

**GENETIC DIVERSITY AND PATH COEFFICIENT ANALYSIS
IN OAT (*Avena sativa* L.)**

by

Miss. Wagh Vandana Ramdas

Reg. No. 016/039

A Thesis submitted to the
**MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI - 413 722, DIST. AHMEDNAGAR,
MAHARASHTRA, INDIA**

in partial fulfilment of the requirements for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

**AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)**



DEPARTMENT OF AGRICULTURAL BOTANY

**POST GRADUATE INSTITUTE,
MAHATMA PHULE KRISHI VIDYAPEETH,
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2018

CANDIDATE'S DECLARATION

I hereby declare that this thesis or part
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by me or other person to any
other University or Institute
for a Degree or
Diploma

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Dated : / /2018

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LIST OF ABBREVIATIONS

%	:	Percent
h^2 (b.s.)	:	Broadsense heritability
Cov	:	Covariance
°C	:	Degree celcius
C.D.	:	Critical difference
C.V.	:	Coefficient of variation
cm	:	Centimetre
D.F.	:	Degree of freedom
DMY	:	Dry matter yield
EMP	:	Environment mean sum of products
<i>et al.</i>	:	et alli (and others)
Fig.	:	Figure
G.A.	:	Genetic advance
GAM	:	Genetic advance as per cent of mean
GCV	:	Genotypic coefficient of variation
GFY	:	Green forage yield
GM	:	General mean
GMP	:	Genotypic mean sum of squares
Gm	:	Gram(s)
ha.	:	hectare(s)
i.e.	:	that is
L/S ratio	:	Leaf stem ratio
MSS	:	Mean sum of squares
N. S.	:	Non significant
PCV	:	Phenotypic coefficient of variation
RBD	:	Randomized block design
S.E.	:	Standard Error
S.S	:	Sum of squares
spp.	:	Species
<i>viz.,</i>	:	Videlicet (Namely)

ABSTRACT

“GENETIC DIVERSITY AND PATH COEFFICIENT ANALYSIS IN OAT (*Avena sativa* L.)”

by

MISS. VANDANA RAMDAS WAGH

A candidate for the degree

of

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Research Guide	: Prof. A. H. Sonone
Department	: Agricultural Botany
Major discipline	: Genetics and Plant Breeding

The present investigation entitled “Genetic diversity and path coefficient analysis in oat (*Avena sativa* L.) was conducted with twenty seven forage oat genotypes in a randomized block design with two replications at research farm of AICRP on Forage Crops and Utilization, MPKV, Rahuri during *rabi* 2016-17.

Observations were recorded for plant height at 50 per cent flowering, number of tillers per meter row length, number of leaves per tiller, leaf length, leaf width, leaf/stem ratio, stem thickness, green forage yield, dry matter content, crude protein content. Data on morphological characters like plant growth habit, hairiness of sheath of lowest leaf, hairiness of margins of leaf below flag leaf, internode exposed/covered, frequency of plants with recurved flag leaves, orientation of plants with recovered flag leaves, orientation of panicle branches, attitude of panicle branches and attitude of spikelets was also recorded.

The differences among genotypes studied were statistically significant for all the traits except dry matter content. Green forage yield and leaf/stem ratio exhibited highest range while crude protein content and dry

matter content exhibited low range of variation. High values of GCV and PCV were observed for leaf/stem ratio and green forage yield whereas low values were observed for dry matter content and number of leaves per tiller. Seven characters *viz.*, plant height, number of tillers per meter row length, leaf length, leaf width, leaf/stem ratio, stem thickness and green forage yield showed high estimates of heritability (b.s.) accompanied by high genetic advance as percentage of mean indicating these characters were predominantly governed by additive gene action and selection for improvement of these characters will be effective.

Green forage yield was significantly and positively correlated with number of tillers per meter row length, crude protein content, stem thickness, leaf width, plant height and number of leaves per tiller. Leaf width and crude protein content exhibited highest positive direct effect and significant positive correlation with green forage yield.

The D^2 statistics showed that there was adequate diversity among the genotypes with D^2 values ranging from 42.77 to 277.55. On the basis of D^2 values twenty seven genotypes were grouped into six clusters. On the basis of inter cluster distance, cluster means and *per se* performance, a future hybridization programme aiming improvement in green forage yield was suggested.

1. INTRODUCTION

Oat (*Avena sativa* L.) is an important winter cereal in the world. The crop is widely cultivated for use as food, feed and fodder. The bulk of the oats produced in the world are used extensively as feed for livestock (cattle, sheep, poultry and horses) and 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 most environment friendly crop in the US, since it is non-host for major cereal diseases and pests.

The fibre of oats grain has unique physiological properties. Fibre in oats reduces serum cholesterol and helps to promote a more normal blood glucose level in diabetics and is considered to be as healthy food. Feed of oats grain has the highest oil content (10.5 %). Similar to that of barley and maize, oat protein has a relatively well balanced amino acid composition. Oat straw has a higher metabolizable energy (ME) which confirms the traditional view of its superior feeding value.

Crops like berseem, clover and alfalfa remain dormant in hilly areas during winter months whereas, oat can be grown easily during this period. Its popularity as a fodder crop is increasing because of excellent growth habit, quick re-growth and high nutritive value for both milch as well as draft animals. Its cultivation is now extending to the eastern region particularly in those tracts, which are suited to wheat cultivation. It is quick growing, palatable, succulent and nutritious crop. The crop has been well adopted by the farmers because of its multi-cut nature and high yield of nutritious palatable fodder (Bharadwaj, 2012).

The genus *Avena* is large and diverse and contains both wild and cultivated species of polyploidy series with basic chromosome number of $x=7$. *Avena* genus comprises of diploid ($2n=2x=14$) (A and C genomes), tetraploid ($2n=4x=28$) (AB and AC genomes) and hexaploid ($2n=6x=42$) (ACD) species. Tetraploid species resulted from unrelated hybridization events involving an (A) and (B); diploid species

followed by polyploidisation. While as hexaploid species appears to have arisen by two rounds of hybridization followed by chromosome duplication. Out of 27 *Avena* species, the common oat (*Avena sativa* L.) $2n = 6x = 42$; the red oat (*A. byzantina* C. Koch) $2n = 2x = 42$; the Ethiopian oat (*A. abyssinica* Hochst.) $2n = 4x = 28$ and the grey oat (*A. strigosa* Schreb.) $2n = 2x = 14$ species are cultivated. Oat ranks sixth in world cereal production following wheat, maize, rice, barley and sorghum. It is cultivated all over the world and major producing countries are Russia, Canada, Poland and USA. The average annual production of oat in the world is around 23 million tonnes per year. Oat requires a long and cool season for its growth; therefore it is successfully grown in the plains and hilly areas of the country. The total area covered under oat in the country is about 5,00,000 ha. The crop occupies maximum area in Uttar Pradesh (34 %) followed by Punjab (20 %), Bihar (16 %), Haryana (9 %) and Madhya Pradesh (6 %). Forage oat is one of the components of several such high yielding remunerative crop sequences which have resulted in increase in forage productivity per unit area and time. Oats 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. The oat crop is a heavy yielder and the average yield varies from 45-55 tons of green fodder per hectare (Gul Zaffar, 2016).

The cultivated oat is an annual grass. The oat plant has two root systems, the seminal and adventitious. The seminal roots originate during the development of the embryo and they consist of the primary root and two or three lateral roots which arise in the first node. Adventitious roots arise in the nodes of the main stem and of the tillers just beneath the surface of the ground. The adventitious roots constitute the major root system of the oat plant.

Its stem or culm is composed of a series of nodes and internodes. The nodes are solid the elongated internodes of the mature stem are hollow in the center but during early vegetative stage of development the internodes are solid or show only a slight indication of the breakdown of pith.

The position of the leaf on the oat plant and the kinds of plant part produced are similar to those in other grasses. The leaves are solitary, alternate, two ranked and sessile. A completely developed oat leaf consists of terminal portion, the blade, a basal portion, the sheath, and a membranous appendage, the ligule. The blade is elongate, flat, narrow and linear. The margin of blade is entire and its tip is acute. The leaf sheath is an open cylinder. In the young plant the sheaths of the older leaves encloses the stem and younger leaves. At maturity, the leaf sheath encloses all portion of the elongated internode above it. The ligule is a thin membranous appendage which is continuous with the inner margin at the junction of the blade and sheath. The ligule extends upwards and clasps the stem.

The lateral branches of the oat plant arise in the axis of the foliage leaves. The first leaf on a tiller, the prophyllum, differs from a foliage leaf in having two keels and a large vascular bundle in each keel but it is without a blade. The plane of the leaves of a tiller is right angle to that of the parent axis.

The inflorescence is either an equilateral (spreading) or a unilateral (one-sided) panicle is a many-branched, determinate inflorescence. Inflorescence of the oat plant is a panicle composed of a central loose, open rachis with five to seven nodes, from which branches are arise bearing spikelets. Each lateral branch terminates in a single apical spikelet. Other spikelet is born on second or third-order of branches. Each panicle may have 20 to 50 spikelets. The flowers are perfect zygomorphic, bracteates and hypogeous. The flower consists of lemma and a palea, two lodicules, three stamens and one pistil (Bharadwaj, 2012).

Association of one or more characters influenced by a large number of genes is elaborated statistically by correlation coefficients. Genotypic correlation coefficients provide a major of degree and directions of genotypic association between characters.

The method of partitioning the correlations into direct and indirect effects by path coefficient analysis suggested by Wright (1921) provides useful information on the relative merit of the traits in the indirect selection criterion for yield.

The genetic diversity is produced due to inherent genetic differences in germplasm lines/varieties/landraces and is of major interest to the plant breeders. The precise information about genetic divergence is crucial for identification of diverse parent for hybridization.

Therefore, the present investigation entitled “Genetic diversity and path coefficient analysis in oat (*Avena sativa* L.) was undertaken with twenty four oat genotypes along with three checks (RO-11-1, Kent and RO-19) with following objectives.

1. To study genetic diversity in oat.
2. To study direct and indirect effect of component traits on green forage yield (GFY) in oat.

2. REVIEW OF LITERATURE

A comprehensive review of literature is an essential part of any scientific investigation. Review of literature is always necessary to compare the present findings with the previous studies undertaken by the research workers.

The literature pertaining to the present investigation entitled “Genetic diversity and path coefficient analysis in Oat (*Avena sativa* L.) has been reviewed under following different aspects.

2.1 Variability

2.2 Correlation

2.3 Path analysis

2.4 Diversity

2.1 Variability

Fisher (1930) first presented the methods to separate out the genotypic effects based on phenotype and environmental factors. He expressed the genotypic variability in terms of genotypic coefficient of variation.

Burton (1952) has given the use of heritability estimates with genotypic coefficients of variations to give precise estimates of genetic advance.

Singh (1999) studied variability, heritability and genetic advance in oat. The similarities between PCV and GCV estimates combined with high heritability values for plant height, number of leaves/plant, number of tillers/plant, green forage yield (GFY), dry forage yield (DFY) and leaf stem ratio indicated that selection for these characters should be effective. High heritability and genetic advance as a percentage of mean for number of tillers/plant and GFY indicated a predominance of additive gene effects for these traits.

Chaubey *et al.*, (2001) studied variability association and path analysis in forage oat. High heritability was observed for plant height (66.6 %) followed by days to 50 % flowering (64.2 %) in comparison to green fodder yield (47.3 %). The genotypes examined had a range of 74 to 131 days for flowering, 68 to 173 cm for

plant height, 3 to 24 for tiller number, 3 to 8 cm for internode length, 44 to 620 g for green fodder yield and 8 to 93 g for dry fodder yield per plant.

