

# Genetic divergence, variability in oat

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The present investigation on ‘Genetic divergence in oat (*Avena sativa* L.)’ has been undertaken to integrate the genetic variability, heritability, genetic advance, correlation, path analysis and genetic divergence, so that better results may be obtained on yield and other contributing characters. Keeping in view this, the present investigation is aimed to following objectives: to estimate genetic variability, heritability and expected genetic advance; to analyze the inter-character associations between the various characters under study; to estimate direct and indirect effect of various component characters on forage yield through path analysis; and to study the genetic divergence among the genotypes of forage oat in order to facilitate the identification of genetically diverse parents.

**Key words:** *Avena* spp. Genetic advance, Genetic divergence, Genetic variability

OAT (*Avena sativa* L.) belongs to family Gramineae, Sub-class (Monocotyledons), Phylum (Spermatophyta). The genus *Avena* is large and diverse and contains both wild and cultivated species of polyploid series with basic chromosome number of  $\times = 7$ . Normally *Avena* comprises about 30 species, which are the diploids ( $2n=2 \times =14$ ), tetraploid ( $2n=4 \times =28$ ) and hexaploid ( $2n=6 \times =42$ ). All hexaploid *Avena* species belong to genus *Avena* and have genomic constitution of AACCCDD. The hexaploids oats *Avena sativa*, *Avena byzantina*, *Avena fatua* and *Avena sterilis* are inter fertile while the oat ( $2n=6 \times =42$ ) is a natural allopolyploid evolved through cycles of inter-specific hybridization and polyploidization or effective homology combining the three distinct genomes (AACCCDD) are *A. sterilis* and *A. fatua* share the same genome as that of *A. sativa* and *Avena byzantina* is closely related to *Avena sativa* and possibly derived through selection from the latter. The *A.*



*sativa* and *A. byzantina* are the main oats grown for fodder and grain while *Avena sativa* L. is more important cultivated crop and contributed over 80 % of the total world acreage. Oat grain mostly used as live-stock feed for dairy animals because it has more carbohydrate in its composition and it is also the good source of protein, fat, fibre, and minerals. Besides, oats are also the good source of calcium, magnesium, phosphorus and vitamin A, B<sub>1</sub>, B<sub>2</sub> and E. Livestock grain feed is still the primary use of oat crops, accounting for an average of around 74% of the

world's total usage in 1991 to 1992. Oat has been used as fodder and grain as it is a good source of protein, fibre and minerals. It is used as green crop, hay and silage for animal feed alone or in mixture feed to dairy cattle, horses, mules and turkeys, with lesser quantities feed to hogs, beef cattle and sheep. India is increasing on a fast-scale as oat meal, oat granola, baby food and breakfast cereal. Oats have adequate soluble carbohydrates to make good silage. Oat straw is good, palatable roughage and also excellent bedding. Oat in small bags is very popular in

hilly areas. Its forages comprise the largest component of the supplementary cereal forage markets. Oat grain is rich in some important nutrients including silicon, manganese, zinc, calcium, phosphorus and retinol (vitamin A), thiamine (vitamin B<sub>1</sub>), riboflavin (vitamin B<sub>2</sub>) and tocopherol (vitamin E).

D<sup>2</sup> - statistic as multivariate analysis is a powerful tool in the estimating genetic divergence in crop plants. Being a numerical estimate this method has an added advantage over other as it permits precise comparisons among all possible traits of population in a group and its commutation offers the automatic removal of the effects of correlations among the genetic variables involved to its efficiencies and usages. The utility of Mahalanobis's generalized distance D<sup>2</sup> is not only limiting factor for determining the degree of divergence in different populations but also for selecting genetically diverse parents for an efficient breeding programme. The experiment was conducted in *rabi* 2015-2016 at Crop Research Centre (Chirodi) of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U. P.), situated at an elevation of about 297 m above mean sea level with 29°01'N latitude and 77°75'E longitude, representing the north-western plain zone. The experimental material was consisted of thirty-eight diverse genotypes of oat (*Avena sativa* L.). The oat genotypes are given in Table 1.

