed vigour index-I (0.426), seed vigour index-II (0.129) and correlated positively and non-significantly with axis length (0.086), flag leaf length (0.049), seed index (0.041). The negative and significant correlation observed with days to maturity (-0.206), and electrical conductivity (-0.174) while remaining character had shown negative and non-significant correlation.

4.4.1.19 Germination (%) showed positive and significant correlation with seedling length (0.446), seedling dry weight (0.204), seed vigour index I (0.721) and seed vigour index II (0.139), seed yield (0.122), seed index (0.198), green fodder yield (0.157), dry fodder yield (0.171) and negative and significant correlation was found with electrical conductivity (-0.317).

4.4.1.20 Seedling length showed positive and significant correlation with seedling length (0.327), seedling dry weight (0.169), seed vigour index I (0.942), seed vigour index II (0.235), seed index (0.175) while positive and non-significant correlation with seed yield (0.071), green fodder yield (0.022) and dry fodder yield (0.028). It was negatively and significantly correlated found with electrical conductivity (-0.460).

4.4.1.21 Seedling dry weight showed positive and significant correlation with seedling length (0.159), seed vigour index II (0.986) and positive and non-significant correlation found with

seed vigour index I (0.05) and dry matter yield (0.079). It was negatively and significantly correlation found with electrical conductivity (-0.373).

4.4.1.22 Seed vigour index I showed positive and significant correlation with seedling length (0.914) and seed vigour index II (0.163), and positive and non-significant correlation found with dry matter yield (0.099). It was negatively and significantly correlated with electrical conductivity (-0.471).

4.4.1.23 Seed vigour index II showed positive and significant correlation with seed vigour index I (0.185) and positive and non-significant correlation dry matter yield (0.036).

4.4.1.24 Electrical conductivity exhibited negative and significant correlation with seed vigour index I (-0.402) and seed vigour index II (-0.398) while positive and non-significant correlation with dry matter yield (0.004).

Table 4.10: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among 24 characters of 92 genotypes in single cut oat

	PH	DF	DM	FLL	IL	TPL	PL	AL	NOS	SY	SI	LL	LW	GFY	DMY	NOL	CPg	CPf	GP	SL	SDW	SVI	SVII	EC
PH		0.071	-0.074	0.181**	0.055	-0.081	-0.09	0.079	0.129*	0.227**	0.098	0.066	-0.032	0.452**	0.391**	-0.078	-0.062	-0.001	0.099	-0.027	-0.058	0.021	-0.035	-0.081
DF	0.128*		0.099	-0.079	-0.162**	0.023	-0.272**	-0.051	-0.175**	-0.014	-0.227**	-0.08	0.157**	0.137*	0.044	-0.116	-0.129*	-0.037	0.003	0.03	0.005	0.022	0.004	0.162**
DM	-0.098	0.124*		-0.042	-0.121*	0.340**	-0.155**	-0.145*	0.045	-0.049	-0.133*	-0.029	0.034	-0.118	-0.032	0.223**	-0.04	-0.206**	-0.251**	-0.292**	0.006	-0.330**	-0.043	0.178**
FLL	0.209**	-0.104	-0.035		0.216**	-0.091	0.176**	0.327**	0.08	0.186**	-0.006	0.317**	0.077	0.274**	0.254**	-0.123*	-0.095	0.049	0.082	-0.013	0.068	0.025	0.09	-0.150*
IL	0.09	-0.237**	-0.123*	0.274**		0.05	0.242**	0.393**	-0.136*	0.037	0.137*	0.250**	0.202**	0.094	0.140*	-0.025	0.162**	0	0.07	0.103	0.039	0.105	0.052	-0.247**
TPL	-0.104	0.037	0.462**	-0.113	0.053		-0.09	-0.082	0.049	0.023	-0.09	0.015	-0.064	-0.018	-0.022	0.504**	-0.03	-0.109	-0.065	-0.074	-0.157**	-0.083	-0.168**	0.06
PL	-0.101	-0.323**	-0.194**	0.198**	0.305**	-0.131*		0.256**	-0.130*	0.204**	0.035	0.111	0.018	-0.147*	-0.086	0.035	0.044	0.189**	0.05	0.147*	0.130*	0.133*	0.144*	-0.238**
AL	0.172**	-0.054	-0.164**	0.407**	0.498**	-0.09	0.322**		0.059	0.191**	0.073	0.203**	0.283**	0.126*	0.126*	-0.162	0.084	0.086	0.124*	0.128*	0.175**	0.145*	0.202**	-0.065
NOS	0.179**	-0.243**	0.064	0.091	-0.154*	0.082	-0.157**	-0.068		0.087	0.338**	-0.028	-0.059	0.152*	0.085	0.164**	0.112	-0.107	0.041	0.026	0.014	0.038	0.021	-0.127*
SY	0.323**	-0.023	-0.063	0.207**	0.044	0.044	0.227**	0.229**	0.099		0.179**	0.083	0.09	0.189**	0.211**	0.041	-0.138*	0.309**	0.121*	0.071	-0.029	0.107	-0.001	-0.104
SI	0.106	-0.272**	-0.145*	0.01	0.156**	-0.111	0.039	0.094	0.378**	0.196**		-0.077	0.021	0.065	0.027	-0.025	0.153*	0.041	0.198**	0.175**	0.119*	0.219**	0.158**	-0.322**
LL	0.095	-0.098	-0.026	0.414**	0.312**	0.028	0.150*	0.303**	-0.031	0.113	-0.098		0.176**	0.247**	0.181**	0.012	0.03	0.233**	0.015	0.079	0.079	0.066	0.093	-0.039
LW	-0.063	0.221**	0.05	0.101	0.211**	-0.058	0.024	0.359**	-0.077	-0.099	0.02	0.208**		0.009	-0.032	0.033	-0.077	-0.036	-0.107	-0.023	0.194**	-0.068	0.166**	0.071
GFY	0.573**	0.151*	-0.132*	0.321**	0.108	0.01	0.191	0.192**	0.172**	0.221**	0.074	0.340**	0.027		0.654**	0.022	-0.112	-0.037	0.157**	0.022	0.088	0.049	0.053	-0.045
DMY	0.497**	0.007	-0.054	0.338**	0.188**	0.038	0.116	0.272**	0.08	0.273**	0.048	0.291**	0.014	0.641**		0.023	-0.034	0.021	0.171**	0.028	0.079	0.099	0.036	0.004
NOL	-0.093	-0.137*	0.345**	-0.182**	0.06	0.738**	-0.009	-0.246**	0.277**	0.047	-0.023	0.079	0.018	0.055	-0.089		-0.042	-0.084	-0.171**	-0.11	-0.238**	-0.156**	-0.270**	0.147*
CPg	-0.079	-0.154*	-0.045	-0.089	0.159**	-0.088	0.057	0.105	0.144*	-0.152*	0.171	0.015	-0.086	-0.134	-0.047	-0.097		0.138*	0.232**	0.213**	0.065	0.264**	0.114	-0.179**
CPf	0	-0.022	-0.227**	0.054	0.004	-0.192**	0.206**	0.105	-0.131*	0.350**	0.044	0.277	-0.036	-0.038	0.034	-0.155*	0.149*		0.049	0.459**	0.117	0.376**	0.124*	-0.153*
GP	0.197**	-0.043	-0.344**	0.061	0.125*	-0.105	0.04	0.238**	0.062	0.141*	0.284**	0.05	-0.112	0.213**	0.236**	-0.259**	0.328**	0.051		0.327**	0.153*	0.679**	0.054	-0.228**
SL	-0.023	0.021	-0.325**	0.008	0.11	-0.137*	0.192**	0.155**	0.037	0.079	0.201**	0.106	-0.026	0.033	0.04	-0.142*	0.256**	0.520**	0.446**		0.159**	0.914**	0.219**	-0.393**
SDW	-0.07	0.013	0.007	0.076	0.036	-0.200**	0.148*	0.204**	0.014	-0.028	0.121*	0.103	0.215**	0.094	0.085	-0.348**	0.073	0.122*	0.204**	0.169**		0.05	0.976**	-0.350**
SVI	0.052	-0.003	-0.375**	0.03	0.124*	-0.142*	0.165**	0.201**	0.051	0.111	0.260**	0.101	-0.066	0.05	0.117	-0.201**	0.320**	0.426**	0.721**	0.942**	0.05		0.185**	-0.402**
SVII	-0.034	-0.003	-0.045	0.092	0.059	-0.212**	0.158**	0.247**	0.023	0	0.167**	0.116	0.192**	0.058	0.045	-0.392**	0.126*	0.129*	0.139	0.235**	0.986**	0.163**		-0.398**
EC	-0.092	0.233**	0.194**	-0.169**	-0.277**	0.086	-0.254**	-0.06	-0.147*	-0.127*	-0.344**	-0.076	0.074	-0.061	-0.008	0.216**	-0.229**	-0.174**	-0.317**	-0.460**	-0.373**	-0.471**	-0.425**	

** Significant at 1%, * Significant at 5%.

4.4.2 Correlation coefficient analysis in Ist cut multi-cut variety

4.4.2.1 Plant height exhibited positive and significant correlation with green fodder yield (0.323), dry matter yield (0.191), and germination percentage (0.336), seedling length (0.142), seed vigour index-I (0.230), crude protein at 65 days (0.219) while positive and non-significant correlation with seedling dry weight (0.011). This character showed negative and significant correlation with electrical conductivity (-0.279) and it showed negative and significant correlation tillers per plant (-0.419).

4.4.2.2 Number of tillers/plant exhibited positive and significant correlation with electrical conductivity (0.174) and while positive and non-significant correlation observed in green fodder yield (0.039) and dry matter yield (0.084) and the negative and significant correlation found with remaining characters.

4.4.2.3 Green fodder yield exhibited positive and significant correlation with plant height (0.488), dry matter yield (0.873), germination % (0.133) and it was correlated positively and non-significantly with number of tillers per plant (0.072), seedling length (0.074), seedling dry weight (0.104), seed vigour index-I (0.103), seed vigour index-II (0.102) while this character was found negatively and non-significantly correlated with remaining characters.

4.4.2.4 Dry matter yield exhibited positive and significant correlation with plant height (0.471), green fodder yield (0.868) and seed vigour index-II (0.123). It was found negatively and significantly correlated with crude protein at 65 days (-0.129) while it was found positively and non-significantly with remaining characters.

4.4.2.5 Forage crude protein showed positive and significant correlation with plant height (0.137), germination % (0.177), seedling length (0.387) and seed vigour index-I (0.366) and it was correlated positively and non-significantly with seed vigour index-II (0.077). The negative and non-significant correlation was observed with green fodder yield (-0.003), dry fodder weight (-0.063) while remaining character had shown negative and non-significant correlation.

Table 4.11: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among 11 characters of 92 genotypes in 1st cut of multi cut oat

	PH	TPL	GFY	DMY	CP	GP	SL	SDW	SVI	SVII	EC
PH		-0.274**	0.488**	0.471**	0.137*	0.172**	0.092	0.011	0.142*	0.049	-0.188**
TPL	-0.419**		0.072	0.116	-0.126*	-0.120*	-0.113	-0.261**	-0.135*	-0.284**	0.127*
GFY	0.323**	0.039		0.868**	-0.003	-0.088	-0.075	-0.088	-0.097	-0.106	-0.068
DMY	0.191**	0.084	0.873**		-0.063	-0.105	-0.074	-0.073	-0.103	-0.096	-0.037
CP65	0.219**	-0.209**	-0.018	-0.129*		0.148*	0.281**	0.038	0.280**	0.065	-0.208**
GP	0.336**	-0.180**	0.125*	0.016	0.177**		0.327**	-0.153*	0.679**	0.054	-0.228**
SL	0.142*	-0.202**	0.074	0.078	0.387**	0.446**		0.159**	0.914**	0.219**	-0.393**
SDW	0.011	-0.328**	0.104	0.097	0.047	-0.204**	0.169**		0.05	0.976**	-0.350**
SVI	0.230**	-0.217**	0.103	0.118	0.366**	0.721**	0.942**	0.05		0.185**	-0.402**
SVII	0.067	-0.360**	0.102	0.123*	0.077	-0.039	0.235**	0.986**	0.163**		-0.398**
EC	-0.279**	0.174**	-0.086	-0.057	-0.277**	-0.317**	-0.460**	-0.373**	-0.471**	-0.425**	

** Significant at 1%, * Significant at 5%.

4.4.3 Correlation coefficient analysis in 2nd cut multi-cut variety

4.4.3.1 Plant height exhibited positive and significant correlation with flag leaf length (0.222), internode length (0.527), peduncle length (0.173), axis length (0.495), seed index (0.211), leaf length (0.315), leaf width (0.170), green fodder yield (0.179) & dry matter yield (0.163), and germination percentage (0.128) while positive and non-significant correlation with seedling length (0.006), seedling dry weight (0.055), seed vigour-I (0.042), and seed vigour index-II (0.09). This character showed negative and significant correlation with electrical conductivity (-0.266) and it found negative and non-significant with rest of the characters.

4.4.3.2 Days to 50% flowering exhibited positive and significant correlation with green fodder yield (0.177) dry matter yield (0.152), number of leaves per plant (0.345) and tillers per plant (0.487) while negative and non-significant correlation with plant height (-0.035), flag leaf length (-0.037), crude protein (0.021) and seedling dry weight (0.013) and negative and non-significant correlation with internode length (-0.132), peduncle length (-0.183), crude protein forage at second cut (-0.245) while remaining characters were positively and non-significantly correlated with this character.

4.4.3.3 Flag leaf length exhibited positive and highly-significant correlation with leaf length (0.344), peduncle length (0.239), internode length (0.309) and plant height (0.186). Negative and significant correlation was found with electrical conductivity (-0.194) and tillers per plant (-0.128) while negative and non significant correlation was observed with crude protein in grains (-0.089) and days to 50% flowering (-0.044) and remaining character showed positive and non-significant correlation.

4.4.3.4 Internode length exhibited positive and significant correlation with plant height (0.325), flag leaf length (0.227), peduncle length (0.257), leaf length (0.297), leaf width (0.219), seed index (0.177), germination % (0.143) and seed vigour index-I (0.145) while negative and significant correlation was observed with electrical conductivity (-0.306) and days to 50% flowering (-0.126), and had negative and non-significant correlation with number of leaves per plant (-0.088). This character showed positive and non-significant correlation with remaining characters.

4.4.3.5 Number of tillers/plant exhibited positive and significant correlation with plant height (0.123), number of leaves per plant (0.996), days to 50% flowering (0.360), electrical conductivity (0.174), while positive and non-significant correlation was observed with leaf length (0.028), green fodder yield (0.007), dry matter yield (0.002) and the negative and significant correlation found with crude protein at second cut (-0.237), germination % (-0.180), seedling length (-0.202), seedling dry weight (-0.328), seed vigour index-I (-0.217), and seed vigour index-II (-0.360) and remaining character had shown negative and non-significant correlation.

4.4.3.6 Peduncle length exhibited positive and significant correlation with plant height (0.123), flag leaf length (0.200), internode length (0.198), axis length (0.325), leaf length (0.126), crude protein forage (0.199), seedling length (0.136), seedling dry weight (0.120), seed vigour index-I (0.149) and seed vigour index-II (0.142) . It has negative and significant correlation with days to 50% flowering (-0.140) and electrical conductivity (-0.225. This character showed negative and non-significant correlation with number of tillers/plant (-0.075), number of leaves per plant (-0.083) and leaf width (-0.035), and it showed positive and non-significant correlation with remaining characters.

4.4.3.7 100 seed weight showed positive and significant correlation with internode length (0.141), germination % (0.284), seedling length (0.201), seedling dry weight (0.121), seed vigour index-I (0.260), seed vigour index-II (0.167) while negative and significant correlation was found with days to 50% flowering (-0.133), electrical conductivity (-0.344) and leaf length (-0.127) and negative and non-significant correlation with, number of leaves per plant (-0.023). This character showed positive and non-significant correlation with remaining characters.

4.4.3.8 Leaf length had positive and significant correlation with plant height (0.304), flag leaf length (0.271), internode length (0.198), peduncle length (0.122), leaf width (0.295), crude protein at second cut (0.253), seedling length (0.162) and seed vigour index-II (0.140) whereas it showed negative and non-significant correlation with seed index (-0.104) and days to 50% flowering (-0.057), and had positive and non-significant correlation with remaining characters.

4.4.3.9 Leaf width had positive and significant correlation with plant height (0.130), internode length (0.200), seed index (0.284), leaf length (0.247), dry matter yield (0.132), seedling dry weight (0.215), seed vigour index-II (0.192) while positive and non-significant correlation was observed with days to 50% flowering (0.034), flag leaf length (0.089), seed index (0.021), green fodder yield (0.109), number of leaves per plant (0.018) and electrical conductivity (0.073) whereas it showed negative and non-significant correlation with remaining characters.

4.4.3.10 Green fodder yield exhibited positive and significant correlation with plant height (0.196), days to 50% flowering (0.129), leaf length (0.247), dry matter yield (0.976), germination % (0.133) and seedling dry weight (0.153) and it was correlated positively and non-significantly with flag leaf length (0.094), seed index (0.004), leaf length (0.051), leaf width (0.077), number of leaves per plant (0.001), seedling length (0.023), seed vigour index-I (0.102) and seed vigour index-II (0.109) while this character was found negatively and non-significantly correlated with remaining characters.

4.4.3.11 Dry matter yield exhibited positive and significant with plant height (0.205), green fodder yield (0.965) and germination % (0.138), and it was correlated positively and non-

significantly with days to 50% flowering (0.104), seed index (0.003), seedling length (0.021), seedling dry weight (0.019), seed vigour index-I (0.21), seed vigour index-II (0.018) and tillers per plant (0.101). It was found negatively and significantly correlated with crude protein at second cut (-0.157) while it showed negatively and non-significant with remaining characters.

4.4.3.12 Number of leaves per plant were correlated positively and significantly with days to 50% flowering (0.223), tillers per plant (0.555) and electrical conductivity (0.216) while positive and non-significant correlation was found with peduncle length (0.006), leaf width (0.32), green fodder yield (0.009) and dry matter yield (0.015). This character showed negative and non-significant correlation with plant height (-0.107), internode length (-0.028) and seed index (-0.025) whereas remaining characters were negatively and significantly correlated.