Shankar *et al.*, (2002) studied variation and association in oat. They reported that, high estimates of genotypic and phenotypic coefficient of variation (GCV and PCV, respectively) were observed in GY, L:S, GW, G, GFY and DMY. GFY, G, GW and GY showed high heritability coupled with high PCV. High GCV and heritability estimates associated with greater genetic advance were observed for GFY, DMY, G, GW and GY.

Prasad *et al.*, (2003) studied nature of genetic variability and diversity in large exotic collection of forage oat. All the characters examined exhibited moderate to high variability. Plant height and number of days to flowering exhibited high heritability.

Pundir *et al.*, (2003) studied genetic variability for forage characters in oat. Results showed that high heritability estimates with high genetic advance were observed for green and dry fodder yield, number of leaves per plant, leaf length, leaf breadth, leaf weight and dry leaf weight. Green fodder yield per plant and leaf breadth had the maximum and minimum genotypic and phenotypic coefficients of variation, respectively. All characters studied showed higher values of expected genetic advance, along with higher estimates of heritability.

Kumar *et al.*, (2004) studied genetic variability and correlation in fodder oat. Analysis of variance showed significant difference among all the germplasm lines for all the characters. High estimates of coefficient of variation were observed for number of tillers, flag leaf length, green fodder yield, number of leaves, dry matter yield and longest internode length.

Gautam *et al.*, (2006) studied genetic variability and association of morpho-physiological characters in oat. In general, the estimates of phenotypic coefficient of variation (PCV) were higher than the genotypic coefficient of variation (GCV) for all characters. Maximum variation was observed for dry matter yield (10.5-45.10 g) and green fodder yield (40.33-180.20 g). High heritability coupled with high genetic advance was recorded for green fodder yield, leaf : stem ratio, grain

yield, tillers per plant and flag leaf length, indicating the importance of additive effects for these characters.

Bahadur and Chaubey (2008) found considerable variability existed for all the characters. The magnitude of genotypic coefficient of variation was quite close to the estimates of phenotypic coefficient of variation in almost all the traits. High heritability was observed for almost all the characters including quality traits, whereas genetic advance was reasonably high for green and dry fodder yield/plant.

Bahadur *et al.*, (2008) studied character association and path coefficient analysis in oat. Genotypic and phenotypic coefficient of variation was high for almost all the fodder yield traits. Heritability was high for all the characters, whereas genetic advance was high for most of the characters.

Singh and Singh (2010) studied genetic variability and Divergence analysis in oat under rainfed Environment of intermediate Himalayan hills. They reported that in general the estimates of PCV were better than estimates of GCV for all the traits. This suggested that the role of environment in the expression of the characters. High estimates of GCV were obtained for dry matter yield, green fodder yield, plant height and tillers per plant. While moderate estimates obtained for dry matter percentage. Low estimates of GCV were observed for days to flowering, crop duration and L/S ratio. Dry matter yield, green fodder productivity, green fodder yield, tillers per plant and plant height exhibited high GCV, heritability and high genetic advance indicating predominance of additive gene effects in controlling these characters. As such selection could be effective as such as these characters could effectively used in selection.

Kapoor *et al.*, (2011) studied correlation and path coefficient analysis in oat. High heritability along with high genetic advance (GA) was recorded for internode length (cm), number of tillers per plant, flag leaf length (cm), plant height (cm), axis length (cm), axis branch number, number of seeds per panicle and seed yield g/plant. High estimates of genotypic coefficient of variation and phenotypic coefficient of variation (GCV and PCV) were observed for internode length, number of tillers per plant, axis branch number, number of seeds per plant and seed yield per

plant, suggesting that selection based on these characters would facilitate successful isolation of desirable types.

Sofi *et al.*, (2012) studied selection parameters for improvement of green fodder yield and seed yield in oats. Perusal of variability parameters revealed that the range of variation was high in traits like seed yield per hectare, seed breadth, tillers per m², seed length and green fodder yield as indicated by higher values of C.V. per cent. 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. Heritability (b.s.) estimates were generally high for all traits ranging from 79.236 per cent for seed length to 97.228 per cent for tillers per m². Genetic gain was high for all traits especially seed yield per hectare, tillers per m², seed breadth, seed length and green fodder yield per hectare.

Montilla–Bascon *et al.*, (2013) studied genetic diversity and population structure among oat cultivars and landraces. Cultivars showed less diversity than the landraces indicating a reduction of genetic diversity during breeding, whereas white oat landraces showed higher diversity than red ones.

Nirmala Kumari *et al.*, (2013) studied trait association and path analysis for grain yield in oat in the western zone of Tamil Nadu. The estimate of genotypic coefficient variation (GCV) and phenotypic coefficient of variation (PCV) were high for number of basal tillers per plant, number of productive tillers per plant, and number of grains per panicle. Broad sense heritability estimates for various traits ranged from 71 to 96 per cent. The highest heritability and genetic advance were recorded for the traits *viz.*, number of productive tillers per plant (86.00 and 85.06 %), number of grains per panicle (92.00 and 64.87 %) and panicle length (96.00 and 37.23 %).

Jaipal and Shekhawat (2016) studied genetic variability and divergence in oats for green fodder and grain yield. High heritability along with high genetic advance was observed for tillers per meter row length, leaf : stem ratio, seed index and straw yield (q/ha) and green fodder yield (q/ha).

Bind *et al.*, (2016) studied genetic variability, heritability and genetic advance for different characters on green fodder yield in oat. The magnitude of PCV as expected was greater than the corresponding GCV for all the characters indicating importance of environment in expression of characters on the basis of result out of 11 characters studied seeds per panicle, dry matter yield per plant, green fodder yield per plant and harvest index showed that high GCV and heritability coupled with high genetic advance as per cent of mean which revealed that these four traits might be under control of additive gene effects and therefore they are more reliable for effective selection.

2.2 Correlation

Chaubey *et al.*, (2001) reported that, green fodder yield exhibited a significant positive association with tiller number (0.61), plant height (0.43 cm), leaf width (0.43 cm), and dry fodder yield (0.80 g).

Shankar *et al.*, (2002) studied variation and associations in oat. They reported that, GY was positively and significantly correlated with DF, G and GW. In contrast, GFY had negative and significant correlation with DF, GW and GY. Positive and significant association of GFY with L : S and DMY, and negative but significant association of GY with GFY and L:S were also observed.

Kumar *et al.*, (2004) reported that, green fodder yield per plant was strongly and positively correlated with plant height, number of leaves and number of tillers per plant, flag leaf length and width, longest leaf length and width, stem thickness, longest internode length and dry matter yield per plant.

Mall *et al.*, (2005) green yield was strongly and positively correlated with tiller number, grain number, dry matter yield and harvest index. Tiller number was strongly and positively correlated with green fodder yield, dry matter yield, harvest index and green yield. Grain number/panicle and dry matter was also observed between green fodder yield and dry matter yield per plant.

Gautam *et al.*, (2006) reported that, green fodder yield showed significant positive association with tillers per plant and grain yield per plant. Grain yield had positive association with tillers per plant, flag leaf length, green fodder yield

and dry matter yield. It is concluded that direct selection for tillers per plant, flag leaf length and dry matter yield will be more effective in enhancing fodder and grain yield in forage oat.

Bahadur *et al.*, (2008) reported that, green and dry fodder yield was positive and significantly correlated with plant height, stem diameter, number of leaves per plant, leaf length and leaf breadth.

Bukhari *et al.*, (2009) studied correlation and path coefficient analysis in fodder oat. From correlation and path coefficient analysis they reported that the traits like days to 50 per cent flowering, plant height (cm), number of tillers (sq^{-1}), green fodder yield (q ha^{-1}), dry fodder yield (q ha^{-1}), leaf area index, leaf stem ratio, crude protein play a major role for improvement of yield potential of fodder oats.

Kapoor *et al.*, (2011) found that, traits like number of leaves, internode length (cm), flag leaf width (cm), axis length (cm), axis branch number and number of seeds per panicle had positive and significant correlation at genotypic as well as phenotypic level with seed yield and the selection based on these traits will result in improving the seed yield in oat.

Sofi *et al.*, (2012) reported that green fodder per hectare was highly correlated with plant height and tillers per m^2 , while as seed yield per hectare had significant positive correlation with seed breadth, 1000-seed weight, plant height 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.

2.3 Path analysis

In the improvement of any crop, the knowledge of any one or more characters associated with yield is useful in selecting the individual. Such association between plant characters is statistically elaborated by correlation coefficients. But the correlation between the dependent and independent characters and direct and indirect effects of the independent characters are completely separate things. Sometimes, the correlation between two characters may be highly positive but the direct effect of the independent characters on the dependent one may be negative. Hence mere correlation can not serve the purpose of selection in crop improvement programme.

Therefore, the method of partitioning the direct and indirect effects of independent characters on the dependent characters i.e. path coefficient analysis was detailed by Wright (1921).

Further Dewey and Lu (1959) gave the detailed procedure for path analysis of replicated trials which was quite different technique in eliminating the environmental variance.

Chaubey *et al.*, (2001) studied variability associations and path analysis in forage oat. Number of tillers (0.66) and leaf width (0.41) showed high positive direct effects on green fodder yield. It was suggested that selection for optimum plant height with more tillers and leaves per plant coupled with longer leaf and flag leaf length should result in progenies with high green fodder yield potential in forage oat.

Kumar *et al.*, (2004) studied path analysis in oat. They reported that the number of tillers per plant, plant height and flag leaf length were most important traits with high direct contribution towards green fodder yield.

Mall *et al.*, (2005) studied correlation and path analysis in oat. Harvest index, biological yield, tiller number and grain number exerted positive direct effect on grain yield/plant, while days to 50 per cent flowering, and green fodder yield/plant showed negative direct effect on grain yield.

Bahadur and Chaubey (2007) studied path analysis in oat. They found that plant height, stem diameter, number of tillers/plant, number of leaves/plant, leaf breadth and length were the principal components of green as well as dry fodder yield. They advocated that selection should be based on these characters for accelerating genetic improvement of fodder yield in oat.

Kapoor *et al.*, (2011) studied correlation and path analysis in oat. They reported that, traits like number of leaves, internode length, flag leaf width, axis length, axis branch number and number of spikelets per panicle showed high direct effect on seed yield per plant. Selection for more number of leaves, axis branches and number of seeds per panicle along with broader flag leaf will be significant for the improvement of seed yield in oat.

Nirmala Kumari *et al.*, (2013) studied path analysis in oat. It was concluded that number of productive tillers per plant and number of grains per panicle were major yield contributing factors in selecting high yielding oat genotypes.

2.4 Diversity

The concept of D^2 statistics for measuring the divergence between two populations was introduced by Mahalanobis (1936). It gives a result based on the magnitude of divergence and is independent of size of sample.

Allard (1961) described the relationship between genetic diversity and consistency of performance in different environment by using three distinct levels of genetic diversity. He concluded that, genetic diversity and productivity were completely related and according that many factors determined the productivity of mixed population. According to him genetic diversity and stability on contrast appeared more related.

Murthy and Arunachalam (1966) stated that, a change in the breeding structure could bring a substantial change in character association and the pattern of distribution of genetic variability, geographical distribution and genetic diversity could not be directly related in many of the crops examined by them. Genetic drift and selection in different environment may cause greater diversity than geographic diversity.