The estimates of heritability in broad sense, expected genetic advance, genotypic and phenotypic coefficients of variability for the eleven characters under study. A comparative study of the genotypic and phenotypic coefficients of variation for most of the characters studies showed a relatively similar contribution of the genotypic variation in determining the phenotypic variation. The genotypic coefficient of variation ranged between 6.48 and 34.52 for days to 50% flowering and stem girth, respectively. The phenotypic coefficient of variation ranged between (7.58) to (34.61) for days to

**Table 1.** Genotypes of oats.

Sl. No.	Germplasm	Sl. No.	Germplasm	Sl. No.	Germplasm
1.	EC-246128	14.	UPO-201	27.	JHO-2004-1
2.	JHO 99-2	15.	UPO-240	28.	OL -125
3.	UPO -202	16.	EC- 246206	29.	JHO-2000-4
4.	UPO 2005-1	17.	Kent	30.	AOS- 1-1
5.	EC -1176404	18.	OS 7	31.	UPO -268
6.	JHO -851	19.	JHO -2002-7	32.	JHO- 2002-6
7.	EC 246198	20.	OS -6	33.	EC-576061
8.	EC -246184	21.	JHO-2001-1	34.	UPO- 276
9.	NDO 1	22.	UPO -272	35.	EC-246205
10.	EC -246199	23.	EC- 529095	36.	EC-246190
11.	UPO 94	24.	UPO -06-1	37.	JHO 2003-78
12.	JHO -822	25.	EC -246207	38.	EC-246197
13.	EC-2676176	26.	EC-246299		

50% flowering and stem girth, respectively.

All the characters under study showed high heritability (> 60%) for namely, days to 50% flowering (73.18), plant height (85.34), number of leaves per plant (92.23), flag leaf area (95.78), number of tillers per plant (96.84), stem girth (99.84), number of green pods per spike (94.37), length of spike (93.22), leaf stem ratio (97.40), dry fodder yield per plant (96.94) and green fodder yield per plant (97.64).

Expected genetic advance expressed as percentage of mean was observed high (>20%) for number of leaves per plant (27.96), stem girth (23.93), number of green pods per spike (20.45), leaf stem ratio (39.10), dry fodder yield per plant (36.75) and green fodder yield per plant (49.85), while, moderate (10-20%) genetic advance as percentage of mean was recorded for days to 50% flowering (11.42), plant height (19.30), number of tillers per plant

(10.57) and length of spike (15.74). Low genetic advance as percentage of mean (<10) was found for flag leaf area.

#### Estimation of correlation coefficient

Investigations were carried out with the experimental data to determine the coefficient of correlation at the phenotypic and genotypic levels at Sardar Vallabh Bhai Patel University of Agriculture and Technology, Modipuram . The inter-character phenotypic correlation coefficients are presented in Table 3. The significant and positive correlation of green fodder yield per plant was observed with plant height (0.37), flag leaf area (0.46), stem girth (0.53) and dry fodder yield per plant (0.40), while exhibited negative but non-significance correlation of green fodder yield per plant with days to 50% flowering (-0.08), number of green pods per spike (-0.05) and leaf stem ratio (-0.03) and showed positive but non-significant

**Table 2.** Estimates of variability parameters for eleven characters in oat (*Avena sativa* L.)

Characters	Heritability % (broad sense)	Genetic Advance	Genetic Advance (as %of mean)	GCV (%)	PCV (%)
Days to 50% flowering	73.18	10.91	11.42	6.48	7.58
Plant height	85.34	21.09	19.30	10.14	10.98
No. of leaves per plant	92.23	1.18	27.96	14.13	14.72
Flag leaf area (cm <sup>2</sup> )	95.78	9.72	8.08	18.89	19.30
No. of tillers per plant	96.84	4.04	10.57	25.94	25.99
Stem girth (mm)	99.80	21.18	23.93	34.52	34.61
No. of green pods per Spike	94.37	19.57	20.45	20.21	20.81
Length of spike (cm)	93.22	8.95	15.74	17.97	18.61
Leaf stem ratio (w/w)	97.40	20.15	39.10	29.07	29.46
Dry fodder yield per plant (g)	96.94	24.06	36.75	25.05	25.41
Green fodder yield per plant (g)	97.64	29.37	49.85	29.40	29.76