4.4.3.13 Crude protein forage showed positive and significant correlation with seed index (0.180), leaf length (0.195), germination % (0.211), seedling length (0.548), seed vigour index-I (0.503) and seed vigour index-II (0.142) and it was correlated positively and non-significantly with flag leaf length (0.075) and seedling dry weight (0.108). The negative and significant correlation was observed with days to 50% flowering (-0.229), green fodder weight (-0.134), dry fodder weight (-0.123) and electrical conductivity (-0.351) while remaining character had shown negative and non-significant correlation this character.

Table 4.12: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among 20 characters of 92 genotypes in 2nd cut of multi cut oat

	PH	DM	FLL	IL	TPL	PL	AL	SI	LL	LW	GFY	DMY	NOL	CP	GP	SL	SDW	SVI	SVII	EC
PH		-0.035	0.186**	0.325**	0.123*	0.123*	0.425**	0.162**	0.304**	0.130*	0.196**	0.205**	-0.107	-0.015	0.06	0.004	0.041	0.026	0.051	-0.199**
DM	-0.05		-0.044	-0.126*	0.360**	-0.140*	-0.118	-0.133*	-0.057	0.034	0.129*	0.104	0.223**	-0.229**	-0.251**	-0.292**	0.006	-0.330**	-0.043	0.178**
FLL	0.222**	-0.037		0.227**	-0.087	0.200**	0.287**	0.001	0.271**	0.089	0.068	0.058	-0.127*	0.075	0.062	-0.018	0.064	0.013	0.082	-0.153*
IL	0.527**	-0.132*	0.309**		-0.039	0.198**	0.392**	0.141*	0.198**	0.200**	-0.084	-0.076	-0.028	0.057	0.076	0.116	0.06	0.117	0.073	-0.256**
TPL	-0.211**	0.487**	-0.128*	-0.061		-0.075	-0.092	-0.087	0.044	-0.033	0.322**	0.311**	0.555**	-0.161**	-0.120*	-0.113	-0.261**	-0.135*	-0.284**	0.127*
PL	0.173**	-0.183**	0.239**	0.257**	-0.089		0.264**	0.035	0.122*	-0.028	-0.182**	-0.171**	-0.006	0.160**	0.062	0.089	0.102	0.097	0.118*	-0.210**
AL	0.495**	-0.151*	0.350**	0.559**	-0.163**	0.325**		0.112	0.371**	0.284**	-0.027	-0.01	-0.175**	0.053	0.142*	0.140*	0.163**	0.162**	0.196**	-0.058
SI	0.211**	-0.145*	-0.001	0.177**	-0.118	0.035	0.121*		-0.104	0.021	0.004	0.003	-0.025	0.180**	0.198**	0.175**	0.119*	0.219**	0.158**	-0.322**
LL	0.315**	-0.075	0.344**	0.297**	0.036	0.126*	0.233**	-0.127*		0.247**	0.051	0.054	0	0.195**	0.096	0.094	-0.003	0.112	0.021	0.012
LW	0.170**	0.051	0.111	0.219**	-0.08	-0.035	0.346**	0.021	0.295**		0.077	0.086	0.032	-0.088	-0.107	-0.023	0.195**	-0.068	0.166**	0.071
GFY	-0.179**	0.177**	0.056	-0.151*	0.007	-0.272**	-0.094	0.001	0.026	0.109		0.965**	-0.009	-0.134*	-0.092	-0.132*	0.113	-0.140*	0.099	-0.01
DMY	-0.163**	0.152*	0.05	-0.129*	-0.002	-0.254**	-0.073	-0.004	0.026	0.132*	0.976**		0.015	-0.123*	-0.091	-0.114	0.139*	-0.126*	0.126*	-0.025
NOL	-0.159**	0.345**	-0.201**	-0.088	0.996**	-0.083	-0.255**	-0.023	0.055	0.018	0.001	0.023		-0.072	-0.171**	-0.11	-0.238**	-0.156**	-0.270**	0.147*
CP	-0.024	-0.245**	0.096	0.075	-0.237**	0.199**	0.085	0.208**	0.253**	-0.11	-0.166**	-0.157**	-0.135*		0.155**	0.469**	0.094	0.428**	0.125*	-0.306**
GP	0.128*	-0.344**	0.032	0.143*	-0.180**	0.113	0.261**	0.284**	0.162**	-0.111	-0.133*	-0.138*	-0.259**	0.211**		0.327**	-0.153*	0.679**	0.054	-0.228**
SL	-0.006	-0.325**	0	0.129*	-0.202**	0.136*	0.157**	0.201**	0.102	-0.026	-0.229**	-0.204**	-0.142*	0.548**	0.446**		0.159**	0.914**	0.219**	-0.393**
SDW	0.055	0.007	0.075	0.061	-0.328**	0.120*	0.195**	0.121*	0	0.215**	0.153*	0.186**	-0.348**	0.108	-0.204**	0.169**		0.05	0.976**	-0.350**
SVI	0.042	-0.375**	0.013	0.145*	-0.217**	0.149*	0.212**	0.260**	0.140*	-0.066	-0.224**	-0.207**	-0.201**	0.503**	0.721**	0.942**	0.05		0.185**	-0.402**
SVII	0.08	-0.045	0.085	0.088	-0.360**	0.142*	0.240**	0.167**	0.029	0.192**	0.139*	0.172**	-0.392**	0.142*	-0.039	0.235**	0.986**	0.163**		-0.398**
EC	-0.266**	0.194**	-0.173**	-0.306**	0.174**	-0.225**	-0.09	-0.344**	0.002	0.073	-0.007	-0.019	0.216**	-0.351**	-0.317**	-0.460**	-0.373**	-0.471**	-0.425**	

** Significant at 1%, * Significant at 5%

4.5 Path coefficient analysis

Simple correlation coefficient values do not make a complete picture of complex situation of association among different characters therefore the assessment of real contribution of each individual character towards seed yield/plant is important to decide about selection indices. Path coefficient analysis provides more realistic picture of the relationship among the characters. The path coefficient analysis reveals whether the association of each individual character with yield is due to its direct effect on yield or is a consequence of indirect effects *via* other component characters. Thus, path coefficient is essential to know the effectiveness of selection for simultaneous improvement in these characters.

In the present study, path coefficient analysis was done on the basis of genotypic correlation coefficients.

4.5.1 Path coefficient analysis in single cut

Direct and indirect effects of different characters on dry matter yield per plant were calculated in single cut which have been presented in Table 4.13.

Direct effect

A critical perusal of path coefficient analysis exhibited high direct and positive effects of green fodder yield (0.5709), tillers per plant (0.1931), plant height (0.1554) and seed yield per meter row length (0.1596) while days to 50% flowering (-0.2288), peduncle length (-0.036), axis length (-0.0445), number of spikelets (-0.0006), and number of leaves per plant (-0.4082) had negative direct effects on dry matter yield per plant. This indicated that the green fodder yield, tillers per plant, plant height and seed yield per meter row length were important traits so far their association with dry matter yield is concerned.

Indirect effect

Plant height (0.3272), flag leaf length (0.18302), seed yield (0.1263), leaf length (0.1942), had high positive indirect effects via green fodder yield while peduncle length (-0.1092) and days to maturity (-0.0756) had negative indirect effect via green fodder yield.

Residual effects calculated were 0.45574. This indicated that a considerable magnitude of variation was presented for association of dry matter yield with dependent traits.

Table 4.13: Path coefficient analysis for 24 characters of 92 genotypes in single cut

	PH	DF	DM	FLL	IL	TPL	PL	AL	NOS	SY	SI	LL	LW	GFY	NOLS	CPg	CPf	GP	SL	SDW	SVI	SVII	EC
PH	0.15539	-0.02933	-0.01154	0.01018	0.00361	-0.02	0.00363	-0.00763	-0.0001	0.05159	-0.00209	0.00604	-0.0042	0.32715	0.0378	-0.00431	0.00004	0.04709	-0.03441	0.12842	-0.08201	-0.05797	-0.01992
DF	0.01992	-0.2288	0.01465	-0.00505	-0.00953	0.00718	0.01163	0.00242	0.00014	-0.00373	0.00535	-0.00626	0.01464	0.08645	0.05611	-0.00839	0.002	-0.01038	0.03161	-0.02288	0.00477	-0.00525	0.05059
DM	-0.01516	-0.02833	0.11832	-0.00172	-0.00495	0.08918	0.00697	0.00731	-0.00004	-0.01011	0.00286	-0.00168	0.00335	-0.0756	-0.14064	-0.00247	0.02064	-0.08223	-0.48547	-0.01269	0.59149	-0.07513	0.04203
FLL	0.03246	0.0237	-0.00419	0.04872	0.01101	-0.02178	-0.00715	-0.01809	0.00005	0.03308	0.00019	0.02639	0.00668	0.18302	0.07442	-0.00486	-0.00487	0.01464	0.01205	-0.13958	-0.04682	0.15536	-0.03663
IL	0.01399	0.0543	-0.01458	0.01337	0.04013	0.01016	-0.011	-0.02215	0.00009	0.007	-0.00307	0.01992	0.01397	0.06164	0.02436	0.00871	-0.00036	0.02982	0.16355	-0.06614	-0.19548	0.10041	-0.06016
TPL	-0.01609	-0.0085	0.05464	-0.0055	0.00211	0.19311	0.00471	0.004	-0.00005	0.00706	0.00218	0.00181	-0.00381	-0.00558	-0.30128	-0.00481	0.01745	-0.02508	-0.20419	0.36654	0.22323	-0.35817	0.01869
PL	-0.01563	0.07382	-0.02289	0.00967	0.01225	-0.02525	-0.036	-0.01433	0.00009	0.03631	-0.00077	0.00957	0.00159	-0.1092	0.00381	0.0031	-0.0187	0.00945	0.28684	-0.26978	-0.26043	0.26607	-0.05504
AL	0.02665	0.01245	-0.01943	0.01981	0.01998	-0.01737	-0.01161	-0.0445	0.00004	0.0365	-0.00185	0.01937	0.02381	0.10938	0.10059	0.00575	-0.00951	0.0568	0.23194	-0.37288	-0.31715	0.41619	-0.01303
NOS	0.02778	0.05565	0.00753	-0.00444	-0.00617	0.01585	0.00565	0.00303	-0.0006	0.01573	-0.00743	-0.00199	-0.00512	0.09823	-0.11299	0.00786	0.01193	0.01476	0.0548	-0.02562	-0.08076	0.03828	-0.03196
SY	0.05023	0.00535	-0.00749	0.0101	0.00176	0.00854	-0.0082	-0.01017	-0.00006	0.15961	-0.00384	0.00718	-0.00659	0.1263	-0.01933	-0.00829	-0.03177	0.03379	0.11753	0.05066	-0.17495	-0.00034	-0.02748
SI	0.01653	0.06232	-0.01721	-0.00047	0.00627	-0.02144	-0.00142	-0.00419	-0.00021	0.03125	0.01963	-0.00623	0.00135	0.04246	0.00955	0.00935	-0.004	0.06796	0.29935	-0.22166	-0.40984	0.28221	-0.07457
LL	0.01471	0.02246	-0.00311	0.02015	0.01252	0.00547	-0.00541	-0.0135	0.00002	0.01796	0.00192	0.06382	0.01378	0.1942	-0.0324	0.00079	-0.02512	0.01199	0.15832	-0.18763	-0.15966	0.19609	-0.01656
LW	-0.00984	-0.05053	0.00597	0.00491	0.00846	-0.01111	-0.00087	-0.01598	0.00004	-0.01586	-0.0004	0.01327	0.06628	0.01515	-0.00746	-0.00472	0.00326	-0.02669	-0.03916	-0.39274	0.10398	0.3239	0.01602
GFY	0.08906	-0.03465	-0.01566	0.01562	0.00433	-0.00189	0.00689	-0.00852	-0.0001	0.03531	-0.00146	0.02171	0.00176	0.57085	-0.02258	-0.00732	0.00343	0.05079	-0.0487	0.17158	-0.07885	-0.0976	-0.01314
NOLS	-0.01439	0.03145	0.04077	-0.00888	-0.00239	0.14253	0.00034	0.01096	-0.00015	0.00756	0.00046	0.00507	0.00121	0.03157	-0.4082	-0.00528	0.01404	-0.06185	-0.212	0.63648	0.31684	-0.66201	0.0468
CPg	-0.01225	0.03512	-0.00534	-0.00434	0.00639	-0.017	-0.00204	-0.00468	-0.00008	-0.02421	-0.00336	0.00093	-0.00573	-0.07645	0.0394	0.05466	-0.01352	0.07825	0.38272	-0.1336	-0.50466	0.21191	-0.04961
CPf	-0.00006	0.00503	-0.0269	0.00262	0.00016	-0.03712	-0.00742	-0.00466	0.00007	0.05586	-0.00087	0.01766	-0.00238	-0.02155	0.06313	0.00814	-0.0908	0.0123	0.7755	-0.22256	-0.67103	0.21708	-0.03778
GP	0.03063	0.00994	-0.04072	0.00299	0.00501	-0.02027	-0.00143	-0.01058	-0.00003	0.02258	-0.00558	0.0032	-0.00741	0.12137	0.10569	0.0179	-0.00467	0.2389	0.66542	0.3727	-0.13525	-0.06554	-0.06892
SL	-0.00358	-0.00485	-0.03849	0.00039	0.0044	-0.02643	-0.00693	-0.00691	-0.00002	0.01257	-0.00394	0.00677	-0.00174	-0.01863	0.05799	0.01402	-0.04717	0.10653	0.49218	-0.30926	-0.48437	0.39737	-0.09981
SDW	-0.01091	-0.00286	0.00082	0.00372	0.00145	-0.03871	-0.00532	-0.00907	-0.00001	-0.00442	-0.00238	0.00655	0.01424	-0.05357	0.14209	0.00399	-0.01105	-0.0487	0.25238	-0.2885	-0.07921	0.66501	-0.08087
SVI	0.00809	0.00069	-0.04442	0.00145	0.00498	-0.02736	-0.00596	-0.00896	-0.00003	0.01773	-0.00511	0.00647	-0.00437	0.02857	0.0821	0.01751	-0.03867	0.17216	0.40602	-0.09194	-0.5753	0.27578	-0.10224
SVII	-0.00534	0.00071	-0.00527	0.00448	0.00239	-0.04098	-0.00568	-0.01097	-0.00001	-0.00003	-0.00328	0.00741	0.01272	-0.03301	0.1601	0.00686	-0.01167	-0.00928	0.35131	-0.80377	-0.2574	0.68783	-0.09236
EC	-0.01426	-0.05332	0.02291	-0.00822	-0.01112	0.01662	0.00914	0.00267	0.00008	-0.0202	0.00674	-0.00487	0.00489	-0.03455	-0.088	-0.01249	0.0158	-0.07584	-0.68603	0.68114	0.74193	-0.71812	0.21709

** Significant at 1%, * Significant at 5%.

4.5.2 Path coefficient analysis in Ist cut of multi-cut

Direct and indirect effects of different characters on dry matter yield per plant were calculated in Ist cut of multi-cut which have been presented in Table 4.14 number of genotypes in each cluster,

Direct effect

A critical perusal of path coefficient analysis exhibited high direct and positive effects of green fodder yield (0.8902), tillers per plant (0.1516) and plant height (0.1041) while forage crude protein (-0.1341) had negative direct effects on dry matter yield per plant. This indicated that the green fodder yield, tillers per plant and plant height were important traits so far as their association with dry matter yield is concerned.

Indirect effect

Plant height (0.2874) had high positive indirect effects via green fodder yield. Tillers per plant (0.1518) had positive indirect effect via green fodder yield per meter row length.

Residual effects calculated were 0.04638. This indicated that a considerable magnitude of variation was presented for association of dry matter yield with dependent traits.

Table 4.14: Path coefficient analysis for 11 characters of 92 genotypes in 1st cut of multi cut oat

	PH	TPL	GFY	CP	GP	SL	SDW	SVI	SVII	EC
PH	0.1401	0.06355	0.28744	-0.02938	0.11437	0.13989	-0.00448	-0.27888	0.0212	0.01689
TPL	0.05867	0.15175	0.0343	0.02798	-0.06134	-0.19953	0.13663	0.26307	-0.11322	-0.01055
GFY	-0.04524	0.00585	0.89019	0.00236	-0.04262	-0.07265	0.04314	0.12508	-0.03845	0.00521
CP	-0.03069	0.03165	-0.01568	-0.1341	0.06034	0.38183	-0.01943	-0.44364	0.02413	0.01676
GP	0.04709	0.02736	-0.11149	-0.02378	0.34025	0.44047	0.08492	-0.87378	-0.01222	0.01922
SL	0.01984	0.03066	-0.06547	-0.05185	0.15173	0.98774	-0.07047	-1.1425	0.07411	0.02783
SDW	0.00151	0.04977	-0.09216	-0.00625	-0.06935	0.16706	0.41664	-0.06097	0.31051	0.02255
SVI	0.03222	0.03292	-0.09183	-0.04907	0.2452	0.9307	-0.02095	0.81251	0.05143	0.02851
SVII	0.00944	0.05459	-0.10874	-0.01028	-0.01321	0.23254	-0.41101	-0.19812	0.31477	0.02576
EC	-0.00944	0.05459	-0.10874	-0.01028	-0.01321	0.23254	-0.41101	-0.19812	0.31477	0.02576

** Significant at 1%, * Significant at 5%.

4.5.3 Path coefficient analysis in 2nd cut of multi-cut

Direct and indirect effects of different characters on dry matter yield per plant were calculated in 2nd cut of multi-cut which have been presented in Table 4.14 number of genotypes in each cluster,

Direct effect

A critical perusal of path coefficient analysis exhibited high direct and positive effects of green fodder yield (0.9164), tillers per plant (0.2341) and plant height (0.1401) while days to 50% flowering (-0.089), leaf length (-0.0769), axis length (-0.0945), and number of leaves per plant (-0.1473) had negative direct effects on dry matter yield per plant. This indicated that the green fodder yield, tillers per plant and plant height were important traits so far their association with dry matter yield is concerned.

Indirect effect

Plant height (0.1821), days to 50% flowering (0.1803), leaf width (0.1105), had high positive indirect effects via green fodder yield and numbers of tillers per plant (1467) via number of leaves per plant while inter-node length (-0.1537) and peduncle length (-0.2761) had negative indirect effect via green fodder yield.