Prasad *et al.*, (2003) grouped 247 genotypes into 16 clusters. Genotypes from different places of collection often grouped together in the same cluster, suggesting some degree of ancestral relationship among the genotypes. Based on genetic divergence and mean performance for yield and yield characters, 20 genotypes were found superior.

Kumar *et al.*, (2005) based on Mahalanobis D^2 statistics they classified 100 lines into 9 clusters. Cultivars of the same geographic origin were classified under different clusters, indicating that the grouping pattern did not show a significant relationship between genetic diversity and geographical diversity. Based on genetic divergence, and mean performance for yield and other characters, diverse and

superior genotypes (HFO-604, HFO-566, HFO-552, HFO-161, HFO-699, HFO-14, HFO-305, HFO-244 and HFO-502) were selected.

Mall and Vishwakarma (2006) grouped forty eight genotypes into 7 clusters. Cluster I was the largest with 37 lines, followed by cluster II with 6 lines. The remaining 5 clusters consisted of one line each and were highly diverse from one another. 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 high amount of hybrid vigour and good recombinants.

Bahadur and Chaubey (2008) studied genetic diversity in forage oat. They grouped fifty genotypes into 9 clusters. The clustering pattern revealed that there was no relation between geographic origin and genetic diversity of the genotypes. The intracluster distances ranged from 0.00 to 99.37 and 0.00 to 99.20, whereas intercluster distances varied from 194.78 to 6060.81 and 230.33 to 9938.09, under normal- and late-sown conditions, respectively. Promising genotypes grouped in different clusters should be used in hybridization programmes to obtain transgressive segregants followed by selection to improve fodder yield and quality in forage oat.

Singh and Singh (2010) grouped seventy oat genotypes into 7 clusters and two ungrouped clusters on the basis of D^2 analysis. Cluster I was the largest and contain 16 genotypes. The genotype belonging to ungrouped cluster IX, namely, SJO-47 showed promise for green fodder yield, dry matter yield, green fodder productivity per day, tillers per plant and dry matter (%).

Ahmed *et al.*, (2011) studied genetic diversity and clustering pattern in seventy five germplasm lines of oat for yield and contributing traits using D^2 analysis. Clustering pattern grouped the germplasm lines into nine different clusters. Cluster IV consisted of 21 lines, cluster I and II had 20 lines each, cluster V had 9 lines. Cluster

IV is characterized by lines having prominent traits like high green fodder yield, high grain yield, and tall plants, long and broad leaves. Contribution towards genetic divergence was more from days to 50 % flowering, grain yield, leaf-stem ratio and green fodder yield, so the direct selection for these traits would be helpful.

Jaipal and Shekhawat (2016) studied genetic variability and divergence in oats. On the basis of multivariate analysis based on Mahalanobis D^2 statistic, thirty genotypes were grouped only into four clusters. Cluster I was the largest and consisted of 23 genotypes followed by II with five genotypes followed by III with five genotypes. Rest of the cluster IV had single genotype in each cluster.

3. MATERIAL AND METHODS

The present investigation entitled, “Genetic diversity and path coefficient analysis in oat (*Avena sativa* L.)” was conducted at AICRP on Forage Crops and Utilization, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar, Maharashtra during *rabi* 2016-17. The details of the material used and methods adopted for the conduct of the present investigation are given in this chapter.

3.1 Climatic condition

The Mahatma Phule Krishi Vidyapeeth, Rahuri comes under semi-arid, sub-tropical and geographically situated between 19° 47' to 19° 57' north latitude and 74° 32' to 74° 19' east longitude and at altitude of 657 meters above mean sea level. The annual rainfall ranges between 310-620 mm with an average rainfall 520 mm. The distribution of rain is erratic and the number of rainy days varies from 25-45 in different years. Most of the rainfall is received through south west monsoon during June to September. The annual minimum temperature ranges from 8 to 28.5° C and maximum 26.2 to 42.8° C.

3.2 Experimental material

The experimental material consisted of twenty seven oat genotypes. Out of which twenty four genotypes were provided by the IGFRI, Jhansi and three checks from AICRP on Forage Crops and Utilization, MPKV, Rahuri. The list of twenty seven genotypes is given in table 1.

Table 1. List of twenty seven forage oat genotypes

Sr. No	Name of genotype	Sr. No.	Name of genotype
A.	IGFRI, Jhansi		
1.	ROG-15-1	13.	ROG-15-13
2.	ROG-15-2	14.	ROG-15-14
3.	ROG-15-3	15.	ROG-15-15
4.	ROG-15-4	16.	ROG-15-16
5.	ROG-15-5	17.	ROG-15-17
6.	ROG-15-6	18.	ROG-15-18
7.	ROG-15-7	19.	ROG-15-19

Table 1 contd....

Sr. No	Name of genotype	Sr. No.	Name of genotype
8.	ROG-15-8	20.	ROG-15-20
9.	ROG-15-9	21.	ROG-15-21
10.	ROG-15-10	22.	ROG-15-22
11.	ROG-15-11	23.	ROG-15-23
12.	ROG-15-12	24.	ROG-15-24
B.	Forage improvement project, MPKV, Rahuri		
25.	RO-11-1 (Check)	26.	RO-19 (Check)
27.	Kent (Check)		

3.3 Experimental details

The experiment was laid out in randomized block design (RBD) with two replications having twenty four genotypes with three checks. The sowing was done on 16 December, 2016.

1. Design : Randomized Block Design
2. Replication : 2
3. Treatments : 27 (24 + 03 checks)
4. Plot Size : Two rows of 3.00 m length
5. Spacing : Line sowing in rows spaced 30 cm apart
6. Fertilizer Dose : 100:50:40, N:P:K kg/ha
50:50:40, N:P:K kg/ha - Basal
50:00:00, N:P:K kg/ha – 30 DAS
7. Season : Rabi, 2016-17
8. Location : AICRP on Forage Crops and Utilization,
MPKV, Rahuri.
9. Date of sowing : 16 December, 2016

3.4 Cultural practices

The land was prepared by ploughing followed by two cross harrowing. The basal dose of 50 kg N, 50 kg P₂O₅ and 40 kg K₂O per hectare was applied at the time of sowing. Sowing was carried out on 16 December 2016. Fertilizer application of 50 kg N per hectare was given 30 days after sowing as top dressing. The cultural

practices like irrigation, plant protection, weeding were followed to obtain good growth of the crop.

3.5 Observations recorded

The observations were recorded on five randomly selected plants in each replication for all the characters except number of tillers per meter row length, leaf stem ratio and green forage yield (Kg/m row length).

3.5.1 Forage yield and ancillary characters

3.5.1.1 Plant height (cm) at 50 % flowering

Plant height was measured in centimeters from ground level to the top of the main tiller of the selected plants at the time of 50% flowering in all replications and mean for each replication was worked out.

3.5.1.2 Number of tillers per meter row length

Number of tillers in one meter row length were counted and recorded in each replication and averages were worked out.

3.5.1.3 Number of leaves per tiller

Main tiller of the five observational plants were taken and number of leaves per tiller were counted in each replication. Mean number of leaves per tiller were then worked out.

3.5.1.4 Leaf length (cm)

Leaf length of third leaf from top of the main tiller of the five randomly selected plants was measured in centimeter. Average leaf length was then worked out.

3.5.1.5 Leaf width (cm)

Leaf width of third leaf from top of the main tiller of the five randomly selected plants was measured in centimeters at the middle portion of the leaf where leaf is most widened and observations were recorded.

3.5.1.6 Leaf/stem ratio (L/S)

Hundred gram composite sample of leaves and stems was taken at the time of harvesting for estimation of leaf/stem ratio. All the leaves and stems were

separated and weighed in grams. The leaf/stem ratio was calculated by using the following formula,

$$\text{L/S ratio} = \frac{\text{Weight of the leaves (gm)}}{\text{Weight of the stem (gm)}}$$

3.5.1.7 Stem thickness (mm)

Stem of the main tiller was taken from the selected plant. Diameter of the stem at first internode from the base of the main stem was recorded with the help of thread and measured in mm with the help of measuring scale.

3.5.1.8 Green forage yield (kg/m row length)

Green forage yield was recorded from one meter row length in each plot of and the average was worked out in kilograms per meter of the row.

3.5.1.9 Crude protein content (%)

Oven dried samples of the green fodder was grinded in a grinder and 0.2 gm of the grinded sample was analyzed in laboratory for the estimation of crude protein content. Nitrogen content in dry fodder was determined by Microkjeldahl's method (Thimmaiah, 1999). Percent nitrogen was calculated by using the formula,

$$\% \text{ N} = (A-B) \times (N \times \text{Equivalent wt. of N}) \times \frac{\text{Volume made}}{\text{Volume taken}} \times \frac{100}{0.2}$$

Where,

A = Pipette reading

B = Burette reading

N = Normality of H₂SO₄

Per cent protein content was calculated by using following formula,

$$\text{Crude protein content (\%)} = \text{Nitrogen \%} \times 6.25$$

3.5.1.10 Dry matter content (%)

Two hundred and fifty gram sample of green fodder was taken at the time of harvesting and dried in a hot air oven at 60⁰ C temperature until constant dried weight was observed. Weight of the dried samples were recorded and dry matter content was worked out in percentage with the help of following formula,

$$\text{Dry matter (\%)} = \frac{\text{Weight of oven dry sample (gm)}}{250} \times 100$$

3.5.2 Morphological characters

Eight morphological characters were observed and observations were recorded into different categories.

3.5.2.1 Plant growth habit

Plant growth habit was recorded after the 25-29 DAS of the crop. Growth habit was assessed visually from the attitude of the leaves and tillers of the selected plant. The angle formed by the outer leaves and the tillers with an imaginary vertical axis used. Observations were recorded and categorized into five categories viz., erect, semi-erect, intermediate, semi-prostrate and prostrate.

3.5.2.2 Hairiness of sheath of lowest leaf

Hairiness of sheath of the lowest leaf was recorded after the 25-29 DAS of the crop. This assessed visually from the selected plant and observations were recorded. Observations were recorded and categorized into five categories viz., absent or very weak, weak, medium, strong and very strong.

3.5.2.3 Hairiness of margins of leaf below flag leaf

The leaf just below the flag leaf was selected after the 40-45 DAS from the five randomly selected plants and hairiness of margins of leaf was recorded. . Observations were recorded and categorized into five categories viz., absent or very weak, weak, medium, strong and very strong.

3.5.2.4 Internode exposed or covered

Stem of the main tiller was taken from the five randomly selected plant. First internode from the base of the main stem was observed. . Observations were recorded and categorized into two categories viz., internode exposed and internode covered.

3.5.2.5 Frequency of plants with recurved flag leaves

Frequency of plants with recurved flag leaves was recorded after 47-51 DAS. Flag leave from the selected plants was taken were categorized according to intensity of recurved flag leaves.

3.5.2.6 Orientation of panicle branches

Orientation of panicle branches were observed 70-75 DAS of the crop. A panicle was selected from the five randomly selected plants and panicle branches were observed and categorized into three categories viz., unilateral, sub-unilateral and equilateral.

3.5.2.7 Attitude of panicle branches

Attitude of panicle branches were observed 70-75 DAS of the crop. A panicle was selected from the five randomly selected plants and panicle branches were observed. Observations were recorded and categorized into five categories viz., erect, semi-erect, horizontal, drooping and strongly drooping.

3.5.2.8 Attitude of spikelets

Attitude of spikelets were observed 70-75 DAS of the crop. A panicle was selected from the five randomly selected plants and spikelets were observed. Observations were recorded and categorized into two categories viz., erect and pendulous.