Residual effects calculated were 0.20186. This indicated that a considerable magnitude of variation was presented for association of dry matter yield with dependent traits.

Table 4.15: Path coefficient analysis for 20 characters of 92 genotypes in 2nd cut of multi cut oat

	PH	Df	FLL	IL	TPL	PL	AL	SI	LL	LW	GFY	NOLS	CP	G	SL	SDW	SVI	SVII	EC
PH	0.10405	0.00442	0.00189	0.01969	-0.04928	0.00378	-0.04677	-0.0059	-0.02418	0.00953	0.18212	0.02336	-0.00156	-0.00099	0.00212	0.05194	0.01965	-0.06622	-0.02618
Df	-0.00517	-0.089	-0.00031	-0.00492	0.1141	-0.00401	0.01424	0.00407	0.00576	0.00284	0.18027	-0.05075	-0.01592	0.00266	0.11172	0.00651	-0.17605	0.03699	0.01907
FLL	0.02314	0.00326	0.0085	0.01156	-0.02992	0.00523	-0.0331	0.00003	-0.02642	0.00621	0.05707	0.02958	0.00623	-0.00024	0.00007	0.07016	0.00595	-0.07048	-0.017
IL	0.05486	0.01171	0.00263	0.03735	-0.01422	0.00564	-0.05282	-0.00494	-0.02281	0.0123	-0.1537	0.01297	0.00489	-0.0011	-0.04416	0.05733	0.06789	-0.07299	-0.03014
TPL	-0.0219	-0.04336	-0.00109	-0.00227	0.23411	-0.00196	0.01541	0.0033	-0.00277	-0.00447	0.00723	0.14667	-0.0154	0.00139	0.06937	-0.30736	-0.10173	0.29895	0.01717
PL	0.01796	0.01627	0.00203	0.0096	-0.02094	0.02192	-0.03074	-0.00099	-0.00969	-0.00194	-0.2761	0.01224	0.01293	-0.00088	-0.04656	0.11204	0.06981	-0.11843	-0.02219
AL	0.05152	0.01342	0.00298	0.02089	-0.03819	0.00713	-0.0945	-0.00338	-0.01788	0.01943	-0.0954	0.03757	0.00553	-0.00202	-0.05387	0.18235	0.09952	-0.19959	-0.0089
SI	0.02195	0.01294	-0.00001	0.00661	-0.02765	0.00078	-0.01141	-0.0279	0.00973	0.00117	0.00133	0.00345	0.01349	-0.0022	-0.06889	0.11362	0.12198	-0.13896	-0.03384
LL	0.03274	0.00667	0.00292	0.01109	0.00844	0.00276	-0.02197	0.00354	-0.0769	0.01655	0.02688	-0.00813	0.01641	-0.00125	-0.03511	-0.00019	0.0655	-0.02445	0.00023
LW	0.01766	-0.0045	0.00094	0.00818	-0.01863	-0.00076	-0.03269	-0.00058	-0.02266	0.05613	0.1105	-0.00264	-0.00717	0.00086	0.00891	0.20164	-0.0308	-0.15983	0.00724
GFY	-0.01864	-0.01578	0.00048	-0.00565	0.00167	-0.00595	0.00886	-0.00004	-0.00203	0.0061	0.91641	-0.00018	-0.01079	0.00103	0.07855	0.14332	-0.10508	-0.1154	-0.00067
NOLS	-0.0165	-0.03065	-0.00171	-0.00329	0.23314	-0.00182	0.02409	0.00065	-0.00424	0.001	0.00124	-0.1473	-0.00876	0.002	0.04879	-0.32624	-0.0943	0.32598	0.02124
CP	-0.00249	0.02181	0.00082	0.00281	-0.0555	0.00436	-0.00804	-0.0058	-0.01942	-0.00619	-0.16885	0.01986	0.06495	-0.00163	-0.1881	0.10111	0.23602	-0.11806	-0.03453
G	0.01334	0.03062	0.00027	0.00533	-0.0422	0.00249	-0.02468	-0.00795	-0.01244	-0.00626	-0.13545	0.03813	0.01369	-0.0077	-0.15313	-0.19104	0.33789	0.03227	-0.03128
SL	-0.00064	0.02894	0	0.0048	-0.04729	0.00297	-0.01482	-0.00561	-0.00786	-0.00146	-0.23251	0.02093	0.03558	-0.00344	-0.3434	0.15852	0.4418	-0.19567	-0.04529
SDW	0.00577	-0.00062	0.00064	0.00228	-0.07677	0.00262	-0.01838	-0.00339	0.00002	0.01208	0.15543	0.05127	0.00701	0.00157	-0.05808	0.93725	0.02358	-0.81987	-0.0367
SVI	0.00436	0.0334	0.00011	0.00541	-0.05079	0.00326	-0.02005	-0.00727	-0.01074	-0.00369	-0.22778	0.02962	0.0327	-0.00556	-0.32356	0.04713	0.46887	-0.1358	-0.0464
SVII	0.00829	0.00396	0.00072	0.00328	-0.08421	0.00312	-0.02268	-0.00467	-0.00226	0.01079	0.14112	0.05777	0.00923	0.0003	-0.08085	0.92458	0.07661	-0.8311	-0.04191
EC	-0.02765	-0.01722	-0.00147	-0.01143	0.04079	-0.00494	0.00853	0.0096	-0.00018	0.00412	-0.00694	-0.03175	-0.02277	0.00245	0.15787	-0.34914	-0.22082	0.35361	0.09851

** Significant at 1%, * Significant at 5%.

4.6 Genetic divergence

The mean sum of squares due to genotypes for all the traits studied were highly significant from the analysis of variance table (Table 4.1, 4.2 and 4.3) thereby, revealing sufficient amount of genetic variation among the genotypes for all the characters studied, but the extent of genetic diversity present among the genotypes taken for the investigation could not be explained with analysis of variance table.

To quantify genetic divergence between any two genotypes or group of genotypes, Mahalanobis' D^2 statistics (1936) as described by Rao (1952) was used and the genotypes were grouped into different clusters on the basis of ward 's minimum variance method. All 92 oat genotypes were grouped into nine clusters based on the relative magnitude of their D^2 values, in such a way that genotypes in each cluster had smaller D^2 value than between the clusters.

4.6.1 Genetic divergence: single cut

Table 4.16 revealed the distribution pattern of 92 genotypes in different clusters. Cluster pattern revealed that cluster IX and VI were the largest ones with 18 and 17 genotypes each, followed by cluster V with 13 genotypes, cluster III with 10 genotypes, cluster VII with 9 genotypes, cluster II and IV each with 6 genotypes and cluster I with 5 genotypes.

4.6.1.1 Intra and inter cluster average D^2 values

The intra and inter cluster D^2 values among 92 genotypes are given in table 4.16. The results show that inter cluster distances are more than intra cluster distances which indicates the presence of narrow genetic variation within a cluster. The highest intra cluster D^2 value was observed for cluster VII (6.512) followed by cluster IX (6.238), cluster II (6.292), cluster VI (5.578), cluster V (5.558), cluster III (5.550), cluster IV (5.483), cluster VIII (5.481) and cluster I (5.012).

When diversity was studied among the clusters based on the inter cluster D^2 values, it showed a range of 5.012 to 8.304. The average inter-cluster distance was found to be highest between cluster IV and IX (8.304), cluster I and VIII (8.161), cluster III and IX (7.741) whereas the lower inter cluster distance was observed between cluster V and VI (6.243), followed by cluster III and V (6.323). The higher inter cluster distance indicated the presence of more diversity among the genotypes included between these clusters.

Table 4.16: Average intra (diagonal) and inter (above diagonal) cluster D² values in 92 genotypes of oat

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	5.012	6.908	7.324	6.956	7.018	7.069	7.663	8.161	7.598
II		6.292	7.215	7.141	7.16	7.081	7.384	7.192	7.089
III			5.55	6.564	6.323	6.427	6.835	7.53	7.741
IV				5.483	6.568	6.601	7.588	7.576	8.304
V					5.558	6.243	7.154	6.921	7.191
VI						5.578	6.907	7.012	7.062
VII							6.512	6.924	7.289
VIII								5.481	6.673
IX									6.238

4.6.1.2 Mean values of different clusters for 24 characters

The cluster means for dry matter yield and its component characters are presented in Table 4.17.1, 4.17.2 and 4.17.3. The data revealed considerable differences among all the clusters for most of the characters studied. It was evident that plant height was lowest in cluster VIII (96.67) and the highest in cluster I (131.87). Cluster I recorded the highest flag leaf length (26.93) while cluster VII recorded the lowest (18.85). Peduncle length was recorded minimum for cluster VII (20.17) and maximum for cluster V (33.280). Cluster I revealed the highest mean value for inter-node length (20.60), whereas cluster IX had the lowest mean value (13.50). For axis length, cluster V (24.95) had the highest mean value while cluster VII had the lowest mean value (17.78).

Cluster IV showed the maximum mean value (84.33) for number of spikelets/panicle and cluster II showed the lowest mean value (64.50). For number of tillers/plant, the highest mean value was possessed by cluster II (10.30) and the lowest value was possessed by cluster V (8.69). Days to 50% flowering was the highest in cluster II (96.44) and the lowest in cluster IV (91.13). Cluster VIII recorded the highest mean value of days to maturity (128.33) and the lowest in cluster VII (114.67). 100 seed weight was recorded maximum for cluster IV (3.92) and the minimum for cluster IX (2.97).

Cluster IV showed the maximum mean value (144.56) for seed yield and cluster VII showed the lowest mean value (81.44). For leaf length, the highest mean value was possessed by cluster II (38.00) and the lowest value was possessed by cluster VIII (29.13). leaf width was the highest in cluster II (2.028) and the lowest in cluster V (1.280). Cluster II recorded the highest mean value of number of leaves per plant (47.333) and the lowest in cluster VI (37.216).

Cluster I showed the maximum mean value (1.494) for green fodder yield and cluster VIII showed the lowest mean value (0.624). For dry matter yield, the highest mean value was possessed by cluster I (0.309) and the lowest value was possessed by cluster VIII (0.144). crude protein in grain was the highest in cluster IV (13.57) and the lowest in cluster I (11.81). Cluster V recorded the highest mean value of crude protein in forage (13.67) and the lowest in cluster VIII (12.87).

Table-4.17.1: Cluster mean for 24 characters in oat germplasm in single cut

Characters Clusters	Plant height (cm)	Das to 50%flowering	Days to maturity	Flag leaf length (cm)	Internode length (cm)	Tillers per plant	Peduncle length (cm)	Axis length (cm)
I	131.87	93	118.53	26.93	20.60	8.99	24.10	23.73
II.	120.67	96.44	120.89	23.17	17.33	10.3	23.78	19.75
III.	107.5	92.17	116.53	24.1	16.83	8.8	29.63	24.02
IV.	121.28	92.78	122.17	26.5	17.89	9.29	28.43	24.31
V.	108.59	91.62	114.87	25.95	19.10	8.69	33.28	24.95
VI.	113.8	94.73	118.73	25.53	17.57	8.71	24.03	24.52
VII.	108.78	92.74	114.67	18.85	16.22	8.90	20.17	17.78
VIII	96.67	91.13	128.33	19.63	16.42	9.62	25.38	19.40
IX	100.65	95.26	121.54	21.65	13.50	9.00	23.00	20.86

Table-4.17.2: Cluster mean for 24 characters in oat germplasm in single cut

Characters Clusters	Number of spikelets	Seed yield (g)	Seed index (g)	Leaf length (cm)	Leaf width (cm)	Green fodder yield (Kg)	Dry matter yield (Kg)	Number of leaves per plant
I	70.60	135.07	3.41	36.00	1.707	1.494	0.309	41.267
II.	64.50	104.00	3.36	38.00	2.028	1.088	0.199	47.333
III.	65.87	96.20	3.33	36.50	1.753	0.948	0.203	39.967
IV.	84.33	144.56	3.92	36.61	1.822	1.277	0.230	45.278
V.	67.26	119.74	3.40	36.00	1.277	0.872	0.159	41.974
VI.	67.22	94.82	3.36	34.00	1.815	1.006	0.206	37.216
VII.	73.56	81.44	3.62	31.26	1.537	0.977	0.158	40.222
VIII	73.21	83.21	3.44	29.13	1.563	0.624	0.144	44.58
IX	62.13	95.72	2.97	31.91	1.822	0.820	0.156	42.481

Table-4.17.3: Cluster mean for 24 characters in oat germplasm in single cut

Characters Clusters	Crude protein grain (%)	Crude protein forage (%)	Germination %	Seedling length (cm)	Seedling dry weight (mg)	Seed vigour index-I	Seed vigour index- II	Electrical conductivity (dS/m/seed)
I	11.81	13.45	86.87	30.639	7.93	2660.33	686.870	0.305
II.	11.89	13.20	86.78	32.512	9.54	2823.44	821.67	0.273
III.	13.20	13.50	90.90	34.957	10.17	3173.23	918.9	0.231
IV.	13.57	13.61	89.22	32.890	12.35	2934.61	1097.67	0.214
V.	12.26	13.66	85.95	31.838	11.13	2734.51	952.72	0.230
VI.	12.66	12.96	86.80	31.985	12.52	2772.94	1081.67	0.242
VII.	13.09	12.94	89.15	31.840	9.62	2839.04	853.56	0.237
VIII	13.01	12.87	83.92	31.127	11.06	2610.5	925.29	0.26
IX	12.19	13.17	84.94	30.265	9.66	2569.83	815.85	0.365