3.6 Statistical analysis

3.6.1 Assessment of variability

a. Analysis of variance

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the randomized block design (Panse and Sukhatme, 1985).

$$Y_{ij} = \mu + G_i + R_j + E_{ij}$$

Where,

$$i = 1, 2, \dots, G$$

$$j = 1, 2, \dots, R$$

$$Y_{ij} = \text{Observation on } i^{\text{th}} \text{ genotype in } j^{\text{th}} \text{ replication}$$

$$\mu = \text{General mean}$$

$$G_i = \text{Effect of } i^{\text{th}} \text{ genotype}$$

$$R_j = \text{Effect of } j^{\text{th}} \text{ replication}$$

$$E_{ij} = \text{Random error associated with } Y_{ij} \text{ observation}$$

ANOVA Table:

Source	d.f.	m.s.	expected m.s.
Replications	r-1	RMS	$\sigma_e^2 + \sigma_r^2$
Treatments	g-1	GMS	$\sigma_e^2 + r\sigma_g^2$
Error	(r-1)(g-1)	EMS	σ_e^2

Where,

r = Number of replications

g = Number of genotypes

σ_g^2 = Variance due to genotypes and

σ_e^2 = Variance due to error

The genotype mean square (GMS) was tested against error mean square (EMS) by 'F' test for $n_1 = (g-1)$ and $n_2 = (r-1)(g-1)$ degrees of freedom, where, g = number of genotypes and r = number of replications. The characters showing significant differences were subjected to further analysis.

Estimation of S. E. and C. D.

$$\text{S.E. of mean (S.Em)} = \sqrt{\sigma_{e/r}^2}$$

$$\text{C.D.} = t \text{ at error d.f.} \times \text{S.E.m} \times \sqrt{2}$$

b. Estimation of mean and range

The mean values for each character were worked out by dividing the total by corresponding number of observations:

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

Where,

\bar{X} = Mean of character

$\sum X_i$ = Total of all the observations for character

N = Number of observations

The lowest and highest values of mean of each character represented the range.

c. Estimation of components of variation

The phenotypic and genotypic variances were calculated using the respective mean squares from variance table (Johnson *et al.*, 1955) as below.

$$\text{Environmental variance } (\sigma^2_e) = \text{EMS}$$

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{GMS} - \text{EMS}}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications

d. Estimation of coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated as per Burton, (1952).

i. Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\sigma^2_g}{\bar{X}} \times 100$$

Where,

σ^2_g = Genotypic variance and,

\bar{X} = Mean of character

ii) Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\sigma^2_p}{\bar{X}} \times 100$$

Where,

σ^2_p = Phenotypic variance and,

\bar{X} = Mean of character

The high, medium and low GCV and PCV estimates were classified as:

Low : 10 per cent

Medium : 10 to 20 per cent

High : > 20 per cent

e. Estimation of heritability (b.s.)

Heritability in broad sense was estimated as suggested by Hanson *et al.*, (1956).

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

Where,

h^2 = Heritability

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The high, medium and low heritability estimates were classified on the basis of values given by Johnson *et al.*, (1955).

Low heritability = < 10 %

Moderate heritability = 10-30 %

High heritability = > 30 %

f. Genetic advance (G.A.)

Genetic advance (at 5 % selection intensity) was calculated using the formula given by Allard (1960)

i. Genetic advance (G.A.)

$$\text{G.A.} = k \times \frac{\sigma^2_g}{\sigma^2_p} \times \sqrt{\sigma^2_p}$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

k = Selection differential (at 5 % selection = 2.06)

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

ii. G.A. as percentage of means (GAM)

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

Where,

G. A. = Genetic advance

\bar{X} = Character mean

GA (As percentage of mean) was classified as

Low : 10 per cent

Medium : 10 to 20 per cent

High : > 20 per cent

3.6.2 Correlation

Analysis of covariance was carried out by taking two characters at a time. The genotypic co-variance was calculated as per Johnson *et al.*, (1955) as below:

Sources	d.f.	Sum of product	Mean sum of product	Expectation of mean sum of product
Replications	(r-1)	RP	RMP	$\text{COVe}_{1.2+g} \text{COV}_{r1.2}$
Genotypes	(g-1)	GP	GMP	$\text{COVe}_{1.2+r} \text{COV}_{g1.2}$
Error	(r-1) (g-1)	EP	EMP	$\text{COVe}_{1.2}$

Environmental covariance (COV. $e_{1.2}$) = EMP

Genotypic covariance (COV. $g_{1.2}$) = $\frac{\text{GMP} - \text{EMP}}{r}$

Phenotypic covariance (COV. $p_{1.2}$) = (COV. $g_{1.2}$) + (COV. $e_{1.2}$)

Where,

GMP = Genotypic mean sum of product

EMP = Error mean sum of product

r = Replication

Appropriate variances and co-variances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et al.*, 1955).

The phenotypic correlation coefficient (r_p) was calculated as:

$$r_{p1.2} = \frac{COV_{p1.2}}{\sqrt{(\sigma_{p1}^2)(\sigma_{p2}^2)}}$$

Where,

$r_{p1.2}$ = Phenotypic correlation coefficient between character 1 and 2

$COV_{p1.2}$ = Phenotypic covariance between character 1 and 2.

$\sigma_{p1}^2, \sigma_{p2}^2$ = Phenotypic variance of character 1 and 2 respectively.

The significance of the phenotypic correlation coefficient was tested by referring to formula given by Fisher and Yates (1943). The genotypic correlation coefficient (r_g) was calculated as:

$$r_{g1.2} = \frac{COV_{g1.2}}{\sqrt{(\sigma_{g1}^2)(\sigma_{g2}^2)}}$$

Where,

$r_{g1.2}$ = Genotypic correlation coefficient between character 1 and 2

$COV_{g1.2}$ = Genotypic covariance between character 1 and 2

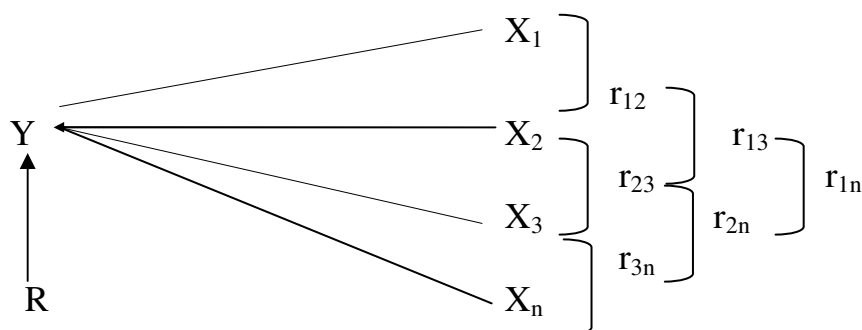
$\sigma_{g1}^2, \sigma_{g2}^2$ = Genotypic variance of character 1 and 2 respectively.

The significance of correlation coefficients was tested from the statistical table of correlation coefficient at 1 and 5 per cent level of significance (Snedcor and Cochran, 1967).

3.6.3 Path analysis

To establish a cause and effect relationship the first step used was to partition genotypic and phenotypic correlation coefficient into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959) and developed by Wright (1921).

The second step in path analysis is to prepare path diagram based on cause and effect relationship. In the present study, path diagram was prepared by taking yield as the effect i.e. function of various components like X_1, X_2, X_3 and these component showed following type of association with each other.



In path diagram the yield is the result of $X_1, X_2, X_3, \dots, X_n$ and some other undefined factors designated by R. The double arrow lines indicated mutual association as measured by correlation coefficient. The single arrow represents direct influence as measured by path coefficient P_{ij} .

Path coefficients were obtained by solving a set of simultaneous equation of the form as per Dewey and Lu (1959).

$$r_{ny} = P_{ny} + r_{n2} P_{2y} + r_{n3} P_{3y} + \dots$$

Where,

r_{ny} = represents the correlation between one component and yield

P_{ny} = represents path coefficient between that character and yield

r_{n2} = represents correlation between that character and each of the other components in turn.

$$\begin{matrix} \text{Matrix A} & & \text{Matrix B} & & \text{C} \\ \begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{ny} \end{pmatrix} & = & \begin{pmatrix} r_{11} & r_{12} & r_{13} & \dots & r_{1n} \\ r_{21} & r_{22} & r_{23} & \dots & r_{2n} \\ r_{n1} & r_{n2} & r_{n3} & \dots & 1 \end{pmatrix} & & \begin{pmatrix} P_{1y} \\ P_{2y} \\ P_{ny} \end{pmatrix} \end{matrix}$$

Where,

$r_{12} = r_{21}$ and so on

r_{1y} = Correlation between one component character and seed yield

The 'B' matrix was inverted $[B]^{-1}$ and path coefficients (P_{ij}) were obtained as,

i.e. $P_{ij} = (B)^{-1} \cdot A$

The indirect effects of a particular character through other characters were obtained by multiplication of direct paths and particular correlation between these characters separately.

$$\text{Indirect effects} = r_{ij} \times p_{iy}$$

Where,

$$i = 1 \text{ to } 9$$

$$j = 1 \text{ to } 9$$

$$P_{iy} = P_{1y}, P_{2y}, \dots, P_{ny}$$

Path coefficient (P_{ij}), correlation coefficient (r_{ij}) and residual factors (R) were diagrammatically presented. The residual factor i.e. variation in yield unaccounted for by these associations was calculated with the following formula:

$$\text{Residual factor (R)} = (1 - R^2)$$

Where,

$$R^2 = P_{1y} r_{1y} + P_{2y} r_{2y} + \dots + P_{ny} r_{ny}$$

$$P_{1y}, P_{2y}, \dots, P_{ny} = \text{Direct path values}$$

$$r_{1y}, r_{2y}, r_{ny} = \text{Correlation coefficient}$$

3.6.4 Diversity

D² analysis

The analysis of divergence was carried out by D² statistics proposed by Mahalanobis (1936) as described by Rao (1952). Analysis of variance for the individual character studied was worked out as per randomized block design analysis to test the significances of differences among the genotypes. All the characters exhibited significant differences so all were used for further analysis of D² statistics. The analysis of covariance for character pair based on plant average was carried out (Cochran and Cox, 1957).

a. Wilk's criteria

After testing differences among populations for ten characters, a simultaneous test of significance of difference between the mean value of number of correlated variables with regard to pooled effect of nine characters considered together was carried out using Wilk's criteria 'Λ' (Wilks, 1932) which was estimated using the relationship.

$$\Lambda = \frac{|E|}{|E + V|}$$

Where,

$|E|$ = The determinant of experimental error sum of squares and sum of products matrix

$|E + V|$ = The determinant of experimental error sum of squares and sum of products plus population sum of squares and product matrix

The significance of Wilk's criteria (Λ) was tested by χ^2 as,

$$\chi^2_{pq} = -m \cdot \log_e (\Lambda)$$

Where,

$$m = n \cdot \frac{(p+q+1)}{2}$$

n = $N_1 + \dots + N_{k-1}$ (Total number of observations-1)

p = Number of significant characters

q = $k-1$ (Number of genotypes -1)

K = Number of genotypes

b. Mahalanobis's generalized distance (D^2)

The generalized distance between any two populations is defined as:

$$D^2 = \sum \sum \lambda_{ij} \delta_i \delta_j$$

Where,

λ_{ij} = Reciprocal matrix to the common dispersion matrix

δ_i = Difference between mean value of the two populations for the i^{th} character

δ_j = Difference between mean value of the two populations for the j^{th} character.