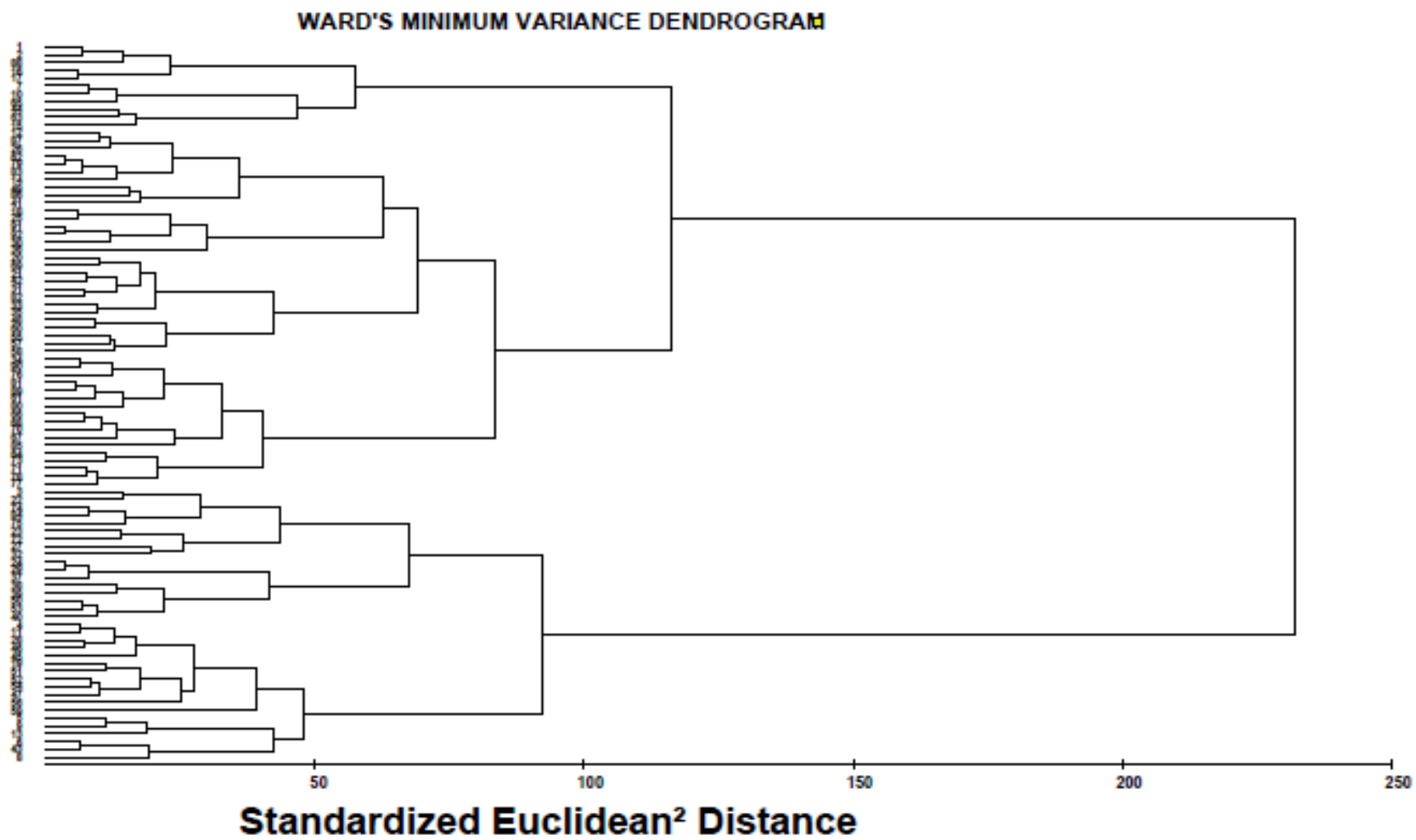


Figure 4.1 Dendrogram showing the clustering pattern of single cut oat genotype

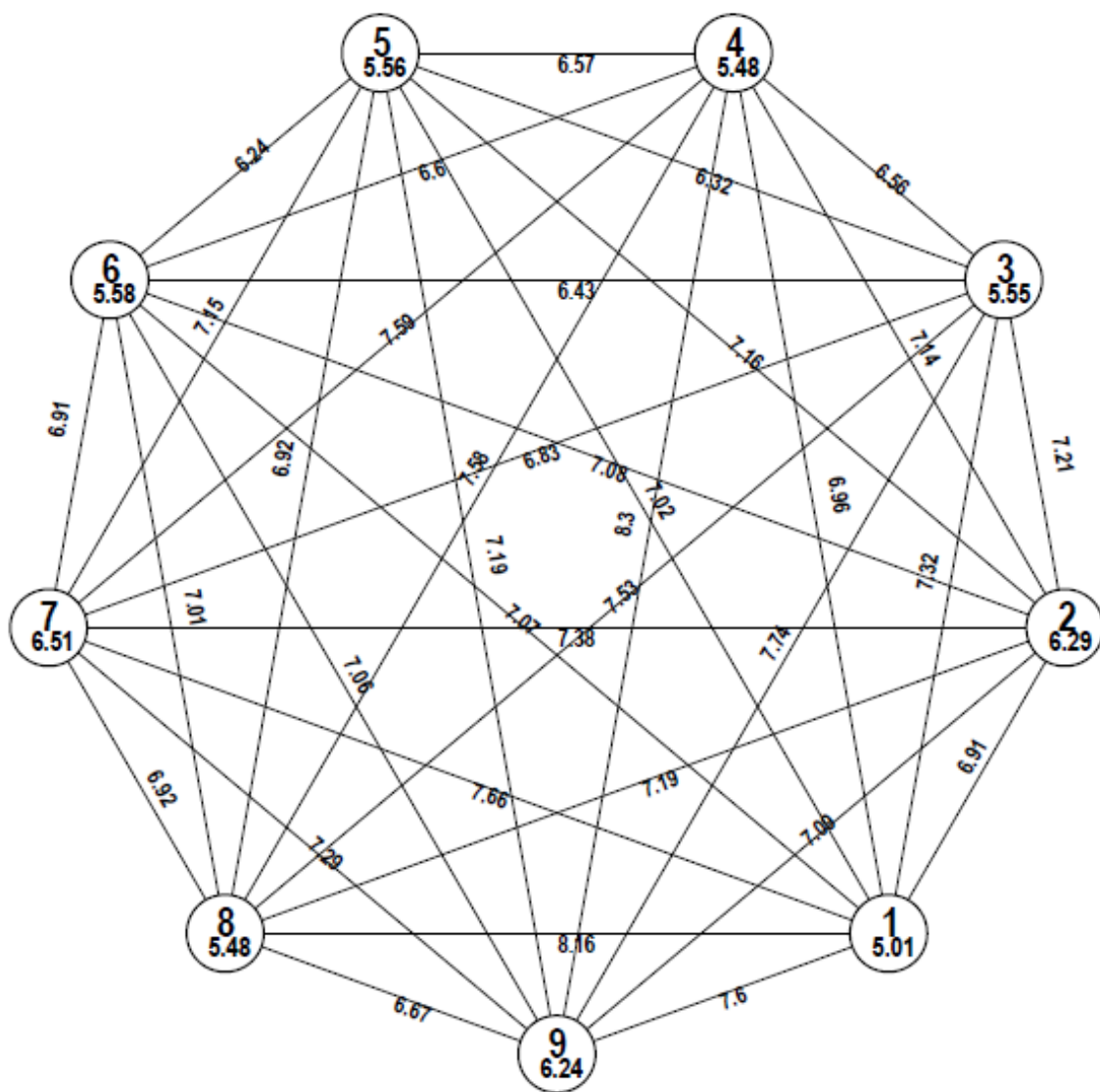


Figure 4.2 Mahalanobis euclidean distances in sinle cut oat

Table 4.18: Clustering of 92 genotypes of oat on the basis of D^2 statistics

Cluster	No. of genotypes	Genotypes
Cluster I	05	1 2 88 16 17
Cluster II	06	7 10 65 44 63 15
Cluster III	10	12 87 26 62 79 83 14 49 86 41
Cluster IV	06	18 25 91 92 30 36
Cluster V	13	20 69 21 42 31 82 33 35 48 60 55 57 58
Cluster VI	17	34 90 76 81 89 61 80 66 68 70 67 85 64 73 71 78 77
Cluster VII	09	3 22 74 84 75 23 72 27 32
Cluster VIII	08	24 29 37 38 39 50 53 40
Cluster IX	18	4 11 28 46 45 19 51 52 54 47 56 59 5 9 13 6 43 8

Cluster III revealed the highest mean value for germination% (90.90) whereas cluster VIII had the lowest mean value (83.92). Cluster III showed the maximum mean value (34.957) for seedling length and cluster IX showed the minimum mean value (30.265). For seedling dry weight, the highest mean value was possessed by cluster VI (12.52) and the lowest value was possessed by cluster VII (7.93). Seed vigour index III was the highest in cluster III (3173.23) and the lowest in cluster IX (2569.83). Seed vigour index II was recorded minimum for cluster I (686.87) and maximum for cluster IV (1097.67). For electrical conductivity, cluster IX (0.365) had the highest mean value while cluster IV had the lowest mean value (0.214).

4.6.2 Genetic divergence: 1st cut of multi-cut oat

Table 4.21 revealed the distribution pattern of genotypes in eleven different clusters. Cluster pattern revealed that cluster VIII and V were the largest ones with 18 and 14 genotypes respectively followed by cluster I and III each with 10 genotypes, cluster VI and XI with 7 genotypes each, cluster IV and X with 6 genotypes each, cluster II and IX each with 5 genotypes each and cluster VII with 4 genotypes.

4.6.2.1 Intra and inter cluster average D² values

The intra and inter cluster D² values among 92 genotypes are given in table 4.19. The results show that inter cluster distances are more than intra cluster distances which indicates the presence of narrow genetic variation within a cluster. The highest intra cluster D² value was observed for cluster V (5.098) followed by cluster IX (4.013), cluster IV (3.740), cluster X (3.600), cluster XI (3.398), cluster II (3.354), cluster III (3.033), cluster I (2.970), cluster VIII (3.904), cluster VI (2.609) and cluster VII (2.602).

When diversity was studied among the clusters based on the inter cluster D² values, it showed a range of 2.602 to 6.826. The average inter-cluster distance was found to be highest between cluster IX and XI (6.826), cluster IV and VII (6.676), cluster IV and XI (6.604) whereas the lower inter cluster distance was observed between cluster V and VI (3.508), followed by cluster VII and VIII (3.717). The higher inter cluster distance indicated the presence of more diversity among the genotypes included between these clusters.

4.6.2.2 Mean values of different clusters for 11 characters

The cluster means for dry matter yield per meter row length and its component characters are presented in Table 4.20. The data revealed considerable differences among all the clusters for most of the characters studied. From the table 4.20, it was evident that plant height were lowest in cluster X (35.44) and the highest in cluster XI (62.91). For number of tillers/plant, the highest mean value was possessed by cluster X (9.33) and the lowest value was possessed by cluster VI (7.51).

Cluster XI showed the maximum mean value (0.322) for green fodder yield and cluster IX showed the lowest mean value (0.141). For dry matter yield, the highest mean value was possessed by cluster XI (0.0751) and the lowest value was possessed by cluster IX (0.0363). Cluster V recorded the highest mean value of crude protein in forage (14.60) and the lowest in cluster X (13.05).

Table 4.19: Average intra (diagonal) and inter (above diagonal) cluster D² values in ninety two genotypes of oat in 1st cut of multicut system

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	2.970	4.071	3.730	5.151	5.036	4.643	3.969	4.16	5.051	4.704	5.081
II		3.354	4.020	4.769	5.330	4.581	5.548	5.463	5.734	6.456	6.544
III			3.033	4.813	4.232	4.072	4.784	4.514	5.947	5.941	4.526
IV				3.740	4.065	4.381	6.676	5.299	5.851	6.349	6.604
V					5.098	3.508	5.845	4.273	5.753	5.758	4.924
VI						2.609	5.200	3.997	5.206	5.646	5.423
VII							2.602	3.717	4.959	4.959	4.678
VIII								2.904	4.375	4.292	4.539
IX									4.013	4.722	6.826
X										3.600	5.859
XI											3.398

Table-4.20.: Cluster mean for different characters in oat germplasm 1st cut of multicut oat

Characters Clusters	Plant height (cm)	Number of tillers per plant	Green fodder yield (Kg)	Dry matter yield (Kg)	Crude protein forage (%)
I	52.13	9.13	0.208	0.0502	13.99
II	54.47	7.95	0.159	0.0386	14.00
III	58.03	8.11	0.243	0.0577	14.24
IV	53.06	8.43	0.169	0.0346	14.51
V	56.43	7.92	0.222	0.0530	14.60
VI	59.52	7.51	0.196	0.0453	14.16
VII	62.58	8.63	0.232	0.0534	13.42
VIII	54.72	8.34	0.218	0.0494	13.97
IX	42.13	8.39	0.141	0.0363	14.03
X	35.44	9.33	0.212	0.0506	13.05
XI	62.91	8.33	0.322	0.0751	13.87

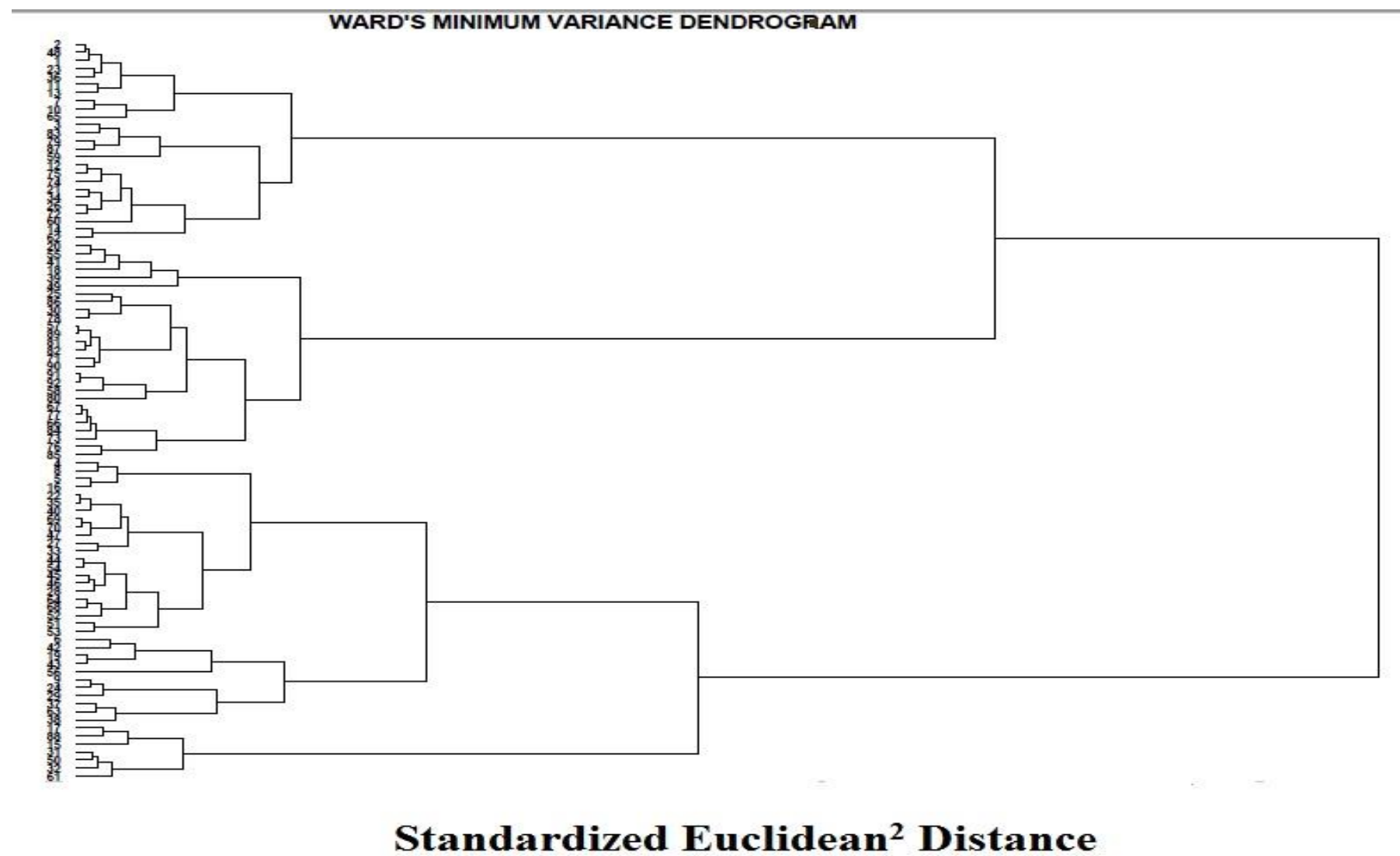


Figure 4.3 Dendrogram showing the clustering pattern of 1st cut of multi cut oat genotype

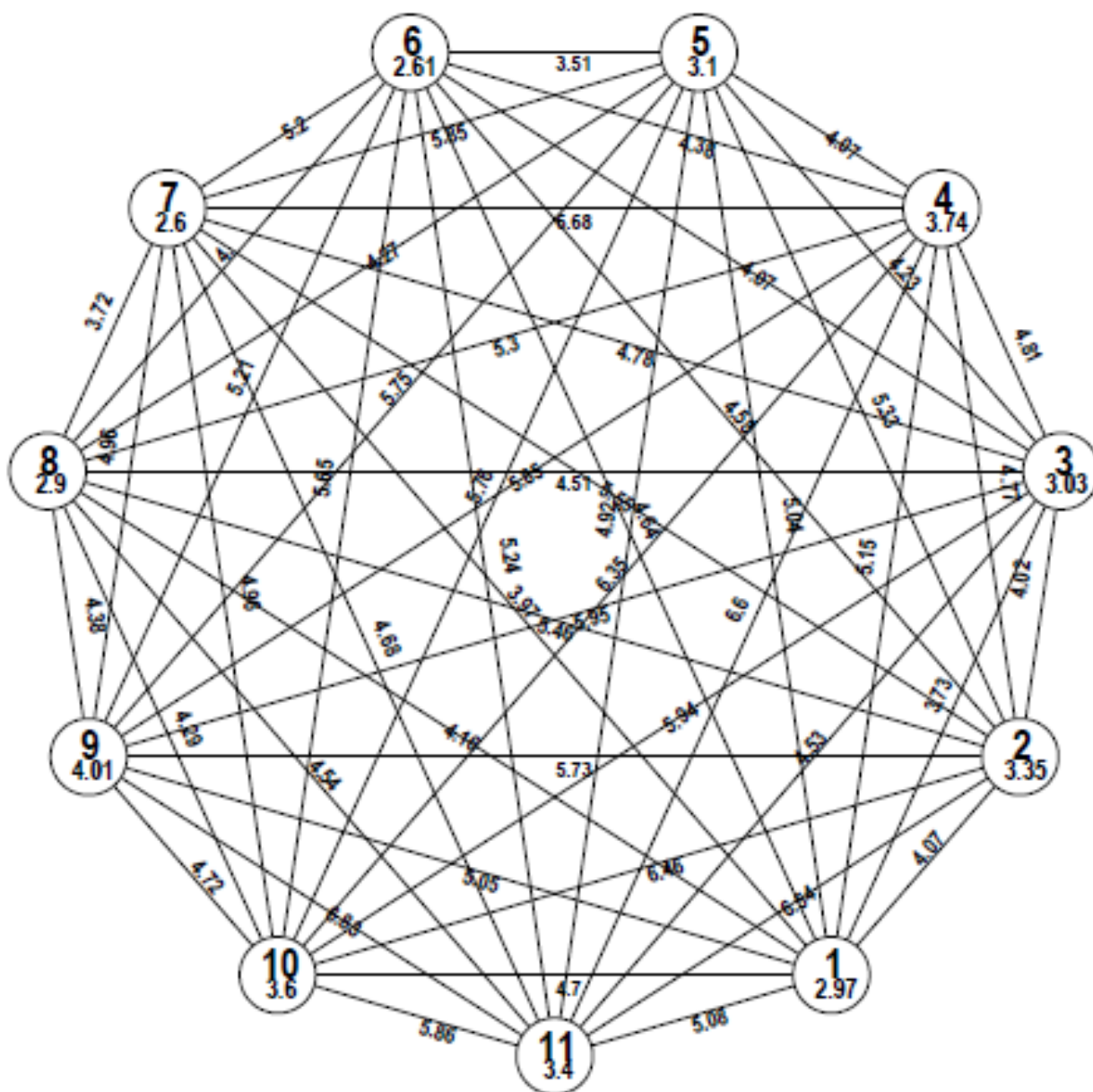


Figure 4.4 Mahalanobis euclidean distances in 1st cut of multi cut oat

Table 4.21: Clustering of 92 genotypes of 1st cut of multicut system

Cluster	No. of genotypes	Genotypes
Cluster I	10	2 48 1 23 36 11 13 7 10 65
Cluster II	05	3 83 79 87 59
Cluster III	10	12 75 74 21 34 26 72 60 14 62
Cluster IV	06	20 55 41 18 39 49
Cluster V	14	25 86 30 78 57 89 81 82 71 90 91 92 58 80
Cluster VI	07	67 77 66 84 73 76 85
Cluster VII	04	4 8 5 16
Cluster VIII	18	22 35 40 69 70 47 27 33 44 54 45 46 28 64 68 52 51
Cluster IX	05	6 42 19 43 56
Cluster X	06	9 24 29 37 63 38
Cluster XI	07	17 88 15 31 50 32 61

4.6.3 Genetic divergence: 2nd cut of multi-cut oat

Table 4.24 revealed the distribution pattern of genotypes in different clusters. Cluster pattern revealed that cluster I and II were the largest ones with 16 genotypes each, followed by cluster IX with 14 genotypes, cluster VI with 13 genotypes, cluster VIII with 10 genotypes, cluster IV and V each with 8 and 7 genotypes, cluster III with 6 genotypes and cluster VII with 2 genotypes.

4.6.3.1 Intra and inter cluster average D² values

The intra and inter cluster D² values among 92 genotypes are given in table 4.22. The results show that inter cluster distances are more than intra cluster distances which indicates the presence of narrow genetic variation within a cluster. The highest intra cluster D² value was observed for cluster VII (6.078) followed by cluster III (5.588), cluster VIII (5.429), cluster IX (5.131), cluster I (5.011), cluster I (5.002), cluster II (4.919), cluster VI (4.908) and cluster IV (4.899).

When diversity was studied among the clusters based on the inter cluster D² values, it showed a range of 4.899 to 8.071. The average inter-cluster distance was found to be highest between cluster II and VII (8.071), cluster III and VI (7.857), cluster III and VII (7.849) whereas the lower inter cluster distance was observed between cluster VI and VIII (5.766), followed by cluster IV and V (5.854). The higher inter cluster distance indicated the presence of more diversity among the genotypes included between these clusters.

4.6.3.2 Mean values of different clusters for 20 characters

The cluster means for dry matter yield per plant and its component characters are presented in Table 4.23.1 and 4.23.2. The data revealed considerable differences among all the clusters for most of the characters studied. From the table 4.23.1 and 4.23.2, it was evident that plant height were lowest in cluster VII (53.67) and the highest in cluster V (85.14). Cluster II recorded the highest flag leaf length (25.46) while cluster VII recorded the lowest (15.83). Peduncle length was recorded minimum for cluster IX (21.46) and maximum for cluster II (29.00). Cluster II revealed the highest mean value for inter-node length (19.63), whereas cluster VII had the lowest mean value (11.17). For number of tillers/plant, the highest mean value was possessed by cluster IV (9.86) and the lowest value was possessed by cluster III (7.71). Days to 50% flowering was the highest in cluster VIII (123.30) and the lowest in cluster VII (113.67).

For leaf length, the highest mean value was possessed by cluster V (35.91) and the lowest value was possessed by cluster VII (26.33). Leaf width was the highest in cluster VII (2.17) and the lowest in cluster VI (1.247). Cluster IV recorded the highest mean value of number of leaves per plant (45.00) and the lowest in cluster III (34.06). Cluster IX showed the maximum mean value (0.661) for green fodder yield and cluster VII showed the lowest mean

value (0.405). For dry matter yield, the highest mean value was possessed by cluster IX (0.1614) and the lowest value was possessed by cluster VII (0.1058). Cluster I recorded the highest mean value of crude protein in forage (12.62) and the lowest in cluster VII (10.98).

Table 4.22: Average intra (diagonal) and inter (above diagonal) cluster D² values in ninety two genotypes of oat

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	5.002	5.952	6.358	5.813	6.072	6.534	7.046	6.602	6.709
II		4.919	6.003	6.300	6.347	6.908	8.071	6.306	6.117
III			5.588	7.684	7.727	7.857	7.849	7.140	6.783
IV				4.899	5.854	6.089	7.458	6.154	6.356
V					5.011	6.191	7.309	6.310	6.541
VI						4.908	6.981	5.766	6.450
VII							6.078	7.252	7.867
VIII								5.429	6.211
IX									5.131

Table-4.23.1: Cluster mean for different characters in oat germplasm in 2nd cut of multicut oat

Characters Clusters	Plant height (cm)	Das to 50%flowering	leaf length (cm)	Internode length (cm)	Tillers per plant	Peduncle length (cm)
I	71.85	115.35	22.02	16.65	8.49	25.98
II.	80.81	118.10	25.46	19.63	8.65	29.00
III.	68.50	114.44	23.50	15.44	7.71	24.08
IV.	75.50	121.50	21.88	17.63	9.86	22.00
V.	85.14	121.14	23.86	17.91	8.92	22.67
VI.	68.72	122.51	19.67	13.92	8.99	22.53
VII.	53.67	113.67	15.83	11.17	8.13	22.42
VIII	65.40	123.30	21.13	15.53	9.11	25.23
IX	80.38	122.14	22.10	15.92	8.64	21.46

Table-4.23.2: Cluster mean for different characters in oat germplasm in 2nd cut of multicut oat

Characters Clusters	Leaf length (cm)	Leaf width (cm)	Green fodder yield (g)	Dry matter yield (kg)	Number of leaves per plant	Crude protein forage (%)
I	29.50	1.496	0.406	0.1065	39.46	12.62
II.	33.10	1.81	0.431	0.1119	39.73	12.22
III.	31.22	1.74	0.433	0.1121	34.06	12.23
IV.	33.29	1.75	0.486	0.1185	45.00	11.61
V.	35.91	2.01	0.411	0.1091	41.00	11.25
VI.	26.15	1.47	0.454	0.1168	42.26	10.98
VII.	26.33	2.17	0.405	0.1058	39.17	12.38
VIII	29.07	2.03	0.455	0.1181	44.23	11.61
IX	31.33	1.91	0.661	0.1614	38.79	11.83

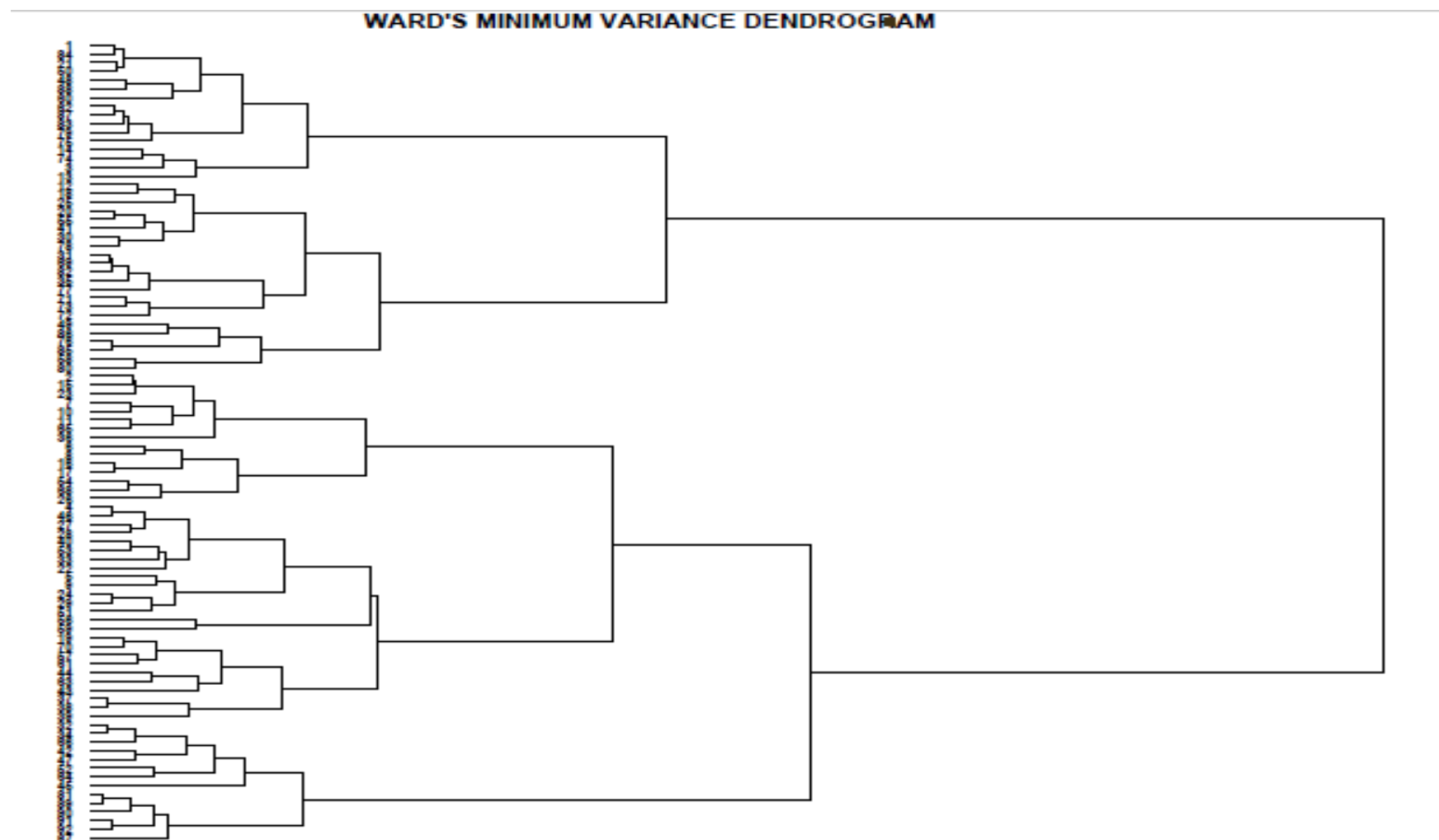


Figure 4.5 Dendrogram showing the clustering pattern of 2nd cut of multi cut oat genotype

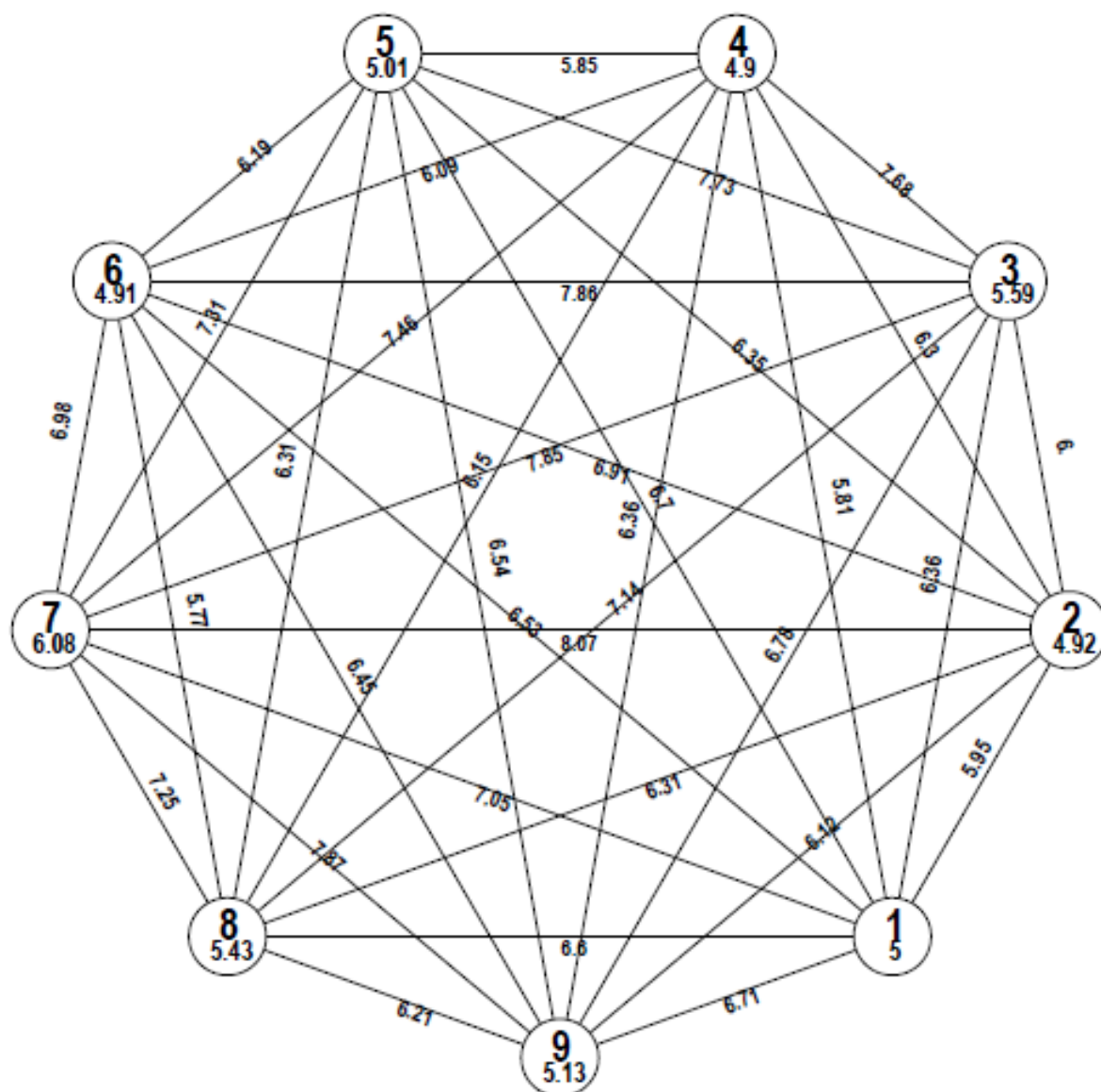


Figure 4.6 Mahalanobis euclidean distances in 2nd cut of multi cut oat

Table 4.24: Clustering of 92 genotypes of oat on the basis of D² statistics

Cluster	No. of genotypes	Genotypes
Cluster I	16	1 84 21 50 48 88 60 62 87 83 79 75 14 74 3 13
Cluster II	16	12 18 25 20 55 41 30 78 31 69 82 35 77 71 73 72
Cluster III	06	49 86 76 85 58 80
Cluster IV	08	2 15 23 7 10 11 65 36
Cluster V	07	6 8 16 17 54 68 26
Cluster VI	13	4 46 27 28 40 53 33 22 5 9 24 29 51
Cluster VII	02	56 59
Cluster VIII	10	19 70 57 61 44 63 43 37 38 39
Cluster IX	14	32 34 66 42 47 52 64 45 81 89 90 91 92 67

4.7 Principal component analysis

Principal component analysis helps in identifying the most relevant characters and presents them in more visualized dimensions through linear combinations of variables that accounts for most of the variation presents in original set of variables.

4.7.1 Principal component analysis in single cut

In the present investigation, principal components with eigen values greater than one were selected for interpretation (Kaiser 1958). The eight principal components had eigen values more than one and altogether explained 70.01% of the total accumulated variability (Table 4.25). The first principal component explained 12.78 % of the total variation. The second, third, fourth, fifth, sixth and seventh principal components explained 10.86, 9.81, 8.34, 8.08, 7.20, 6.89 and 6.04% of the total variance, respectively.

Table 4.25: Total variance explained by different principal components in single cut oat genotypes

Component	Eigen values	Variation Explained %	Cumulative variation Explained %
1	4.178	12.779	12.779
2	2.728	10.862	23.641
3	2.354	9.811	33.452
4	1.884	8.344	41.796
5	1.774	8.080	49.877
6	1.469	7.203	57.080
7	1.369	6.890	63.970
8	1.046	6.035	70.005

Further, principal factor analysis was carried out, because the principal component analysis does not assume a definite model. In principal factor analysis each observed variable is expressed linearly in terms of a common factor and a unique factor. The common factors account for the correlation among the variables. While each unique factor accounts for the remaining variance (including error) of that variable. Moreover, in principal component analysis, the total variation contained in a set of variables is considered, whereas, in factor analysis interest centers on that part of variance which is shared by the common factors. Also in contrast to principal component analysis, here the variables axes are allowed to interact resulting in distortion of mutual orthogonality.

The principal factor analysis carried out without any rotation did not derive the clear picture of interaction among the characters. This did not provide a clear picture regarding the idea of character association with respective principal factor as some factors had very high loading of variable and some have none. This indicated the next alternative of factor analysis i.e. with rotation method Kaiser (1958) was used. To select the relevant characters in various principal factors, the correlation values ($> (\pm 0.5)$) were considered as relevant for that principal factor. Factor loading of different characters with varimax rotation have been presented in Table 4.26.

Table 4.26: Factor loading of different characters with respect to different principal factor (Varimax rotation) in single cut oat

Character	Component							
	PF-1	PF-2	PF-3	PF-4	PF-5	PF-6	PF-7	PF-8
PH	0.22	0.618	-0.037	-0.227	0.291	-0.064	-0.096	0.038
DF	-0.163	0.08	0.095	-0.577	-0.04	0.545	0.126	0.226
DM	-0.482	0.031	0.173	0.278	0.216	0.359	0.04	-0.159
FLL	0.342	0.435	0.384	0.084	-0.134	-0.123	-0.062	-0.223
IL	0.392	0.197	0.257	0.408	-0.251	-0.161	0.377	0.016
TPL	-0.357	0.164	-0.155	0.549	0.022	0.492	0.078	-0.042
PL	0.371	-0.152	0.187	0.407	-0.366	-0.245	-0.277	0.096
AL	0.496	0.239	0.404	0.152	-0.204	-0.047	0.237	0.281
NOS	0.044	0.119	-0.303	0.28	0.650	-0.054	-0.002	0.105
SY	0.293	0.377	-0.058	0.135	0.007	0.047	0.605	0.335
SI	0.386	-0.032	-0.233	0.252	0.460	-0.24	0.053	0.378
LL	0.309	0.35	0.317	0.226	-0.217	0.244	-0.008	0.513
LW	0.069	0.021	0.506	0.042	-0.063	0.254	0.379	0.033
GFY	0.221	0.773	0.011	-0.177	0.24	0.093	0.045	-0.099
DMY	0.273	0.720	0.01	-0.142	0.138	0.048	0.032	-0.184
NOLS	-0.409	0.2	-0.238	0.628	0.023	0.323	-0.06	0.098
CPg	0.316	-0.258	-0.252	0.172	0.048	-0.025	0.391	-0.305
CPf	0.467	-0.114	-0.098	-0.031	-0.305	0.298	-0.502	-0.026
GP	0.547	0.126	-0.494	-0.13	-0.066	-0.022	0.319	0.027
SL	0.697	-0.246	-0.363	-0.035	-0.142	0.386	-0.013	0.023
SDW	0.39	-0.432	0.598	-0.027	0.452	0.186	-0.115	-0.083
SVI	0.752	-0.141	-0.483	-0.077	-0.139	0.292	0.113	0.024
SVII	0.491	-0.409	0.521	-0.046	0.448	0.182	-0.063	-0.088
EC	-0.631	0.195	0.066	-0.205	-0.278	0.019	0.042	0.164

Data presented in Table 4.26 clearly indicated that PF-1 was loaded on germination %, seedling length and seed vigour index-I. With similar logic, PF-2 showed a strong and positive factor with the traits like plant height, green fodder yield and dry matter

yield. The PF-3 was loaded with leaf width. The PF-4 showed the diversity among accessions based on number of leaves per plant and numbers of tillers per plant and days to maturity. PF-5 confirms the variation observed by number of spikelets per panicle and seed index. PF-6 was loaded with days to 50% flowering. PF-7 showed the strong and positive factor with seed yield. PF-8 loaded with leaf length.

Among these principal factors, PF-2 and PF-7 regarded as fodder yield factors and seed yield factors.

4.7.2 Principal component analysis in 1st cut of multi-cut

The three principal components had eigen values more than one and altogether explained 67.95% of the total accumulated variability (Table 4.27). The first principal component explained 26.24% of the total variation. The second and third principal components explained 21.84 and 19.87% of the total variance, respectively.