This quantity is estimated by D^2 statistic (Mujumdar and Rao, 1958) as:

$$D^2 = \sum \sum S_{ij} \delta_i \delta_j$$

Where,

S_{ij} , δ_i , δ_j are the sample estimates of λ_{ij} , δ_i and δ_j respectively, since this formula for computation requires inversion of tenth order determinant and then evaluation of 10 (10+1) terms, whose sum is D^2 .

c. Computation of D^2 values

For each combination, D^2 was calculated. Thus total 351 D^2 values [(27)(26)/2] were worked out.

d. Determination of population constellation

No rules can be laid down for the finding the clusters, because cluster is not well defined term. The only criteria appears to be that, any two groups belonging to same cluster should be at least, on an average show a smaller D^2 value than those belonging to two different.

The simple method suggested by Tocher (Rao, 1952) for cluster formation is to start with two closely related groups and find third group which has a smaller average D^2 value from the first two. Similarly, the fourth group is chosen to have smaller average D^2 values from the first three and so on. While proceeding further from cluster formation at any stage, the average D^2 value of

the group appears to be high than those already listed, then this group does not fit in that format group and taken outside of that cluster.

The genotypes included in first cluster are then omitted and the rest are treated similarly to form next cluster.

e. Average intra-cluster distances

The intra cluster distances were calculated as,

$$\frac{\sum Di^2}{n}$$

Where,

$\sum Di^2$ = Sum of distances between all possible combinations

n = Number of genotypes included in a cluster

f. Average inter-cluster distances

The procedure followed for calculating inter-cluster distances was first to measure the distance between cluster-I and cluster-II, between cluster-I and cluster-III, and between cluster-I and cluster-IV and so on. Likewise the clusters were taken one by one and the distances between other clusters were calculated. The average inter-cluster distances were they calculated as,

$$\frac{\sum Di^2}{(ni.nj)}$$

Where,

ni = Number of genotypes in cluster 'i'

nj = Number of genotypes in cluster 'j'

g. Cluster diagram

The intra and inter-cluster distances (D values) were obtained by taking square root of average D^2 values of respective groups.

With the help of D^2 values between the clusters, a diagram showing the relationship between different populations was drawn.

4. RESULT AND DISCUSSION

The results obtained in the present investigation entitled “Genetic diversity and path coefficient analysis in oat (*Avena sativa* L.)” have been presented and discussed in this chapter under appropriate sub headings.

4.1 Genetic variability and heritability

There can be little doubt that the existence of genetic variability is advantageous to the evolutionary survival of a species. Yield improvement in any crop can be brought about through plant breeding but necessary variability upon which selection is to be practiced must be available in the genetic material. Therefore, before proceeding for any plant breeding programme, the plant breeder must survey and assess the variability present with respect to yield and its attributes. The variability for a given agronomic or yield component character can be estimated through variance, coefficient of variability i.e. GCV and PCV, heritability and genetic advance.

4.1.1 Analysis of variance

The analysis of variance revealed significant genotypic differences for all the characters except dry matter content (%) (Table 2).

Ahmed *et al.*, (2011) reported significant differences among the genotypes of oat for the traits *viz.*, plant height, number of leaves per plant, leaf length, leaf width, leaf/stem ratio and green forage yield.

Bind *et al.*, (2016) reported significant differences among the genotypes of oat for the traits *viz.*, number of tillers per plant, green forage yield plant height. These results were in conformity with those obtained in the present investigation.

4.1.2 Mean performance

The mean values of the twenty seven forage oat genotypes for ten different characters studied are given in table 3.

Table 2. Analysis of variance for ten different characters in forage oat

Sr. No.	Character	Mean sum of squares	
		Genotype	Error
1.	Plant height at 50% flowering (cm)	508.5697**	26.7789
2.	Number of tillers per m. row length	513.3732**	32.9458
3.	Number of leaves per tiller	0.6219*	0.1910
4.	Leaf length (cm)	79.0778**	4.0974
5.	Leaf width (cm)	0.3621**	0.0411
6.	Leaf /Stem (L/S) ratio	0.0687**	0.0033
7.	Stem thickness (mm)	73.1571**	7.2922
8.	Green forage yield (kg/m row length)	0.4881**	0.0137
9.	Dry matter content (%)	0.6283	0.3747
10.	Crude protein content (%)	1.4309**	0.3175

*,** = significant at 5% and 1 % levels, respectively.

4.1.2.1 Plant height at 50 % flowering (cm)

The range of variation for plant height was from 89.50 cm (ROG -15-4) to 151.80 cm (RO-19). Six genotypes recorded significantly more height than trial mean (112.54).

4.1.2.2 Number of tillers per meter row length

The range of variation for number of tillers per meter row length was from 58.00 (ROG -15-15) to 113.00 (ROG -15-11) with overall mean performance of 88.92. Highest number of tillers per meter row length was observed for ROG-15-11(113.00) followed by ROG -15-13 (109.00) and ROG -15-16 (108.00). Seven genotypes recorded significantly more number of tillers per meter row length over overall mean (88.92).

4.1.2.3 Number of leaves per tiller

The range of variation for number of leaves per tiller was from 4.70 (ROG-15-1) to 7.40 (RO-11-1) with overall mean performance of 6.46. Highest

Table 3. Mean performance of twenty seven genotypes of forage oat for ten different characters

Sr. No.	Name of genotype	Plant height at 50 % flowering	No. of tillers per m. row length	No. of leaves per tiller	Leaf length (cm)	Leaf width (cm)	L/S ratio	Stem thickness (mm)	Green forage yield (kg/m row length)	Dry matter content (%)	Crude protein content (%)
1.	ROG- 15-1	98.50	85.00	4.70	29.00	1.58	0.38	17.50	0.58	19.53	5.79
2.	ROG -15-2	106.80	80.50	6.60	44.90	1.81	0.49	18.55	1.15	21.27	7.65
3.	ROG -15-3	124.10*	107.00**	6.20	46.20	2.22	0.51	28.20	2.27**	21.45	7.65
4.	ROG -15-4	89.50	78.50	6.00	41.10	1.62	0.75**	22.30	1.16	20.85	5.79
5.	ROG -15-5	117.80	65.00	6.50	47.20	1.75	0.64	22.53	1.04	20.16	5.79
6.	ROG -15-6	103.70	90.00	5.80	49.70**	1.70	0.67	18.20	1.17	19.48	7.00
7.	ROG -15-7	92.40	70.00	6.40	41.55	1.77	0.63	25.40	1.08	19.97	5.58
8.	ROG -15-8	104.30	72.00	7.10	37.50	1.81	0.63	17.60	0.90	21.40	6.56
9.	ROG -15-9	109.50	99.50	6.45	38.00	2.02	0.40	24.50	1.42	20.43	6.89
10.	ROG -15-10	129.10**	69.50	6.60	42.10	2.13	0.66	28.40*	0.93	21.57	7.32
11.	ROG -15-11	126.60	113.00**	6.50	51.80**	2.65**	0.44	28.50*	2.27**	20.36	7.37
12.	ROG -15-12	127.70**	104.00**	6.60	42.90	2.83**	0.88**	26.80	1.88**	20.03	7.22
13.	ROG -15-13	91.80	109.00**	5.90	51.40**	2.51	0.88**	17.40	1.81*	20.55	7.69
14.	ROG -15-14	104.40	94.00	6.20	39.20	1.77	0.66	26.00	1.47	20.54	7.03
15.	ROG -15-15	133.00**	58.00	6.20	52.10**	2.61	0.42	31.90*	1.58	20.19	6.01
16.	ROG -15-16	89.90	108.50**	5.80	51.50**	2.41	0.51	14.80	1.51	20.02	6.05
17.	ROG -15-17	105.20	102.00	6.55	36.70	2.07	0.33	25.90	1.50	19.65	6.95
18.	ROG -15-18	115.80	94.00	7.10	42.60	2.40	0.40	22.40	1.81*	19.75	7.78
19.	ROG -15-19	107.30	91.00	6.40	45.00	2.00	0.66	26.60	2.15**	20.01	5.85
20.	ROG -15-20	96.40	74.00	6.50	53.55**	2.00	0.40	18.00	1.47	20.30	6.27
21.	ROG -15-21	110.70	70.00	7.00	42.80	2.40	0.88**	19.80	1.11	19.76	6.00
22.	ROG -15-22	114.20	73.50	7.30	52.60**	3.13	0.83**	20.50	1.00	20.74	5.79
23.	ROG -15-23	105.50	86.50	6.40	45.00	2.28	0.61	27.10	1.55	19.86	8.36*
24.	ROG -15-24	143.20**	102.00	6.40	52.90**	2.96**	0.37	25.50	1.87**	20.61	6.89
25.	RO-11-1 (Check)	118.10	107.50**	7.40*	37.40	2.27	0.25	25.80	2.58**	20.37	7.80
26.	Kent (Check)	121.40	90.00	7.10	39.60	2.20	0.30	24.30	2.89**	20.11	7.94
27.	RO-19 (Check)	151.80**	107.00**	6.90	46.90	2.74*	0.50	29.30*	2.01**	20.49	7.90
	Mean	112.54	88.92	6.46	44.67	2.20	0.56	22.73	1.52	20.36	6.85
	S.E. ₊	3.65	4.05	0.30	1.43	0.14	0.04	1.90	0.08	0.43	3.39
	C.D.5%	10.63	11.79	0.89	4.16	0.41	0.11	5.55	0.24	N.S.	1.15
	C.D.1%	14.37	15.94	1.21	5.62	0.56	0.16	7.50	0.32	N.S.	1.56

*, ** = significant at 5 % and 1 % levels, respectively

number of leaves per tiller was observed for RO-11-1 followed by ROG -15-22 (7.30) and ROG-15-7 and ROG-15-18 (7.10). Only one genotype *viz.*, RO-11-1(7.10) recorded significantly more number of leaves per tiller over the trial mean (6.46).

4.1.2.4 Leaf length (cm)

The range of variation for leaf length was from 29.00 cm (ROG -15-1) to 53.55 cm (ROG-15-20) with mean performance of 44.67 cm. Highest leaf length was observed for ROG-15-20 (53.55) followed by ROG-15-22(52.60) and ROG-15-11(51.80). Eight genotypes recorded significantly more leaf length than trial mean (44.67).

4.1.2.5 Leaf width (cm)

The range of variation for leaf width was from 1.58cm (ROG-15-1) to 3.13 cm (ROG-15-22) with mean performance of 2.20 cm. Highest leaf width was observed in ROG-15-22 (3.13) followed by ROG-15-24(2.96) and ROG-15-12 (2.83). Four genotypes recorded significantly higher leaf width over the trial mean (2.20).

4.1.2.6 Leaf/Stem ratio (L/S)

The range of variation for L/S ratio was between 0.25 (RO-11-1) and 0.88. (ROG-15-12), (ROG-15-13) and (ROG-15-21). Five genotypes recorded significantly higher leaf/stem ratio than overall mean (0.56).

4.1.2.7 Stem thickness (mm)

The range of variation for stem thickness was between 14.80 mm (ROG-15-16) and 31.90 mm (ROG-15-15) with mean performance of 22.73 mm. Four genotypes recorded significantly higher stem thickness than overall mean (22.73).

4.1.2.8 Green forage yield (Kg/m. row length)

Lowest green forage yield observed in ROG-15-1 (0.58 kg) and highest green forage yield observed in check Kent (2.89 kg) with mean performance of 1.52 kg. Ten genotypes recorded significantly more green forage yield than overall trial mean (1.52).