Table 4.27: Total variance explained by different principal components in 1st of multi-cut cut oat genotypes

Component	Eigen values	Variation Explained %	Cumulative variation Explained %
1	3.249	26.244	26.244
2	2.190	21.843	48.087
3	2.035	19.865	67.952

Table 4.28: Factor loading of different characters with respect to different principal factor (Varimax rotation) in 1st cut of multi-cut oat

Character	Component		
	PF-1	PF-2	PF-3
PH65	0.316	0.11	0.635
TPL	-0.224	-0.451	-0.261
GFY65	-0.112	-0.050	0.922
DMY65	-0.150	-0.037	0.902
CP65	0.484	0.095	0.035
GP	0.776	-0.153	-0.017
SL	0.834	0.194	-0.038
SDW	-0.067	0.976	-0.097
SVI	0.953	0.083	-0.038
SVII	0.066	0.962	-0.1
EC	-0.504	-0.478	-0.159

Data presented in Table 4.28 clearly indicated that PF-1 was loaded on germination %, seedling length and seed vigour index-I. The PF-2 was loaded with seedling dry weight and seed vigour index-II and with similar logic, PF-3 showed a strong and positive factor with the traits like plant height, green fodder yield and dry matter yield.

Among these principal factors, PF-3 regarded as fodder yield factors.

4.7.3 Principal component analysis in 2nd cut of multi-cut

The seven principal components had eigen values more than one and altogether explained 73.34% of the total accumulated variability (Table 4.29). The first principal component explained 15.31 % of the total variation. The second, third, fourth, fifth, sixth and seventh principal components explained 11.94, 11.79, 10.54, 10.40, 7.38 and 5.97 % of the total variance, respectively.

Table 4.29: Total variance explained by different principal components in 2nd multi-cut of oat genotypes

Component	Eigen values	Variation Explained %	Cumulative variation Explained %
1	4.261	15.311	15.311
2	2.692	11.942	27.253
3	2.195	11.795	39.048
4	1.809	10.538	49.586
5	1.452	10.402	59.989
6	1.182	7.382	67.370
7	1.076	5.966	73.336

Data presented in Table 4.26 clearly indicated that PF-1 was loaded on seedling length and seed vigour index-I. With similar logic, PF-2 showed a strong and positive factor with the traits like green fodder yield and dry matter yield. The PF-3 was loaded with internode length. The PF-4 showed the diversity among accessions based on green fodder yield and dry matter yield. PF-5 confirms the variation observed by number of leaves per plant and seedling dry weight. PF-6 was loaded with seed index and leaf length. PF-7 showed the strong and positive factor with leaf width.

Among these principal factors, PF-2 and PF-4 regarded as fodder yield factors.

Table 4.30: Factor loading of different characters with respect to different principal factor (Varimax rotation) in 2nd cut of multi-cut oat

Character	Component						
	PF-1	PF-2	PF-3	PF-4	PF-5	PF-6	PF-7
PH	0.326	0.310	0.523	0.062	-0.149	-0.304	-0.119
DM	-0.494	0.238	0.075	0.138	0.378	-0.059	-0.006
FLL	0.280	0.318	0.390	-0.008	-0.162	0.382	-0.292
IL	0.430	0.203	0.575	0.038	0.008	-0.217	-0.032
TPL	-0.517	-0.068	0.303	0.582	0.391	-0.047	-0.02
PL	0.379	-0.018	0.320	-0.170	0.239	0.149	-0.401
AL	0.493	0.314	0.507	-0.064	-0.107	-0.101	0.211
SI	0.373	-0.009	-0.078	0.243	0.027	0.617	-0.177
LL	0.249	0.300	0.443	0.217	0.042	0.506	0.095
LW	0.084	0.443	0.237	-0.048	0.059	-0.094	0.671
GFYMC	-0.240	0.626	-0.310	0.522	-0.353	0.07	-0.079
DMYMC	-0.216	0.639	-0.309	0.525	-0.33	0.071	-0.061
NOLS	-0.480	-0.176	0.287	0.491	0.492	-0.045	0.052
CPMC	0.537	-0.238	-0.115	0.193	0.176	0.361	-0.085
G	0.525	-0.369	-0.002	0.298	-0.364	-0.134	0.081
SL	0.701	-0.329	-0.200	0.330	0.156	0.145	0.253
SDW	0.415	0.618	-0.413	-0.214	0.435	-0.012	0.040
SVI	0.745	-0.404	-0.156	0.379	-0.024	0.063	0.225
SVII	0.511	0.566	-0.417	-0.162	0.375	-0.032	0.047
EC	-0.638	-0.093	0.164	-0.255	-0.201	0.161	0.368

Oat (*Avena sativa* L.) is the most important cereal (graminaceous) forage crop grown during winter season, which is fed in the form of green and dry fodder as well as silage. Crop improvement in any crop depends on the extent of genetic diversity in the gene pool. The knowledge of nature and extent of genetic variation available in the germplasm helps the breeders for planning sound breeding programmes. Plant breeders are engaged in developing the newer varieties of crops for betterment of fodder yield and seed yield so that the demand for fodder can be fulfilled.

The variability in the population is largely due to genetic cause with least environment effect, the possibility of selecting superior genotype is a prerequisite for obtaining higher yield, which is the ultimate expression of various yield contributing characters. But the maximum genetic variability which was present in genotypes has already exhausted and further selection in these genotypes has narrowed genetic variability. The basic material utilized in finding genetic variability is germplasm. The crosses involving diverse parents within compatible range could be intercrossed to obtain high heterotic expression and also to recover desirable transgressive segregants in the subsequent generations.

Considering the above facts, it is, therefore, essential to identify and classify the variability present among the genotypes based on various criteria such as morphology, geographical distribution and genetic diversity. In the present investigation, an attempt has been done to evaluate 92 genotypes of oat for the estimation of proportion of variability, broad sense heritability, predicted genetic advance, GCV and PCV with respect to 24 characters. The associations among these characters and their direct and indirect effects on dry matter yield per meter row length have also been studied with Mahalanobis D^2 analysis and principal component analysis to assess genetic diversity among the genotypes.

The results presented in previous chapter are discussed under following headings:

- 5.1 Variability, heritability and genetic advance analysis
- 5.2 Correlation coefficient analysis
- 5.3 Path coefficient analysis
- 5.4 Diversity Analysis
- 5.5 Principal component analysis

5.1 Variability, heritability and genetic advance analysis

The analysis of variance investigated during the study indicated significant differences among the genotypes for all the characters studied viz. plant height (cm), number

of days to 50% flowering, number of days to maturity, flag leaf length (cm), internode length (cm), number of tillers/plant, peduncle length (cm), axis length (cm), number of spikelets/panicle, seed yield (g), 100-seed weight (g), leaf length(cm), leaf width (cm), green fodder yield (kg), dry matter yield (kg) and number of leaves/plant, germination (%), seedling length (cm), seedling dry weight (mg), seed vigour index I, seed vigour index II and electrical conductivity (mS/cm/seed), forage crude protein (%) and seed crude Protein (%). These results indicate that there is a great scope for the improvement of germplasm through selection and heterosis breeding. The results clearly indicate that all the oat genotypes studied showed high variability for grain and fodder yield and its component traits. The genotypes showed a wide range of variation, which helps in the selection of superior and desirable genotypes for further improvement and exploitation through selection, hybridization, heterosis and combination breeding.

The earlier researchers Singh and Singh (2009); Shehzad *et al.* (2011); Chakraborty *et al.* (2014); Cattivelli *et al.* (2011); Ahmed *et al.* (2011); Bibi *et al.* (2012); Kapoor and Bajaj (2013); Arora (2013); Khan *et al.* (2014), Krishna *et al.* (2014); Surje *et al.* (2014); Bind *et al.* (2016) and Shekhawat and Jaipal (2016) also observed a large and exploitable variation in oat germplasm, it could be stated that there is enough scope for improvement through selection for the traits investigated in the present material.

Among dry matter yield and its component characters, plant height possessed the highest range, followed by seed yield/meter row length, 100 seed weight, flag leaf length and green fodder yield. This shows that these characters are responsible for wide variation in seed yield of various genotypes. Bibi *et al.* (2012) and Siloriya *et al.* (2014) also reported similar results for plant height. High variability for dry matter yield/meter row length and green fodder yield per meter row length in first and second cut of multi-cut was also reported by Arora (2013).

The estimates of heritability, PCV, GCV, and genetic advance are useful in determining the method of selection to improve a particular population for a specific trait. It is always not necessary for high heritability to be associated with high genetic advance. High heritability coupled with high genetic advance indicates that there are additive genetic effects and simple selection may be effective for improvement of that character. The magnitude of phenotypic coefficient of variance was higher than genotypic coefficient of variance for all the characters studied indicating the influence of environment in the expression of these characters. Similar results were reported by Singh and Singh (2009); Singh and Singh (2011) and Jaipal & Shekhawat (2016). The highest estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for 100-seed weight followed by seed yield per meter row length, internode length, forage crude protein (%), grain crude protein (%), seedling length, seedling dry weight seed vigor index-I and seed vigor index-II.

Therefore, selection for these characters would be effective for the improvement of yield in oat. Moderate estimates of GCV and PCV was observed for traits like plant height at fodder stage, leaf length, axis length and dry matter yield,; low GCV and PCV was observed for days to 50% flowering, days to maturity, leaves per plant and number of tillers per plant. Similar findings were reported by Singh and Singh (2011); Bibi *et al.* (2012); Chakraborty *et al.* (2014) and Shekhawat and Jaipal (2016) for one or more characters. Singh and Singh (2011) and Bind *et al.* (2016) found low GCV and PCV for days to flowering and days to maturity which supported the present finding. Dubey *et al.* (2014) recorded low GCV and PCV for traits like leaves per plant, tillers per plant and axis length while high GCV and PCV for dry matter yield per meter row length and green fodder yield per meter row length also reported by Jaipal & Shekhawat (2016). GCV and PCV relatively showed very small difference. A close proximity between GCV and PCV indicated very less influence of environment in the expression of the characters. This was supported by the findings of Surje and De (2014).

GCV together with heritability and genetic advance was considered as good estimates of genetic gain to be expected from selection on phenotypic basis. A trait having high heritability and high genetic advance signifies the usefulness of plant selection based on phenotypic performance.

The high estimates of heritability (broad sense) were recorded for almost all the characters studied. These findings are in accordance with the results of Singh and Singh (2011); Chakraborty *et al.* (2014); Dubey *et al.* (2014) and Bind *et al.* (2016). Also, genetic advance as percent of mean was high for characters like flag leaf length, internode length, peduncle length, axis length, leaf length, leaf width, green fodder yield per plant, dry matter yield, seed yield and hundred seed weight, while the estimates of genetic advance as percent of mean was moderate for plant height, number of tillers per plant, number of leaves per plant, forage crude protein and grain crude protein indicating that the improvement of these through selection as well as their exploitation through combination breeding. However, the estimates of high heritability coupled with high genetic advance were observed for the characters viz., flag leaf length, days to maturity, leaf length, leaf width, tillers per plant, peduncle length, internode length, number of spikelets per panicle, axis length, green fodder yield, dry matter yield, seed yield, hundred seed weight and plant height suggesting that simple selection could be done for the improvement of these traits in the existing material.

Sangwan *et al.* (2012) and Shekhawat and Jaipal (2016) observed high heritability with high genetic advance for tillers per plant and green fodder yield. Singh and Singh (2011) also recorded high heritability and genetic advance were for characters like tillers per plant, green fodder yield and dry matter yield. Chakraborty *et al.* (2014) observed high heritability along with high genetic advance for characters like green fodder yield, 100 seed weight and seed yield per plant. These results underline the scope for improvement through selection in

these characters. Pundir *et al.* (2008) studied the genotypic and phenotypic coefficient of variation, heritability, expected genetic advance in 36 genotypes of oat over four environments.

5.2 Correlation coefficient analysis

Yield is a complex character which is contributed by a large number of component traits. Therefore, to determine the relative importance of the component characters and to initiate an effective selection programme, correlation studies are practised. In forage oat, dry fodder yield is an important character on which animal performance is dependent. Hence, dry fodder yield per meter row length was taken as dependent character for correlation studies in this investigation.

Correlation between different characters could arise due to linkage or pleiotropy. Correlation due to linkage can be manipulated or changed through recombination but it would be impossible to overcome the correlation due to pleiotropy. In the later case, genetic improvement in one trait is not eventually possible without bringing a change in the associated component characters.

High magnitude of genotypic correlation coefficient to that of phenotypic correlation coefficient shows a good amount of strong inherent association between different attributes. Bibi *et al.* (2012) and Krishna *et al.* (2014) also reported that genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for most of the characters studied.

Plant height exhibited positive correlation with flag leaf length, axis length, spikelets/panicle, number of tillers/plant, days to 50% flowering, days to maturity, seed yield, green fodder yield and dry matter yield and negative correlation with peduncle length, and 100 seed weight. Ziya *et al.*, (2001), Kumar *et al.*, (2004), Lorencetti *et al.* (2006), Bahadur *et al.* (2008), Sofi *et al.* (2012), Ahmed *et al.* (2013) and Krishna *et al.* (2014) also reported similar results.

Flag leaf length was positively associated with peduncle length, internode length, number of tillers/plant, days to 50% flowering, days to maturity, 100 seed weight, seed yield green fodder yield and dry matter yield, and negatively correlated with axis length and spikelets/panicle. Similar results were recorded by Kumar *et al.*, (2004) and Ahmed *et al.* (2013).

Number of spikelets/panicle showed positive correlation with plant height, number of tillers/plant, 100 seed weight, seed yield, green fodder yield and number of leaves per plant and negative correlation with days to 50% flowering. Surje and De (2014) also reported similar to the present findings.

Number of tillers/plant showed positive correlation with spikelets/panicle, days to maturity and seed yield and negative correlation with days to 50% flowering and days to maturity. Ahmed *et al.* (2013) and Krishna *et al.* (2014) also observed similar results.

Days to 50% flowering had positive correlation with days to maturity and negative correlation with seed yield, number of spikelets per panicle and peduncle length. Vaisi *et al.* (2013) and Krishana *et al.* (2014) supported the present findings.

Days to maturity had positive correlation with 100 seed weight and negative correlation with seed yield. Vaisi *et al.* (2013) and Ahmed *et al.* (2013) were in conformity with the present results.

Positive correlations of 100-seed weight were observed with seed yield. Ahmed *et al.* (2013) and Krishna *et al.* (2014) showed similarity with the current findings.

Internode length had positive correlation with peduncle length, axis length, dry matter yield, leaf length and leaf width while negative correlation with days to 50% flowering and number of days to maturity. Kumar *et al.*, (2004), Bahadur *et al.* (2008), and Ahmed *et al.* (2013) agreed with the present results.

Peduncle length had positive correlation with internode length, axis length, leaf length and seed yield while negative correlation with days to 50% flowering and number of days to maturity. These results are in conformity with the findings of Kumar *et al.*, (2004), Bahadur *et al.* (2008), and Ahmed *et al.* (2013).

Seed yield exhibited positive correlation with flag leaf length, axis length, hundred seed weight, number of spikelets/panicle and green fodder yield and dry matter yield and negative correlation with days to 50% flowering and days to maturity. Similar results for one or more characters were reported by many researchers namely; Ahmed *et al.* (2013), Vaisi *et al.* (2013) and Krishna *et al.* (2014).

Green fodder yield had positive correlation with plant height, flag leaf length, axis length, seed yield, leaf length and dry matter yield and showed negative correlation with days to maturity and peduncle length. Kumar *et al.*, (2004), Bahadur *et al.* (2008), Ahmed *et al.* (2013) and Krishna *et al.* (2014) have also observed the similar results.

Dry matter yield showed positive correlation with plant height, flag leaf length, internode length, axis length, seed yield, leaf length and green fodder yield and showed negative correlation with days to maturity and peduncle length. Similar results for one or more characters were reported by researchers, Kumar *et al.*, (2004), Lorencetti *et al.* (2006), Bahadur *et al.* (2008), Ahmed *et al.* (2013) and Krishna *et al.* (2014).

Number of leaves per plant had positive correlation with days to maturity, tillers per plant and number of spikelets per panicle. The results similar to the present findings were also observed by Kumar *et al.*, (2004), Lorencetti *et al.* (2006) and Bahadur *et al.* (2008).

The seedling length was positively correlated with seedling dry weight, seed vigour index-I and seed vigor index-II as these characters primarily depends on length of seedling and they are the multiplication value with germination percentage. Seedling length is directly proportionate with seedling dry weight. As more long is seedling length more will be the seedling dry weight. While electrical conductivity is negative measure of strength. If seed vigour index-I & II so it is negatively correlated with seed quality characters.

These results indicated that plant height, flag leaf length, internode length, axis length, seed yield, 100 seed weight, leaf length, green fodder yield are the major dry matter yield contributing traits to be given more selection pressure for improving dry matter yield.

5.3 Path coefficient analysis

Simple correlation coefficients provide association (positive and negative) between characters but it does not give causal basis of such associations. Path analysis provides the information on direct and indirect effects of various independent components on the dependent character. Both green and dry fodder yield are equally important if we consider morphological characters, however, in case of animal performance and their body maintenance, dry fodder yield is more important. Thus in present study path coefficient analysis was done considering dry fodder yield as a dependent character.

In single cut based on path coefficient analysis at the genotypic level high direct and positive effects were observed for green fodder yield (0.5709), tillers per plant (0.1931), plant height (0.1554) and seed yield per meter row length (0.1596) while days to 50% flowering (-0.2288), peduncle length (-0.036), axis length (-0.0445), number spikelets (-0.0006), and number of leaves per plant (-0.4082) had negative direct effects on dry matter yield per plant. This indicated that the green fodder yield, tillers per plant, plant height and seed yield per meter row length were important traits so far as their association with dry matter yield is concerned while plant height (0.3272), flag leaf length (0.18302), seed yield (0.1263), leaf length (0.1942), had high positive indirect effects via green fodder yield while peduncle length (-0.1092) and days to maturity (-0.0756) had negative indirect effect via green fodder yield.

In 1st cut of multi-cut path coefficient analysis exhibited high direct and positive effects of green fodder yield (0.9164), tillers per plant (0.2341) and plant height (0.1041) while days to 50% flowering (-0.089), peduncle length (-0.036), axis length (-0.0945), and number of leaves per plant (-0.1473) had negative direct effects on dry matter yield per plant. This indicated that the green fodder yield, tillers per plant and plant height were important traits so far as their association with dry matter yield is concerned while plant height (0.1821), flag leaf length (0.1803) and leaf width (0.1105) had high positive indirect

effects via green fodder yield. Tillers per plant (0.1467) had positive indirect effect via number of leaves per plant while peduncle length (-0.2761) and internode length (-0.1537) had negative indirect effect via green fodder yield.

In 2nd cut of multi-cut path coefficient analysis exhibited high direct and positive effects of green fodder yield (0.8902), tillers per plant (0.1518) and plant height (0.1401) while days to 50% flowering (-0.089), peduncle length (-0.036), axis length (-0.0945), and number of leaves per plant (-0.1473) had negative direct effects on dry matter yield per plant. This indicated that the green fodder yield, tillers per plant and plant height were important traits so far their association with dry matter yield is concerned while plant height (0.2874), flag leaf length (0.1803), leaf width (0.1105), had high positive indirect effects via green fodder yield while tillers per plant (-0.0343) had negative indirect effect via green fodder yield. The findings of Choubey *et al.* (2001), Vaisi *et al.* (2013) and Krishna *et al.* (2014) also confirm to our results.

5.4 Diversity Analysis

Development of high yielding plant varieties is recognized as a specific area since exploding population with urbanization and decreasing cultivable lands are the critical factors contributing to fodder insecurity for animals in developing world. Most of the varieties which are available with us were developed by selection. So new varieties have reduced the genetic variability and selection in these genotypes further reduced the genotypic variability. As the genotypic variability for the desirable traits has exhausted. Therefore there is need to identify new genes contributing towards desirable traits (fodder yield, disease and pest resistance etc.).

Diversity in plant genetic resources (germplasm) provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics as germplasm has broad genetic base. Genetic diversity is the outcome of several factors including geographical diversification. Therefore, selection of varieties for hybridization should be strictly based on genetic diversity rather than geographic diversity. The clustering of genotypes from different eco-geographic locations into one cluster could be attributed to the frequent exchange of breeding material from one place to another and its further selection in different geographic regions, which could result in genetic drift

In single cut, 92 genotypes of oat were grouped into nine different clusters. Clustering pattern revealed that cluster IX and VI were the largest ones with 18 and 17 genotypes each, followed by cluster V with 13 genotypes, cluster III with 10 genotypes, cluster VII with 9 genotypes, cluster II and IV each with 6 genotypes and cluster I with 5 genotypes. The cluster distance ranged from 5.012 to 8.304 within the clusters and 5.012 to 6.512 between the clusters. The inter cluster distance were higher than intra cluster distances, which indicated wide genetic diversity among the accessions of different groups than those of same cluster.

In 1st cut of multi-cut, 92 genotypes of oat were grouped into eleven different clusters. Clustering pattern revealed that cluster VIII and V were the largest ones with 18 and 14 genotypes respectively followed by cluster I and III each with 10 genotypes, cluster VI and XI with 7 genotypes each, cluster IV and X with 6 genotypes each, cluster II and IX each with 5 genotypes each and cluster VII with 4 genotypes. The cluster distance ranged from 2.602 to 6.826, within the clusters and 2.602 to 5.058 between the clusters. The inter cluster distance were higher than intra cluster distances, which indicated wide genetic diversity among the accessions of different groups than those of same cluster.

In 2nd cut of multi-cut, 92 genotypes of oat were grouped into nine different clusters. Clustering pattern revealed that cluster I and II were the largest ones with 16 genotypes each, followed by cluster IX with 14 genotypes, cluster VI with 13 genotypes, cluster VIII with 10 genotypes, cluster IV and V each with 8 and 7 genotypes, cluster III with 6 genotypes and cluster VII with 2 genotypes. The cluster distance ranged from 4.899 to 8.071, within the clusters and 4.899 to 6.078 between the clusters. The inter cluster distance were higher than intra cluster distances, which indicated wide genetic diversity among the accessions of different groups than those of same cluster. Kumar *et al.*(2016), Krishna *et al.* (2014), Yadav *et al.* (2011), Ahmed *et al.* (2011) and Mehta *et al.*(2008) also obtained results similar to the present findings.

5.5 Principal component analysis

Principal component analysis (PCA), basically a data reduction technique, initially floated by Pearson (1901) and later on developed by Hotelling (1933) offers solution to the complex problem of large and unmanageable data by transforming the original set of variables into a smaller set of linear combinations that account for most of the variability of the original set. It is useful tool for evaluation of germplasm. This technique is an ordination method often used to simultaneously describe the relationship between set of variables. It tends to reduce the dimension of multivariate data by removing inter-correlation among variables and allow a multi-dimensional relationship to be plotted on two or three principle axes. As a result, PCA allows visualization of difference among the individuals and variables.

In single cut, eight principal components had eigen values more than one and altogether explained 70.01% of the total accumulated variability (Table 4.25). The first principal component explained 12.78 % of the total variation. The second, third, fourth, fifth, sixth, seventh and eighth principal components explained 10.86, 9.81, 8.34, 8.08, 7.20, 6.89 and 6.04% of the total variance, respectively.

PF-1 was loaded on germination %, seedling length and seed vigour index-I. With similar logic, PF-2 showed a strong and positive factor with the traits like plant height, green fodder yield and dry matter yield. The PF-3 was loaded with leaf width. The PF-4 showed the

diversity among accessions based on number of leaves per plant and numbers of tillers per plant and days to maturity. PF-5 confirms the variation observed by number of spikelets per panicle and seed index. PF-6 was loaded with days to 50% flowering. PF-7 showed the strong and positive factor with seed yield. PF-8 loaded with leaf length. Thus, the most important descriptors were those associated with PF-2 and PF-7.

In 1st cut of multi-cut, The three principal components had eigen values more than one and altogether explained 67.95% of the total accumulated variability (Table 4.27). The first principal component explained 26.24% of the total variation. The second and third principal components explained 21.84 and 19.87% of the total variance, respectively. PF-1 was loaded on germination %, seedling length and seed vigour index-I. The PF-2 was loaded with seedling dry weight and seed vigour index-II and with similar logic, PF-3 showed a strong and positive factor with the traits like plant height, green fodder yield and dry matter yield. Among these principal factors, PF-3 regarded as fodder yield factor.

In 2nd cut of multi-cut, seven principal components had eigen values more than one and altogether explained 73.34% of the total accumulated variability (Table 4.29). The first principal component explained 15.31 % of the total variation. The second, third, fourth, fifth, sixth and seventh principal components explained 11.94, 11.79, 10.54, 10.40, 7.38 and 5.97 % of the total variance, respectively.

PF-1 was loaded on seedling length and seed vigour index-I. With similar logic, PF-2 showed a strong and positive factor with the traits like green fodder yield and dry matter yield. The PF-3 was loaded with internode length. The PF-4 showed the diversity among accessions based on green fodder yield and dry matter yield. PF-5 confirms the variation observed by number of leaves per plant and seedling dry weight. PF-6 was loaded with seed index and leaf length. PF-7 showed the strong and positive factor with leaf width. Among these principal factors, PF-2 and PF-4 regarded as fodder yield factors.

Vaisi *et al.* (2013) and Krishna *et al.* (2014) also conducted principal component analysis in oat. Singh *et al.* (2014) and Neeru *et al.* (2015) conducted principal component analysis in Indian mustard and transferred many correlated variables into a few independent principal components explaining much of the variability of the original set.

In the present study, principal factor analysis was carried out using principal component method, which does not require assumption of multivariate normal distribution of population in contrast to the other methods like maximum likelihood method (Jaiswal 2000). Initially the data were analyzed without any rotation but it failed to load all the variables meaning thereby that it could not provide much information regarding the idea of correlation between the variables and the principal factors.

The failure of principal factor analysis without rotation to draw sensible conclusions prompted to go for analysis with rotation. Varimax method of orthogonal rotation (Kaiser

1958) was utilized to rotate the factor axes. This is the most commonly used method and can be placed in a meaningful biological context.

The present investigation entitled “**Evaluation of Oat (*Avena sativa* L.) genotypes for yield and quality characters**” was conducted at Forage Research Area of the Department of Genetics & Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar (Haryana, India) during *rabi* 2015-16. The experimental material comprising of 92 oat genotypes was evaluated following the recommended agronomical package of practices in a Randomized Block Design with three replications in three row plot of three meter length for each genotype.

The observations were recorded on five randomly selected plants of each genotype in each replication for the 16 morphological characters viz., plant height (cm), number of days to 50% flowering, number of days to maturity, flag leaf length (cm), internode length (cm), number of tillers/plant, peduncle length (cm), axis length (cm), number of spikelets/panicle, seed yield (g), 100-seed weight (g), leaf length(cm), leaf width (cm), green fodder yield (kg), dry matter yield (kg) and number of leaves/plant and six seed quality parameters viz. germination (%), seedling length (cm), seedling dry weight (mg), seed vigour index I, seed vigour index II and electrical conductivity (mS/cm/seed) and quality characters such as forage crude protein (%) and seed crude Protein (%).

To evaluate these genotypes for yield and its component traits, the data recorded on 24 characters in single cut, 11 character in 1st cut of multi-cut and 20 characters in 2nd cut of multi-cut system were analyzed to assess the genetic variability, heritability, genetic advance, correlation, path coefficient, genetic divergence and principal component analysis. The salient findings of the present study and conclusions drawn from them are summarized below:

Analysis of Variance (ANOVA) indicated that mean sum of squares due to genotypes were significant for all the traits studied under the single cut and multi-cut system indicating that there was a considerable magnitude of variability among different genotypes of oat for all the traits.

In single cut the genotypes HFO-58, JO-1, JHO-99-1, DULO, UPO-212, KENT, HFO-864, HFO-879, HFO-878 and HFO-409 were identified as promising genotypes for green fodder yield whereas JO-1, JHO-851, JHO-99-1, DULO, HFO-876, KENT, HFO-504, HFO-877, HFO-879, HFO-611, HFO-715, HFO-908, HFO-914, HFO-910, HFO-913 and HFO-912 had high dry matter yield. So these genotypes can be used in oat breeding programme to enhance the fodder yield.

In 1st cut of multi-cut system, genotypes UPO-212, OL-125, SABZAR, JHO99-1, HFO-839, HFO-836, HFO-884, HFO-845, HFO-883, HFO-610, HFO-706, HFO-908, HFO-924 and HFO-912 were identified as promising genotypes for green fodder yield. Whereas UPO-212, ALGERIAN, OL-125, JHO-99-1, HFO-879, HFO-502, HFO-58, HFO-876, HFO-409, HFO-839, HFO-836, HFO-924 and HFO-912 were promising for dry fodder yield. Therefore, these genotypes can be used in oat breeding programme to enhance the fodder yield.

In 2st cut of multi-cut system, the genotypes HFO-114, ALGERIAN, PLP-1, JHO-2006-2, HFO-69, HFO-508, HFO-414, HFO-433, HFO-896, HFO-863, HFO-831, HFO-603, HFO-904, HFO-912 and HFO-902 were identified as promising genotypes for green fodder yield whereas HFO-114, HFO-267, PLP-1, JHO-822, OS-6, HFO-69, HFO-864, HFO-865, HFO-58, HFO-433, HFO-885, HFO-896, HFO-863, HFO-831, HFO-904, HFO-912 and HFO-902 were promising for dry matter yield. Therefore these genotypes can be utilized for oat breeding programme to enhance the fodder yield.

The PCV was slightly higher than the respective GCV for all the traits, indicating that the environmental factors influence their expression to some degree or other.

In single cut the genotypic and phenotypic coefficient of variations in terms of unit of their expression were observed highest for all characters except number of days to 50% flowering, days to maturity, number of tillers per plant and germination percentage, in 1st cut of multi-cut system, the genotypic and phenotypic coefficient of variations in terms of unit of their expression were observed highest for all characters except number of tillers per plant and forage crude protein (%) and in 2nd cut of multi-cut system, the genotypic and phenotypic coefficient of variations in terms of unit of their expression were observed highest for green fodder yield per meter row length, dry matter yield per meter row length, flag leaf length, internode length and peduncle length while low estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for number of days to 50% flowering, number of tillers per plant and forage crude protein.

In single cut the estimates of high heritability were noticed in almost all characters except number of leaves per plant and germination percentage for which moderate heritability was observed.

In 1st cut of multi-cut system, high heritability was noticed in the characters like number of tillers per plant, green fodder yield per meter row length, dry fodder yield per meter row length and forage crude protein while moderate heritability was observed for plant height and in 2nd cut of multi-cut system, the estimates of high heritability were observed for all characters except for number of leaves per plant and plant height where moderate heritability was recorded.

In single cut, positive and significant correlations of dry matter yield per meter row length were recorded for plant height , flag leaf length, internode length, axis length , seed yield per meter row length, leaf length, green fodder yield per meter row length and germination %.

In 1st cut of multi-cut, positive and significant correlations of dry matter yield per meter row length were recorded with plant height, green fodder yield and seed vigour index-II. In 2nd cut of multi-cut, positive and significant correlations of dry matter yield per meter row length were recorded with plant height, green fodder yield and germination %.

The strongly associated characters can be selected. It is also suggested that hybridization of genotypes possessing combination of above characters is most useful for obtaining desirable high dry matter yielding genotypes.

In single cut, path coefficient analysis revealed that characters viz. green fodder yield, number of tillers per plant, plant height and seed yield per meter row length had positive and direct effects on dry matter yield per meter row length, while the characters number of days to 50% flowering, peduncle length, axis length, number of spikelets, and number of leaves per plant showed direct negative effects. Hence, it would be rewarding to lay stress on these characters for the improvement of dry matter yield.

In 1st cut of multi-cut, path coefficient analysis exhibited high direct and positive effects of green fodder yield, numbers of tillers per plant and plant height while days to 50% flowering, peduncle length, axis length and number of leaves per plant had negative direct effects on dry matter yield per plant. In 2nd cut of multi-cut, path coefficient analysis revealed that high direct and positive effects of green fodder yield, tillers per plant and plant height while days to 50% flowering, peduncle length, axis length, and number of leaves per plant had direct negative effects on dry matter yield per plant. Therefore, these characters require great attention for improvement of dry matter yield.

In single cut, the Mahalanobis' D^2 statistics for genetic divergence divided 92 oat genotypes into nine clusters indicating presence of substantial genetic diversity in the evaluated germplasm. The average inter-cluster distance was found to be highest between cluster IV and IX followed by cluster I and VIII. The minimum inter cluster distance was noticed between cluster V and cluster VI. The minimum intra cluster distance was noticed in cluster I and highest intra-cluster distance was observed in cluster VII.

In 1st cut 92 oat genotypes were divided into eleven clusters indicating presence of substantial genetic diversity in the evaluated germplasm. The average inter-cluster distance was found to be highest between cluster IX and XI followed by cluster V and VII. The minimum inter cluster distance was noticed between cluster V and cluster VI. The minimum intra cluster distance was noticed in cluster VII and highest intra-cluster distance observed in cluster V. and in 2nd cut the 92 oat genotypes were divided into nine clusters indicating

presence of substantial genetic diversity in the evaluated germplasm. The average inter-cluster distance was found to be highest between cluster II and VII followed by cluster III and VI. The minimum inter cluster distance was noticed between cluster V and cluster VI. The minimum intra cluster distance was noticed in cluster IV and highest intra-cluster distance observed in cluster VII.

The nine, eleven and nine clusters formed in divergence analysis in single cut, 1st cut and 2nd cut of multi-cut, respectively contained genotypes of heterogenic origin. Therefore, crosses between the members of clusters separated by high inter cluster distance, are likely to throw desirable segregants.

In this context, cluster IX had very high inter-cluster distance from remaining eight clusters in single cut, cluster X and XI had very high inter-cluster distance from remaining eight clusters in 1st cut of multi-cut and cluster VII had very high inter-cluster distance from remaining eight clusters in 2nd cut of multi-cut.

In single cut, a total of eight principal components were extracted on the basis of eigen values more than one and altogether explained 70.01% of the total accumulated variability. The first principal component explained 12.78 % of the total variation. The second, third, fourth, fifth, sixth, seventh and eighth principal components explained 10.86, 9.81, 8.34, 8.08, 7.20, 6.89 and 6.04% of the total variance, respectively.

In 1st cut of multi-cut system, total of three principal components were extracted on the basis of eigen values more than one and altogether explained explained 67.95% of the total accumulated variability. The first principal component explained 26.24% of the total variation. The second and third principal components explained 21.84 and 19.87% of the total variance, respectively.

In 2nd cut of multi-cut system, total of seven principal components were extracted on the basis of eigen values more than one and altogether explained 73.34% of the total accumulated variability. The first principal component explained 15.31 % of the total variation. The second, third, fourth, fifth, sixth and seventh principal components explained 11.94, 11.79, 10.54, 10.40, 7.38 and 5.97 % of the total variance, respectively.

Varimax rotation enabled loading of all the traits on different principal factors in single cut principal factors, PF-2 and PF-7 were regarded as fodder yield factors and seed yield factors, in 1st cut of multi-cut system principal factors, PF-3 was regarded as fodder yield factor whereas in 2nd cut of multi-cut system principal factors, PF-2 and PF-4 were regarded as fodder yield factors.

Total of eight principal components were extracted on the basis of eigen values (>1) and these components explained total of 75% variability. The eigen values of the components were 3.98, 3.24, 2.41, 1.67, 1.50, 1.34, 1.31 and 1.02. All these components shared 18.12%, 14.75%, 10.97%, 7.59%, 6.85%, 6.08%, 5.91% and 4.64% of total variability.