4.1.2.9 Dry matter content (%)

Lowest dry matter content (%) was observed in ROG-15-6 (19.48) while highest dry matter content was observed in ROG-15-10 (21.57) with overall mean performance of 20.36. The treatment differences for dry matter content were non significant.

4.1.2.10 Crude protein content (%)

The crude protein content (%) ranged between 5.58 (ROG-15-7) and 8.36 (ROG-15-23) with overall mean performance of 6.85. ROG-15-23 (8.36) recorded significantly higher crude protein content over the overall mean (6.85).

Highest range was observed for the trait green forage yield followed by leaf/stem ratio, whereas medium for stem thickness, leaf width, number of tillers per meter row length, leaf length, plant height and number of leaves per tiller. Dry matter content and crude protein content exhibited low range.

Prasad *et al.*, (2003) reported high range for green fodder yield, stem girth and number of tillers; medium range for plant height, number of leaves, leaf length and leaf width.

Kapoor *et al.*, (2011) reported high range for number of tillers per plant and stem girth; medium range for plant height, leaf width, leaf length and number of leaves.

Bind *et al.*, (2016) reported medium range for green fodder yield and tillers per plant while plant height showed low range.

Jaipal and Shekhawat (2016) reported high range for green fodder yield and leaf/stem ratio; medium range for tillers per meter row length, leaf length and leaf width.

Singh and Singh (2016) reported high range for green forage yield and plant height whereas medium range for number of tillers per plant and dry matter content. Leaf/stem ratio exhibited low range. These results were in conformity with those obtained in the present investigation.

4.1.3 Estimates of components of variation

The estimates of variability parameters for ten different characters in twenty seven genotypes of forage oat are presented in table 4.

4.1.3.1 Genotypic and phenotypic variance

The phenotypic variance was higher than genotypic variance for all the ten traits studied indicating role of environmental factors in the expression of these characters.

4.1.3.2 Genotypic and phenotypic coefficients of variation

High values of GCV and PCV were recorded for the traits namely, leaf/stem ratio (32.20, 33.81) and green forage yield (31.87, 32.70). Low values of GCV and PCV were observed for two traits *viz.*, dry matter content (1.75, 3.48) and number of leaves per tiller (7.18, 9.96). All the remaining characters recorded medium values of GCV and PCV.

Shankar *et al.*, (2002) reported high values of GCV and PCV for green fodder yield and leaf/stem ratio; medium values of GCV and PCV for plant height, leaf length, leaf width and number of tillers per plant. Low value of GCV and PCV was recorded for stem diameter.

Singh and Singh (2010) reported high values of GCV and PCV for green fodder yield, plant height and tillers per plant; medium values of GCV and PCV for leaf/stem ratio and dry matter content.

Kapoor *et al.*, (2011) reported high values of GCV and PCV for stem girth and number of tillers per plant whereas medium values of GCV and PCV were observed for number of leaves, leaf width, leaf length and plant height.

Bind *et al.*, (2016) reported high values of GCV and PCV for green fodder yield and tillers per plant; low value of GCV and PCV for plant height.

Jaipal and Shekhawat (2016) reported high values of GCV and PCV for green fodder yield and leaf/stem ratio; medium values of GCV and PCV were observed for tillers per meter row length and leaf width. Low values of GCV and PCV for plant height and leaf length. These results were in conformity with those obtained in the present investigation.

Table 4. Estimates of variability parameters for ten different characters in twenty seven genotypes of forage oat

Sr. No.	Name of the character	Range	σ^2_g	σ^2_p	σ^2_e	GCV (%)	PCV (%)	ECV (%)	h^2 (b.s.)	G.A.	G.A. as % of mean
1.	Plant height (cm)	89.50-151.80	240.89	267.67	26.779	13.790	14.537	4.598	90.00	30.331	26.950
2.	Number of tillers per meter row length	58.00-113.0	240.21	273.15	32.945	17.428	18.585	6.454	87.90	29.940	33.668
3.	Number of leaves per tiller	4.70-7.40	0.2154	0.4065	0.1910	7.177	9.859	6.759	53.00	0.696	10.764
4.	Leaf length (cm)	29.00-53.55	37.4902	41.587	4.0974	13.705	14.434	4.530	90.10	11.975	26.805
5.	Leaf width (cm)	1.58-3.13	0.1605	0.2016	0.0411	18.132	20.323	9.180	79.60	0.736	33.325
6.	Leaf/Stem ratio (L/S)	0.25-0.88	0.0327	0.0360	0.0033	32.204	33.812	10.303	90.71	0.354	63.187
7.	Stem thickness (mm)	14.80-31.90	32.9325	40.224	7.2922	25.244	27.899	11.879	81.85	10.696	47.053
8.	Green forage yield (kg/m. row length)	0.58-2.58	0.2372	0.2509	0.0138	31.878	32.790	7.680	94.56	0.975	63.842
9.	Dry matter content (%)	19.48-21.57	0.1268	0.5015	0.3748	1.748	3.477	3.005	52.23	0.3688	1.810
10.	Crude protein content (%)	5.58-8.36	0.5567	0.8742	0.3175	10.892	13.649	8.225	63.64	1.226	17.905

4.1.3.3 Heritability and genetic advance as percent of mean

High estimates of heritability (b.s.) were observed for all characters studied. Seven characters *viz.*, plant height, number of tillers per meter row length, leaf length, leaf width, leaf/stem ratio, stem thickness and green forage yield showed high estimates of heritability (b.s.) accompanied by high genetic advance as percentage of mean.

Genotypic coefficient of variation alone does not indicate the proportion of total heritable variation. The heritability estimates are better indicator in this respect. The broad sense heritability includes the contribution of additive gene effects, dominance and non allelic interaction due to epistasis. Johnson *et al.*, (1955) pointed out that in a selection programme, heritability values as well as estimates of genetic advance are more useful than heritability alone.

Shankar *et al.*, (2002) reported high estimates of heritability accompanied by high estimates of genetic advance as percentage of mean for the characters *viz.*, plant height, leaf length, number of tillers per plant, leaf/stem ratio, green fodder yield and dry matter yield.

Singh and Singh (2010) reported that characters *viz.*, plant height, tillers per plant and dry matter content exhibited high estimates of heritability accompanied by high estimates of genetic advance as percentage of mean.

Kapoor *et al.*, (2011) observed that leaf width, leaf length and number of tillers per plant showed high estimates of heritability accompanied by high estimates of genetic advance as percentage of mean.

Bind *et al.*, (2016) reported high estimates of heritability and genetic advance as percentage of mean for plant height and green fodder yield.

Jaipal and Shekhawat (2016) observed that characters *viz.*, plant height, tillers per meter row length, leaf/stem ratio and green fodder yield exhibited high estimates of and genetic advance as percentage of mean. These results were in conformity with those obtained in the present investigation.

4.2. Correlation

The genotypic correlation coefficients provide an estimate of inherent association between genes controlling any two characters. The underlying genetic mechanism causing such association may be due to complete linkage between the two characters or due to pleiotropic effects. Correlation is of greater significance and can be utilized in formulating an effective selection scheme. It may also help to identify the characters that prove to be of little or no importance in the selection programme.

The genotypic correlation coefficients for ten characters studied in oat are presented in table 5. The only significant correlations either in positive or negative directions are described.

4.2.1 Genotypic association between green forage yield and other characters

It was revealed from table 5 that, green forage yield was significantly and positively associated with tillers per meter row length (0.7342) followed by crude protein content (0.6507), stem thickness (0.5186), leaf width (0.4717) plant height (0.4282) and number of leaves per tiller (0.3475). However, leaf/stem ratio showed significant negative correlation (-0.3210) with green forage yield.

4.2.2 Association among yield contributing characters at genotypic level

4.2.2.1 Plant height at 50 % flowering (cm)

Plant height showed highly significant positive genotypic correlation with leaf width (0.6166), stem thickness (0.4883) number of leaves per tiller (0.4849) and crude protein content (0.4578).

4.2.2.2 Number of tillers per meter row length

Number of tillers per meter row length showed highly significant and positive correlation with crude protein content (0.6593), leaf width (0.3664) and stem thickness (0.2935). However, leaf/stem ratio showed significant negative correlation (-0.2704) with number of tillers per meter row length.

Table 5. Genotypic correlation coefficient of green forage yield with yield contributing characters in twenty seven genotypes of forage oat

Sr. No.	Character	Plant height at 50 % flowering (cm)	Number of tillers per meter row length	Number of leaves per tiller	Leaf length (cm)	Leaf width (cm)	Leaf/stem ratio (L/S)	Stem thickness (mm)	Dry matter content (%)	Crude protein content (%)	GFY (kg/m row length)
1.	Plant height at 50 % flowering (cm)	1.0000	0.1794	0.4849**	0.2125	0.6166**	-0.2285	0.4883**	0.2508	0.4578**	0.4282**
2.	Number of tillers per meter row length		1.0000	-0.1154	0.0024	0.3664**	-0.2704*	0.2935*	-0.0860	0.6593**	0.7342**
3.	Number of leaves per tiller			1.0000	0.0746	0.4594**	-0.0319	0.2133	0.2829*	0.4114**	0.3475*
4.	Leaf length (cm)				1.0000	0.5275**	0.2010	-0.0729	0.0672	0.0089	0.2172
5.	Leaf width(cm)					1.0000	0.1050	0.3633**	-0.1609	0.2910*	0.4717**
6.	Leaf/Stem ratio						1.0000	-0.2078	0.1298	-0.3486**	-0.3210*
7.	Stem thickness (mm)							1.0000	0.2352	0.4373**	0.5186**
8.	Dry matter content (%)								1.0000	0.1242	-0.0979
9.	Crude protein content (%)									1.0000	0.6507**
10.	GFY (Kg/m row length)										1.0000

*,** = significant at 5 % and 1 % levels, respectively

4.2.2.3 Number of leaves per tiller

Number of leaves per tiller showed highly significant and positive correlation with leaf width (0.4594), crude protein content (0.4114) and dry matter content (0.2829).

4.2.2.4 Leaf length (cm)

Leaf length showed highly significant and positive correlation with leaf width (0.5275).

4.2.2.5 Leaf width

Leaf width showed highly positive and significant correlation with stem thickness (0.3633) and crude protein content (0.2910).

4.2.2.6 Leaf/Stem ratio

Leaf/stem ratio showed highly significant and negative correlation with crude protein content (-0.3486).

4.2.2.7 Stem thickness (mm)

Stem thickness showed highly significant and positive correlation with crude protein content (0.4373).

4.2.2.8 Dry matter content (%)

Dry matter content exhibited non significant, positive association (0.1242) with crude protein content.

In the present studies it was observed that green forage yield was significantly and positively correlated with number of tillers per meter row length, crude protein content, stem thickness, leaf width, plant height and number of leaves per tiller. While it showed significant and negative association with leaf/stem ratio.

Chaubey *et al.*, (2001) reported significant positive association of green fodder yield with tiller number, plant height and leaf width.

Kumar *et al.*, (2004) reported significant positive association of green fodder yield with plant height, number of leaves and number of tillers per plant and stem thickness.

Mall *et al.*, (2005) reported significant positive association of green fodder yield with tiller number.

Bahadur *et al.*, (2008) reported significant positive association of green fodder yield with plant height, stem diameter and number of leaves per plant.

Bukhari *et al.*, (2009) reported significant positive association of green fodder yield with plant height, number of tillers and leaf/stem ratio.

Sofi *et al.*, (2012) reported significant positive association of green fodder yield with plant height and tillers per m². These results were in conformity with those obtained in the present investigation.

4.3 Path analysis

Direct effect of any component character on yield gives an idea about the reliability of indirect selections to be made through those characters to bring about improvement in green forage yield. If the correlation coefficient between a causal factor and the effect is equal to its direct effect, then correlation explains the true relationship and a selection for that trait will be effective. If the final correlation coefficient is positive, but the direct effect is negative or negligible, in such relations the indirect causal factors are to be considered simultaneously for selection. The residual effect determines how best the causal factors accounts for the variability of the dependent factor.

The genotypic correlation coefficients being more important, were only partitioned into direct and indirect effects which are presented in table 6.

4.3.1 Direct effect of independent traits on green forage yield

Leaf width exhibited highest positive direct effect (8.4470) on green forage yield followed by crude protein content (5.0533) and dry matter content (3.3570). On the other hand number of tillers per meter row length (-5.3403) showed highest negative direct effect on green forage yield followed by characters *viz.*, leaves per tiller (-4.9242), plant height (-3.4724), leaf length (-3.1188), leaf/stem ratio (-2.0425) and stem thickness (-1.8882).

Chaubey *et al.*, (2001) observed high direct effects of number of tillers and leaf width on green fodder yield. These results were in conformity with those obtained in the present investigation.

Kumar *et al.*, (2004) reported high direct effects of number of tillers per plant and plant height on green fodder yield. These results were in contrast to those obtained in the present investigation.

4.3.2 Indirect effect of different independent traits on green forage yield

4.3.2.1 Plant height at 50% flowering (cm)

Plant height showed negative direct effect of magnitude (-3.4724) on green forage yield. However its genotypic correlation with green forage yield was (0.4287**). It was due to high and positive indirect effect *via* leaf width (5.21) and crude protein content (2.31).

4.3.2.2 Number of tillers per meter row length

Number of tillers per meter row length exhibited negative direct effect of magnitude (-5.3403), however, it was significantly and positively associated with green forage yield (0.73**). This was due to high and positive indirect effects of number of tillers on green forage yield *via* crude protein content (3.33) and leaf width (3.09).

4.3.2.3 Number of leaves per tiller

Leaves per tiller exhibited negative direct effect (-4.9242), however it was significantly and positively associated with green forage yield. It was due to high and positive indirect effect of number of leaves per tiller *via* leaf width (3.88) and crude protein content (2.08).

4.3.2.4 Leaf length (cm)

Leaf length exhibited negative direct effect of magnitude (-3.1188). It showed positive indirect effect through leaf width (4.4562), dry matter content (0.2257), stem thickness (0.1376) and crude protein content (0.0448).

4.3.2.5 Leaf width (cm)

Leaf width exhibited highest positive direct effect of magnitude (8.4470), and also it was significantly and positively associated with green forage yield.

Table 6. Genotypic path coefficient of nine independent variables on green forage yield in forage oat

Sr. No.	Character	Plant height at 50 % flowering (cm)	Number of tillers per meter row length	Number of leaves per tiller	Leaf length (cm)	Leaf width (cm)	Leaf/stem ratio (L/S)	Stem thickness (mm)	Dry matter content (%)	Crude protein content (%)	Genotypic correlation with GFY
1.	Plant height at 50 % flowering (cm)	-3.4724	-0.9579	-2.3878	-0.6627	5.2087	0.4668	-0.9220	0.8420	2.3135	0.4282**
2.	Number of tillers per meter row length	-0.6229	-5.3403	0.5685	-0.0075	3.0950	0.5523	-0.5542	-0.2886	3.3319	0.7342**
3.	Number of leaves per tiller	-1.6838	0.6165	-4.9242	-0.2327	3.8808	0.0651	-0.4027	0.9497	2.0788	0.3475*
4.	Leaf length (cm)	-0.7378	-0.0128	-0.3673	-3.1188	4.4562	-0.4105	0.1376	0.2257	0.0448	0.2172
5.	Leaf width (cm)	-2.1412	-1.9567	-2.2623	-1.6453	8.4470	-0.2145	-0.6860	-0.5400	1.4707	0.4717**
6.	Leaf/Stem ratio	0.7936	1.4442	0.1569	-0.6268	0.8871	-2.0425	0.3924	0.4357	-1.7617	-0.3210*
7.	Stem thickness (mm)	-1.6956	-1.5674	-1.0501	0.2273	3.0687	0.4245	-1.8882	0.7895	2.2100	0.5186**
8.	Dry matter content (%)	-0.8710	0.4592	-1.3931	-0.2097	-1.3588	-0.2651	-0.4440	3.3570	0.6276	-0.0979
9.	Crude protein content (%)	-1.5897	-3.5210	-2.0256	-0.0277	2.4583	0.7120	-0.8258	0.4169	5.0533	0.6507**

Residual effect=1.4751, Bold figures indicate direct effect

*, ** = significant at 5 % and 1 % levels, respectively

4.3.2.6 Leaf/stem ratio

Leaf/stem ratio exhibited negative direct effect of magnitude (-2.0425), and also it was significantly and negatively associated with green forage yield (-0.3210*)

4.3.2.7 Stem thickness (mm)

Stem thickness exhibited negative direct effect of magnitude (-1.8882). However, its association with green forage yield was significant and positive (0.5186**). This was due to high and positive indirect effects of stem thickness on green forage yield *via* leaf width (3.07) and crude protein content (2.21).

4.3.2.8 Dry matter content (%)

Dry matter content had high and direct effect (3.3570) on green forage yield. However, its association with green forage yield was negative and non significant. This was due to high and negative indirect effects *via* number of leaves (-1.39) and leaf width (-1.36).

4.3.2.9 Crude protein content (%)

Crude protein content recorded high and positive direct effect (5.033) on green forage yield. Its association with green forage yield was also positive and significant. Indirect effect of crude protein content *via* leaf width was high and positive (2.4583).

4.4 Diversity

Genetic divergence, which is due to genetic factors, is the basis for heritable improvement. The plant breeders have always therefore, been fascinated by great amount of diversity in crop plants as could serve as raw material for crop improvement program. The precise information about the genetic divergence is therefore, crucial for effective breeding programme. The genetically diverse parents are known to produce higher heterotic effects and consequently give desirable recombinants in the breeding material. D^2 statistic proposed by Mahalanobis (1936) is a measure that appraises the genetic diversity quantitatively among a set of genotypes.

The aim of cluster formation and measuring inter and intra cluster divergence is to provide the basis for selection of parents for hybridization

programme. The theoretical concept behind such grouping is that, the genotypes grouped into the same cluster presumably are less diverse from each other than those belonging to the different clusters and will not give expected desired heterotic response and segregants in further generations.

Consequently tentative parents are selected from different clusters with wider genetic diversity. Therefore the criterion for parent selection should be high inter cluster distance, high *per se* performance and high cluster mean for the character under consideration.

4.4.1 Cluster formation

The cluster formation was done by following Tocher's method, as described by Rao (1952). All the twenty seven genotypes studied were grouped into six clusters (Table 7). Cluster I with ten genotypes emerged as the largest cluster followed by Cluster II and cluster III with seven genotypes each. Cluster IV, V and VI were solitary clusters.

Table 7. Grouping of twenty seven oat genotypes into different clusters by Tocher's method

Cluster No.	Number of Strains	Genotypes included in the cluster
I	10	ROG-15-9, ROG-15-17, ROG-15-18, Kent, ROG-15-23, ROG-15-14, ROG-15-2, ROG-15-20, ROG-15-6, ROG-15-16
II	7	ROG-15-4, ROG-15-7, ROG-15-8, ROG-15-21, ROG-15-10, ROG-15-5, ROG-15-22
III	7	ROG-15-3, ROG-15-11, RO-19, ROG-15-24, ROG-15-12, ROG-15-19, ROG-15-13
IV	1	ROG-15-15
V	1	RO-11-1
VI	1	ROG-15-1

Prasad *et al.*, (2003) grouped 247 oat genotypes into sixteen clusters. Kumar *et al* (2005) grouped 100 oat germplasm lines into nine clusters. Singh and Singh (2010) grouped seventy oat genotypes into seven clusters. Ahmed *et al.*, (2011)

grouped seventy five exotic and indigenous oat germplasm lines into nine clusters. Jaipal and Shekhawat (2016) grouped thirty oat genotypes into four clusters.

4.4.2 Intra and inter cluster divergence

The average intra and inter cluster D and D² values are presented in Table 8.

Table 8. Average intra and inter cluster distance (D) and (D²) values

Clusters	I	II	III	IV	V	VI
I	6.54 (42.77)	9.29 (86.30)	8.60 (73.96)	9.16 (83.90)	11.13 (123.87)	9.96 (99.20)
II		7.10 (50.41)	11.62 (135.04)	8.49 (72.08)	16.66 (277.55)	11.00 (121.00)
III			7.59 (57.60)	9.97 (99.40)	10.88 (118.37)	14.35 (205.92)
IV				0.00 (0.00)	16.06 (257.92)	13.79 (190.16)
V					0.00 (0.00)	15.18 (230.43)
VI						0.00 (0.00)

Bold figures denote intra cluster distance

Figures in parenthesis denote D² values

In respect of intra cluster distances, cluster III had the highest value (D=7.59) followed by cluster II (7.10) and cluster I (6.54).

The inter cluster distance (D) range from 8.49 to 16.66. The maximum inter cluster distance (D =16.66) was observed between cluster II and cluster V, followed by cluster IV and V (D = 16.06), cluster V and cluster VI (D = 15.18), cluster III and cluster VI (14.35).The minimum inter cluster distance (D= 6.54) was in cluster II and cluster IV.

4.4.3 Cluster mean

The cluster mean for ten characters studied are presented in table 9. On perusal of table 9, it was revealed that cluster II ranked first for two traits viz., leaf/stem ratio (0.72) and dry matter content (20.64). Cluster II also ranked second for number of leaves per tiller (6.70).

Table 9. Cluster means for ten characters in twenty seven genotypes of forage oat

Cluster No.	Plant height at 50% flowering (cm)	Number of tillers per m. row length	Number of leaves per tiller	Leaf length (cm)	Leaf width (mm)	Leaf/Stem (L/S) ratio	Stem thickness (mm)	Green forage yield kg/m row length	Dry matter content (%)	Crude protein content (%)
I	105.86	91.90	6.45	44.58	2.07	0.48	21.98	1.50	20.14	7.19
II	108.29	71.21	6.70	43.55	2.09	0.72	19.50	1.03	20.64	6.12
III	124.64	104.71	6.41	48.16	2.56	0.61	26.04	2.04	20.50	7.23
IV	133.00	58.00	6.20	52.10	2.61	0.43	31.90	1.59	20.19	6.01
V	118.10	107.50	7.40	37.40	2.27	0.25	25.80	2.59	20.38	7.80
VI	98.50	85.00	4.70	29.00	1.58	0.39	17.50	0.58	19.94	5.80
Population mean	115.23	86.38	6.31	35.20	2.19	0.48	23.78	1.55	20.29	6.69

Cluster III exhibited second highest cluster mean for the characters viz., plant height, number of tillers per meter row length, leaf width, leaf/stem ratio, stem thickness, green forage yield, dry matter content and crude protein content.

Cluster IV ranked first for four characters namely, plant height at 50 % flowering (133.00), leaf length (52.10), leaf width (2.61) and stem thickness (31.90).