REFERENCES

- Ahmed, S., Roy, A. K. and Majumdar, A. B.(2013). Correlation and path coefficient analysis for fodder and grain yield related traits in oats (*Avena sativa*L.). *Annals of Biology*,. **29** (1): 75-78.
- Ahmed, S., Roy, A. K. and Majumdar, A. B. (2011). Genetic diversity and variability analysis in oat (*Avena sativa* L.). *Range Management & Agroforestry*. **32** (2): 96-99.
- Ahmad, M., Zaffar, G., Mir, S.D., Dar, Z.A., Dar, S.H., Iqbal, S., Bukhari, S.A., Khan, G.H. and Gazal A. (2013) Estimation of correlation coefficient on oats (*Avena sativa* L.) for forage yield, grain yield and their contributing traits. *International Journal of Plant and Breeding Research*.**7**(3):188-191.
- Anderson, T. W., Rubin, H. (1956). Statistical Inference in Factor Analysis. *Proceedings of the Third Berkeley Symposium on Mathematical Statistics and Probability*. **5**:111-150.
- Anonymous. (2014). Forage crops and grasses, Handbook of Agriculture. ICAR.
- AOSA. (1983). Seed vigour testing hand book. *Association of Official Seed Analyst. Publications, AOSA Handbook*. **32**
- Arora, R.N.; Chhabra A.K. and Faruqui, S.A.(2012). Oats (*Avena Sativa*L.).In:*Breeding of field crops*,ed Bharadwaj, D.N., AGRIBIOS(India),pp 785-816.
- Arora, R.N. (2013). Characterization and evaluation of one and two-harvest of oats. *Forage research*. **39**(2): 59-63.
- Bahadur, R. and Choubey, R. N. (2008). Morphological variability and genetic diversity in relation to fodder yield and quality traits in oat (*Avena sativa* L.). *Environment and Ecology*. **26**(3):1391-1395
- Bahadur, R. and Choubey, R.N. (2009). Genetic divergence in forage oat (*Avena sativa* L.). *Forage Research*. **34**(4):225-229.
- Bertan, I., A. J. Kurek, F-I-F-de Carvalho, I. C. Assmann, G. O. da Silva and M. L. Cossa (2004). Estimation of genotypic gain through selection in segregating generations of oat. *Scientia Agraria*., **5** (1/2): 29-33.
- Bibi, A., Shahzad, A.N., Sadaqat, H. A., Tahir, M. H. and Fatima, B. (2012). Genetic characterization and inheritance studies of oats (*Avena sativa* L.) for green fodder yield. *International journal of Biology, Pharmacy and Allied Sciences*. **1**(4): 450-460.
- Bind, H., Bharti, B., Pandey, M.K., Kumar, S.,Vishwanath. and Kerkhi, S.A. (2016). Genetic variability, heritability and genetic advance studies for different characters on green fodder yield in oat (*Avena sativa* L.). *Agricultural Science Digest*. **36** (2): 88-91.
- Burgess, P. L., Grant, E. A. and Nickolson, J. W. G. (1972). Feeding value of “forage” oats. *Canadian Journal of Animal Science*. **52**:448-450.

- Burton G.W. and Devane E.M. (1953) Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, 45, 478-481.
- Cattivelli, L., Iannucci, A. and Codianni, P. (2011). Evaluation of genotype diversity in oat germplasm and definition of ideotypes adapted to the mediterranean environment. *International Journal of Agronomy*. 870925: 1-8.
- Chakraborty, J., Arora, R. N., Joshi, U. N. and Chhabra, A. K. (2014). Evaluation of *Avena* species for yield, quality attributes and disease reaction. *Forage Research*. **39** (4):179-184.
- Choubey, R. N., Sai prasad, S. V., Zadoo, S. N. and Roy, A. K. (2001). Assessment of genetic Diversity and inter-relationships among yield contributing traits in forage Oat germplasm. *Forage Research*. **27** (3): 149-154.
- Dillon, W.R. and Goldstein, M. (1984). *Multivariate Analysis: Methods and Applications*. John Wiley & Sons, New York. 283-285.
- Dubey, R. K., R. S. Shukla and M. K. Shrivastava, (2000). Multivariate analysis in oat. *Advances in Plant Sci.*, **13** (2): 467-471.
- Dubey, N., Avinash, H. A., Jaiwar, S. and Chichkhede, L. (2014). Estimates of genetic variability, heritability and genetic advance of oat (*Avena sativa* L.) genotypes for green fodder yield. *Electronic Journal of Plant Breeding*. **5**(4): 881-883.
- Falconer, D.S. (1981). *An Introduction to Quantitative Genetics*, 2nd edition. Longman. New York.
- FAO, 2015. *FAOSTAT*. Food and Agriculture Organization of the United Nations.
- <http://faostat.fao.org/default.aspx>.
- Fisher, R. A. (1925) *Statistical methods for research workers* Oliver & Boyel Edinberg, Tweeddale Court London, Paternoster Row, E C
- Gibson, L. and Benson, G. (2002). Origin, History, and Uses of Oat (*Avena sativa*) and Wheat (*Triticum aestivum*). Deptt. Of Agronomy, Iowa State University.
- Glore, S. R., Van Treeck, D., Knehans, A. W. and Guild, M. (1994). Soluble fiber and serum lipids: a literature review. *Journal of the American Dietetic Association*. **94**: 425–436.
- Greene, N. V., Kenworthy, K. E., Quesenberry, K.H., Unruh, J. B. and J. B. Sartain. (2008). Diversity and relatedness of common carpet grass germplasm. *Crop Science*. **48**(6): 2298–2304.
- Hotelling, H. (1933). Analysis of complex statistical variables into principal components. *Journal. Educaion. Psychology*. **24**: 417.
- Hotelling, H. (1936) Relations between two sets of varieties. *Biometrika*, 28(3-4):321-377
- ISTA. (2009). International rules for seed testing. *Seed Science and Technology*, **27**:1-334
- Jaiswal, U.C. (2000). Principal components analysis and its interpretation. II. Factor analysis and its application in social sciences. In course compendium of “Use of statistical methods in agricultural and allied fields” Jan. 19- Feb. 15, 2000, *Academy of Agricultural Research and Management*, CCS Haryana Agricultural University, Hisar. 166-181.

- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal*. **47**: 314-318.
- Kaiser, H.F. (1958). The varimax criterion for analytic rotation in factor analysis. *Psychometrika*, **23**:187.
- Kapoor, R. and Bajaj, R. K. (2013). Combining ability and heterosis studies in (*Avena sativa* L.) for green fodder yield and component traits. *Society of Plant Research*. **26** (1):272-277.
- Khan, A., Anjum, M.H., Rehman, M.K.U., Zaman, Q. and Ullah, R. (2014). Comparative Study on Quantitative and Qualitative Characters of Different Oat (*Avena sativa* L.) Genotypes under Agro-Climatic Conditions of Sargodha, Pakistan. *American Journal of Plant Sciences*. **5**:3097- 3103.
- Krishna, A., Ahmed, S., Pandey, H.C and Bahukhandi, D. (2013). Estimates of genetic variability, heritability and genetic advance of oat (*Avena sativa* L.) genotypes for grain and fodder yield. *Agricultural Science Research Journals*. **3**(2):56-61.
- Krishna, A., Ahmed, S., Pandey, H.C and Kumar, V. (2014). Correlation, path and diversity analysis of oat (*Avena sativa* L.) genotypes for grain and fodder yield. *Journal of Plant Science & Research*. **1** : **1-9**.
- Kumarmall, Ashutosh and Vishwakarma, D.N. (2006). Genetic divergence in oat (*Avena sativa* L.) *Farm Science Journal*. **15**(1):38-40.
- Kumar, Y., Jhorar, B.S., Sangwan, O. and Singh, P. (2004) Character association between grain yield and its components in oat (*Avena sativa* L.). *National Journal of Plant Improvement*. **6**(1): 4-6.
- Kumar, Y., Jhorar, B.S. and Sangwan, O. (2006). Principal component and factor analysis in oat (*Avena sativa* L.) germplasm. *Haryana Agricultural University Journal of Research*. **36**(1):17-22.
- Kumar, Y., Jhorar, B. S., Singh, R. and Singh, P. (2007). Genetic divergence in oat (*Avena sativa* L.) germplasm using hierarchical cluster analysis. *Environment & Ecology*. **25** (3): 606-609
- Kumar, S., Agrawal, R.K., Dixit A.K., Rai, A.K., Singh, J.B. and Rai, S.K. (2012). Forage Production Technology for Arable Lands. Technology Bulletin No. 01/2012. Available in: <http://www.igfri.res.in/pdf/bulletin_12/Forage%20Production%20Technology%20for%20arable%20Lands.pdf>.
- Kumar, P., Phogat, D.S. and Bhukkar, A. (2016). Genetic diversity analysis in oat. *Forage research*. **42**(2):96-100.
- Kurek A. J., FIF-de Carvalho, AC-de Oliveira, A. Cargnin, V. S. Marchioro and C. Lorencetti (2002). Coefficient of correlation among agronomic traits and of quality of the grain and its usefulness in the selection of plants in oats. *Ciencia-Rural*., **32** (3): 371-376.

- Lorencetti, C., F. I. F. de Carvalho, A. C. de Oliveira, I. P. Valerio, I. Hartwig, G. Benin and D. A. M. Schmidt (2006). Applicability of phenotypic and canonic correlations and path coefficients in the selection of oat genotypes. *Scientia Agricola*, **63** (1): 11-19. 21.
- Mahalanobis, P.C. (1936) On the generalized distance in statistics. *Proceedings of the Natural Institute of Science, (Indian)*, **2**: 49-55.
- Mall, A.K., Vishwakarma, D.N. and Sayeed, A. (2005). Studies on genetic variability, heritability and genetic advances in Oat (*Avena sativa* L.). *Journal of Living World*. **12**(2):18-21.
- Mall, A. K. and Vishwakarma, D.N. (2006). Genetic divergence in oat (*Avena sativa* L.). *Farm Science Journal*. **15**(1):38-40.
- Mehta, A. K., S. K. Bilaiya. and G. S. Rathi. (2008). Genetic divergence in fodder oat (*Avena sativa* L.). *Forage Research*. **34**(3): 146-148.
- Mittelmann, A., FIF-de Carvalho, Neto-J. F. Barbosa, A L-do Amaral, F. Pandini and A. L. Amaral (2001). Heritability for heading date and plant height in oat. *Ciencia Rural*., **31** (6): 999-1002.
- Nadeem, M., Ansar, M., Adeel, A., Ashiq, H. and Khan, S. (2010). Performance Of Winter Cereal-Legumes Fodder Mixtures And Their Pure Stand At Different Growth Stages Under Rainfed Conditions of Pothowar, *Journal Of Agriculture Reseach*. **48**(2):181- 192.
- National Dairy Development Board, Statistics. (2016). Livestock population in India by Species. <http://www.nddb.org/information/stats/pop>
- Neeru, T. N.K., Avtar, R. and Singh, A. (2015) Evaluation and classification of Indian mustard (*Brassica juncea* L.) genotypes using principal component analysis. *Journal of Oilseed Brassica*. **6**(1):167-174.
- Panse, V.G. and Sukhatme, P.V. (1967). *Statistical method for Agricultural works*. ICAR, Publications. New Delhi.
- Pearson, K. (1901). On lines and planes of closest fit to systems of points in space. *Philosophical Magazine*. **2**: 559.
- Peterson, D. M., Wesenberg, D. M., Burrup, D. E. and Erickson C. A. (2005). Relationships among agronomic traits and grain composition in oat genotypes grown in different environments. *Crop Science*. **45**(4):1249–1255.
- Pundir, S.R., Yogya, D. and Grewal, R.P.S. (2003). Genetic variability for forage characters in Oat (*Avena sativa* L.). *Forage Research*. **28**(4):288-229.
- Pundir, S. R. and. Singh, V. P. (2007). Genetic variability and interrelationship for various seedling and forage characters in oats (*Avena sativa* L.). *Forage Research* **32**(4): 254-256.
- Pundir, S. R., Singh, V. P. and Phogat, D. S. (2008). Genetic variability and interrelationship for various grain and seedling characters in oats. *Forage Research*. **33**(4):236-240.
- Rao, C.R. (1952). *Advanced biometrical methods in biometric research*. John Wiley and Sons Inc., New York, 357–363.

- Rao, C. R. (1960). Multivariate analysis: An indispensable statistical aid in applied research. **22**:317-338.
- Rines, H.W., Molnar, S.J., Tinker, N.A. and Phillips RL. (2006). Oats. In: Cereals and millets: genome mapping and molecular breeding in plants (C Koleed). Springer Berlin Heidelberg, New York, 211-242.
- Sangwan, O., Avtar, R., Arora, R. N. and Singh, A. (2012). Variability and character association studies in fodder oat (*Avena sativa* L.). *Forage Research*. **38** (1): 56-58.
- Shankar, S., Jha, P.B., Ghosh, J. and Nirala, R.B.P. (2002). Variation and association studies in Oat (*Avena sativa* L.). *Forage Research*. **28**(2):110-112.
- Shehzad, M; Ayub, M; Nadeem, M.A; Pervez, M; Nadeem, M. and Sarwar, N. (2011) Comparative study on forage yield and quality of different oat (*Avena sativa* L.) varieties under agroecological conditions of Faisalabad, Pakistan, *African Journal of Agricultural Research*, **6** (14): 3388-3391.
- Shekhawat, S. S., Garg, D. K. and Verma, J. S. (2006). Character association and variability study in oats for green fodder yield and related traits. *Forage Research*. **32**(3):163-168.
- Shekhawat, S.S. and Jaipal. (2016). Genetic variability and divergence studies in oats (*Avena sativa* L.) for green fodder and grain yield. *Forage Research*. **42**(1): 51-55.
- Siloriya R.N, Rath G.S. and Meena V.D.(2014) Relative performance of oat (*Avena sativa* L.) varieties for their growth and seed yield. *African Journal of Agricultural Research*, **9**(3):425-431.
- Singh, R.K. and Choudhary, B.D. 1977. Biometrical methods in quantitative genetic analysis. *Kalyani Publishers*. New Delhi. 178-185.
- Singh S.B. and Singh, A.K. (2009) Genetic variability, character association and path analysis for green fodder yield and its component characters in oat (*Avena sativa*). *Progressive Research*. **4**:159–162.
- Singh, S.B. and Singh, A.K. (2011).Genetic Variability and Divergence Analysis in Oat (*Avena sativa*) under Rainfed Environment of Intermediate Himalayan Hills. *Indian Journal of Plant Genetic Resources*. **24**(1): 56–61.
- Sofi, P.A., Zargar, M.Y., Razvi, S.M., Sheikh, F.A., Saba, I. and Shafi, T. (2014). Genetic variability and factor analysis in common bean (*Phaseolus vulgaris* L.) germplasm collection for yield related traits. *Electronic Journal Plant Breeding*. **5**(2):254-259.
- Surje, D.T. and De, D.K. (2014). Correlation Coefficient Study in Oat (*Avena sativa* L.) Genotypes for Fodder and Grain Yield Characters. *Journal of Agricultural Science and Technology*. **1**(1): 89-93.

- Suttie, J.M. and Reynolds, S.G. (2004). Fodder oats: A World Review. Plant Production and Protection Series No. 33. FAO (Rome).
- Tonapi, V.A., Patil, J.V., Dayakan, B., Elengovan, M., Venkatesh, B. and Rao, K.V.R. (2011). Sorghum vision 2030. Directorate of Sorghum Research, Rajendranagar Hyderabad (AP), India 38.
- USDA, Foreign Agriculture Service. (September, 2016). World agriculture production, Circular Series.
- Vaisi, H., Golparvar, A.R., Resaie, A. and Bahraminejad, S. (2013). Factor analysis of some quantitative attributes in oat (*Avena sativa* L.) genotypes. *Scientia Agriculturae*. **3**(3):62-65.
- Vishwakarma, D.N., Ram, C.N., Chauhan, S.S., Maurya, M.L. and Singh, S.P. (2007). Genetic variability for some forage yield characters in oat (*Avena sativa* L.) (In) Abst.National Sympo.on A New Vista to Forage Crop Research. AICRP on Forage Crops, BCKV, Kalyani (WB).
- Whitehead, A., Beck, E.J., Tosh, S. and Wolever, T.M. (2014). Cholesterol-lowering effects of oat β -glucan: a meta-analysis of randomized controlled trials. *The American Journal of Clinical Nutrition*. **100** (6): 1413-1421.
- Yadav, A. K., V. K. Yadav, D. N. Viswakarma, C. N. Ram, Y. Vivek and S. K. Soni (2011). Genetic divergence in oats genotypes. *Plant Archives*., **11** (2): 1013-1016.
- Yanming, M., Zhiyong, L., Tuting, B., Wang, W. and Hao, W. (2006). Study on diversity of oats varieties in Xinjiang. *Xinjiang Agricultural Science*. **43**(6):510-513.
- Ziya, D., R. Kara, T. Dokuyucu and A. Akkya (2001). Correlation and Path Analysis of Grain Yield and Yield Components of some Turkish Oat Genotypes. *Agron. J.*, **43**: 214-218

ABSTRACT

Title of Thesis : **Evaluation of Oat (*Avena sativa* L.) genotypes for yield and quality characters**

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The present study was conducted with 92 genotypes of oat grown in randomized block design in three replications at the Research Farm of forage Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar during rabi 2015-16 to evaluate, categorize and classify them. The analyses of variance revealed highly significant differences among the genotypes for all the characters at genotypic level for single cut and multi-cut. High estimates of GCV and PCV were recorded for green fodder yield, followed by dry matter yield. Highest heritability was recorded for 100 seed weight followed by flag leaf length. The estimates of heritability were high for most of the characters except plant height and number of leaves per plant. Positive and significant correlations of dry matter yield were recorded with green fodder yield, plant height and seed yield. Path coefficient analyses revealed that characters green fodder yield, plant height and number of tillers/plant had positive and direct effects on dry matter yield in single cut and multi-cut. Genetic divergence classified genotypes into nine major clusters. The eight principal components had eigen values more than one and altogether explained 70.01% of the total accumulated variability.

In 1st cut of multi-cut high heritability was observed for green fodder yield and in 2nd cut 100 seed weight and number of days to 50% flowering. Positive and significant correlations of dry matter yield were recorded for green fodder yield in both cuts of multi-cut oat. D² analyses categorized oat genotypes into eleven and nine clusters in 1st & 2nd cut, respectively. The three and seven principal components had eigen values more than one in 1st & 2nd cut, respectively and accounted for 67.95% in 1st & 73.34% in 2nd cut of the total accumulated variability.

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- I played two north-zone tournament and secured 1st position in inter-college during 2011, 2012, 2013, 2016 and 2017 and 2nd position in inter-college Handball game 2014.
- I was selected as Best Handball player of 2012, 2013 & 2016 and also best basketball player 2012, 2013, 2014 and 2016 in inter-college games.
- I was adjudged Best NCC Cadet of my college in Annual College Function 2013 and also got appreciation award in NSS.

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