Cluster V recorded highest cluster means for traits viz., number of tillers per meter row length (107.50), number of leaves per tiller (7.40), green forage yield (2.59) and crude protein content (7.80).

4.4.4 Per cent contribution of various characters for divergence

The per cent contribution of ten characters on genetic divergence is presented in table 10. Green forage yield contributed maximum (23.93%) for divergence followed by leaf/stem ratio (20.80 %), leaf length (14.81 %), plant height (13.39 %), crude protein content (12.25 %), tillers per meter row length (5.70 %), stem thickness (4.27 %), dry matter content (2.85 %) and leaf width (1.99 %).

Table 10. Per cent contribution of ten different characters to genetic diversity in forage oat

Sr. No.	Character	Number of times appearing I in ranking	% contribution
1.	Plant height (cm)	47	13.39
2.	Tillers per m. row length	20	5.70
3.	Leaves per tiller	0	0.00
4.	Leaf length (cm)	52	14.81
5.	Leaf width (cm)	7	1.99
6.	Leaf/stem (L/S) ratio	73	20.80
7.	Stem thickness (mm)	15	4.27
8.	GFY (kg/m row length)	84	23.93
9.	Dry matter (%)	10	2.85
10	Crude protein (%)	43	12.25
11.	Total	--	100.00

Based on cluster mean, *per se* performance and inter cluster distance, a tentative hybridization programme for green forage yield improvement in oat is given below.

1. RO-11-1 x ROG-15-3
2. RO-11-1 x ROG-15-11
3. RO-11-1 x ROG-15-19
4. RO-11-1 x RO-19
5. RO-11-1 x ROG-15-24

4.5 Morphological performance in oat

The twenty seven genotypes of forage oat were classified into different categories for eight morphological characters. The results are presented in table 11.

For plant growth habit twenty seven genotypes of forage oat were grouped into five categories *viz.*, erect (0), semierect(9), intermediate(7), semiprostrate (11) and prostrate(0).

Twenty seven genotypes of oat were classified into into four categories for hairiness of sheath of lowest leaf *viz.*, strong (5), medium (11), low (7) and weak (4).

For hairiness of margins of leaf below flag leaf the morphological classification of oat genotypes was as below, very strong (5), strong (1), medium (5), weak (5) and absent (11).

All the twenty seven genotypes of oat were classified into two categories *viz.*, internode exposed (2) and internode covered (25).

For frequency of plants with recurved flag leaves twenty seven genotypes of forage oat were classified into four categories *viz.*, very high (31), high (0), medium (13) and low (11).

Twenty seven genotypes of oat were classified into into three categories for orientation of panicle branches *viz.*, unilateral (0), sub-unilateral (11), equilateral (16).

Table: 11 Data on eight morphological characters in twenty seven genotypes of forage oat

Sr. No	Genotype	Plant growth habit	Hairiness of sheath of lowest leaf	Hairiness of margins of leaf below flag leaf	Internode exposed/ covered	Frequency of plants with recurved flag leaves	Orientation of panicle branches	Attitude of panicle branches	Attitude of spikelets
1.	ROG-15-1	Semi erect	Medium	Absent	Covered	Low	Sub-unilateral	Semi erect	Pendulous
2.	ROG-15-2	Semi prostrate	Medium	Weak	Covered	Medium	Equilateral	Semi erect	Pendulous
3.	ROG-15-3	Semi erect	Weak	Very strong	Covered	Medium	Equilateral	Semi erect	Pendulous
4.	ROG-15-4	Intermediate	Weak	Medium	Covered	Very high	Sub-unilateral	Semi erect	Pendulous
5.	ROG-15-5	Semiprostrate	Medium	Absent	Covered	Medium	Sub-unilateral	Semi erect	Pendulous
6.	ROG-15-6	Intermediate	Medium	Strong	Covered	Low	Equilateral	Semi erect	Pendulous
7.	ROG-15-7	Semi erect	Low	Weak	Covered	Medium	Equilateral	Semi erect	Pendulous
8.	ROG-15-8	Semi prostrate	Low	Absent	Covered	Medium	Sub-unilateral	Semi erect	Pendulous
9.	ROG-15-9	Intermediate	Medium	Medium	Covered	Low	Sub-unilateral	Semi erect	Pendulous
10.	ROG-15-10	Intermediate	Low	Very strong	Covered	Medium	Equilateral	Semi erect	Pendulous
11.	ROG-15-11	Intermediate	Medium	Absent	Exposed	Very high	Equilateral	Semi erect	Pendulous
12.	ROG-15-12	Semiprostrate	Strong	Weak	Covered	Medium	Equilateral	Semi erect	Pendulous
13.	ROG-15-13	Semierect	Medium	Absent	Covered	Medium	Sub-unilateral	Semi erect	Pendulous
14.	ROG-15-14	Semierect	Weak	Very strong	Covered	Low	Equilateral	Semi erect	Pendulous
15.	ROG-15-15	Semiprostrate	weak	Medium	Covered	Medium	Sub-unilateral	Semi erect	Pendulous
16.	ROG-15-16	Semierect	Low	Absent	Covered	Low	Sub-unilateral	Semi erect	Pendulous
17.	ROG-15-17	Semiprostrate	Medium	Weak	Exposed	Medium	Equilateral	Semi erect	Pendulous
18.	ROG-15-18	Semiprostrate	Strong	Medium	Covered	Low	Equilateral	Semi erect	Pendulous
19.	ROG-15-19	Semierect	Strong	Very strong	Covered	Medium	Equilateral	Semi erect	Pendulous
20.	ROG-15-20	Intermediate	Low	Absent	Covered	Low	Sub-unilateral	Semi erect	Pendulous
21.	ROG-15-21	Semiprostrate	Low	Very strong	Covered	Low	Equilateral	Semi erect	Pendulous
22.	ROG-15-22	Semierect	Medium	Medium	Covered	Medium	Sub-unilateral	Semi erect	Pendulous
23.	ROG-15-23	Semoprostrate	Strong	Absent	Covered	Medium	Equilateral	Semi erect	Pendulous
24.	ROG-15-24	Semiprostrate	Medium	Absent	Covered	Low	Sub-unilateral	Semi erect	Pendulous
25.	RO-11-1	Semierect	Medium	Weak	Covered	Very high	Equilateral	Semi erect	Pendulous
26.	Kent	Intermediate	Low	Absent	Covered	Low	Equilateral	Semi erect	Pendulous
27.	RO-19	Semiprostrate	Strong	Absent	Covered	Low	Equilateral	Semi erect	Pendulous

All the twenty seven genotypes of oat were classified into five categories for attitude of panicle branches *viz.*, erect (0), semi-erect (27), horizontal (0), drooping (0) and strongly drooping (0).

All the twenty seven genotypes of oat were classified into two categories for character attitude of spikelets *viz.*, erect (0) and pendulous (27).

5. SUMMARY AND CONCLUSION

The present investigation entitled, “genetic diversity and path coefficient analysis in oat (*Avena sativa* L.) was conducted during *rabi* season of 2016-17 with the following objectives.

1. To study genetic diversity in oat.
2. To study direct and indirect effect of component traits on green forage yield (GFY) in oat.

Twenty seven genotypes of oat were evaluated in a Randomized Block Design with two replications and observations were recorded on ten characters *viz.*, plant height at 50% flowering (cm), number of tillers per meter row length, number of leaves per tiller, leaf length (cm), leaf width (cm), leaf/stem ratio(L/S), stem thickness (mm), green forage yield (kg/m. row length), dry matter content (%) and crude protein content (%). The genotypes were also classified into different sub categories for eight morphological characters.

5.1 Summary

5.1.1 Variability and genetic parameters

The range of variability, genotypic and phenotypic variances, genotypic and phenotypic coefficient of variation, heritability percentage and genetic advance as percentage of mean were worked out.

Treatment differences were found to be significant for all the characters studied except dry matter content.

High range was observed for green forage yield followed by leaf/stem ratio, whereas medium range was for stem thickness, leaf width, number of tillers per meter row length, leaf length, plant height and number of leaves per tiller. Dry matter content and crude protein content and dry matter content exhibited low range.

The estimates of genotypic as well as phenotypic coefficients of variances were higher for leaf stem ratio followed by green forage yield, stem thickness and leaf width. Seven characters *viz.*, plant height, number of tillers per

meter row length, leaf length, leaf width, leaf/stem ratio, stem thickness and green forage yield showed high estimates of heritability (b.s.) accompanied by high genetic advance as percentage of mean.

5.1.2 Correlation

Green forage yield was significantly and positively correlated with number of tillers per meter row length, crude protein content, stem thickness, leaf width, plant height and number of leaves per tiller. Leaf stem ratio showed significant negative correlation with green forage yield.

5.1.3 Path analysis

Leaf width exhibited highest positive direct effect on green forage yield followed by crude protein content and dry matter content. On the other hand number of tillers per meter row length showed highest negative direct effect on green forage yield followed by characters viz., leaves per tiller, plant height, leaf length, leaf/stem ratio and stem thickness.

5.1.4 Diversity

In the present investigation, the D^2 values between all possible pairs of twenty seven genotypes ranged between 42.77 and 277.50. The genotypes were grouped into six clusters, following Tocher's method as described by Rao (1952). Cluster I had maximum (10) number of genotypes followed by Cluster II and cluster III (with 7 genotypes each) while Cluster IV, V and VI were solitary.

The maximum intra-cluster distance was observed for cluster III followed by cluster II and cluster I.

The maximum inter cluster distance ($D = 16.66$) was observed between cluster II and cluster V, followed by cluster IV and V ($D = 16.06$), cluster V and cluster VI ($D = 15.18$), cluster III and cluster VI (14.35). The minimum inter cluster distance (8.49) was observed between cluster II and cluster IV.

Out of ten characters studied, the character green forage yield (23.93 %) contributed maximum for divergence followed by leaf/stem ratio (20.80 %), leaf length (14.81 %), plant height (13.39 %) and crude protein content (12.25 %).

5.2 Conclusion

5.2.1 Variability

The mean sum of squares due to genotype was highly significant for all the characters studied except dry matter content. A wide range of variability was observed for plant height, number of tillers per meter row length, leaf length, and stem thickness indicating sufficient amount of genetic variation among the genotypes under study.

Three characters *viz.*, leaf/stem ratio, stem thickness and green forage yield showed high estimates of GCV and PCV indicating ample variability for these characters.

Seven characters *viz.*, plant height, number of tillers per meter row length, leaf length, leaf width, leaf/stem ratio, stem thickness and green forage yield showed high estimates of heritability (b. s.) accompanied by high genetic advance as percentage of mean indicating these traits were predominantly govern by additive gene action and selection for these characters will be effective.

5.2.2 Correlation

The characters number of tillers per meter row length, crude protein content, stem thickness, leaf width, plant height and number of leaves per tiller showed significant positive genotypic correlation with green forage yield indicating their importance for indirect selection in green forage improvement programme.

5.2.3 Path analysis

The characters leaf width, crude protein content and dry matter content showed high positive direct effect on green forage yield.

Considering correlation coefficient and path analysis simultaneously, leaf width and crude protein content were found to be true components of green forage yield in oat and emphasis should be given on these characters for green forage improvement in the present set of forage oat genotypes.

5.2.4 Diversity

Twenty seven genotypes of oat were grouped into six clusters.

Based on cluster mean, *per se* performance and inter cluster distance, a tentative hybridization programme for green forage yield improvement in oat was suggested.

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7. VITAE

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