correlation of green fodder yield per plant with number of leaves per plant (0.06), number of tillers per plant (0.13) and length of spike (0.19). Days to 50% flowering revealed positive and significant correlation with plant height (0.31), number of leaves per plant (0.34), flag leaf area (0.26) and leaf stem ratio (0.27), positive and non-significant correlation with number of tillers/plant (0.09), number of green pods/plant (0.09) and length of spike (0.08) and non-significant negative association with stem girth (-0.07) and dry fodder yield/plant (-0.07). Plant height exhibited significant and positive correlation with flag leaf area (0.60), number of green pods per spike (0.45), leaf stem ratio (0.38) and green fodder yield per plant (0.37), positive but non-significant association with number of tillers per plant (0.18), stem girth (0.10), length of spike (0.07) and dry fodder yield per plant (0.06) and non-significant but negative correlation with number of leaves per plant (-0.12). Number of leaves per plant showed positive significant correlation with stem girth (0.28), non-significant positive correlation with dry fodder yield per plant (0.09)

and green fodder yield per plant (0.06) and negative non-significant association with flag leaf area (-0.03), the number of tillers/plant (-0.02), number of green pods/spike (-0.11), length of spike (-0.06) and leaf stem ratio (-0.04). Flag leaf area had positive significant correlation with number of tillers/plant (0.32), stem girth (0.24), length of spike (0.26), dry fodder yield/plant (0.49) and green fodder yield/plant (0.46), non-significant but positive correlation association with number of green pods/spike (0.04) and negative non-significant correlation with leaf stem ratio (-0.05). Number of tillers/plant noted positive significant association with stem girth (0.44) and length of spike (0.48), positive non-significant correlation with number of green pods/spike (0.09), leaf stem ratio (0.03) and green fodder yield (0.13) and negative non-significant correlation with dry fodder yield/plant (-0.02). Stem girth recorded positive significant association with number of green pods/spike (0.33), length of spike (0.39) and green fodder yield/plant (0.53), positive but non-significant correlation with leaf stem ratio (0.01) and dry fodder yield/plant (0.17). Number of green

Pods per spike reported positive significant association with length of spike (0.51) and leaf stem ratio (0.29), positive non-significant correlation with dry fodder yield/plant (0.01) and negative but non-significant correlation with green fodder yield/plant (-0.05). Length of spike was found positive significant association with leaf stem ratio (0.36) and positive but non-significant correlation with dry fodder yield/plant (0.08) and green fodder yield/plant (-0.19). Leaf stem ratio revealed positive significant association with dry fodder yield/plant (0.39) and non-significant negative correlation with green fodder yield/plant (-0.03). Dry fodder yield exhibited positive significant association with green fodder yield/plant (0.40).

The result obtained from the genotypic correlation coefficient for eleven characters under study are given in Table 3. An interpretation of this table is sought in conjunction with the phenotypic correlation coefficient to reveal the fact that values obtained were similar in direction but of a higher magnitude for most of the inter-character associations. Among genotypic

**Table 3.** Estimates of correlation coefficient for genotypic (G) and phenotypic (P) levels among different characters in oat (*Avena sativa* L.)

Characters		Days to 50% flowering	Plant height	No. of leaves per plant	Flag leaf area (cm <sup>2</sup> )	No. of tillers per plant	Stem girth (mm)	No. of green pods per spike	Length of spike (cm)	Leaf stem ratio (w/w)	Dry fodder yield per plant (g)	Green fodder yield per plant (g)
Days to 50% flowering	G	1.00	0.30**	0.32**	0.25**	0.04	-0.05	0.07	0.06	0.26**	-0.05	-0.04
	P	1.00	0.31**	0.34**	0.26*	0.09	-0.07	0.09	0.08	0.27**	-0.07	-0.08
Plant height	G		1.00	-0.11	0.59**	0.16	0.09	0.41**	0.05	0.36**	-0.08	0.36**
	P		1.00	-0.12	0.60**	0.18	0.10	0.45**	0.07	0.38**	0.06	0.37**
No. of leaves per plant	G			1.00	-0.01	-0.02	0.25**	-0.16	-0.05	-0.03	0.07	0.05
	P			1.00	-0.03	-0.02	0.28**	-0.11	-0.06	-0.04	0.09	0.06
Flag leaf area (cm <sup>2</sup> )	G				1.00	0.31**	0.22**	0.03	0.25**	-0.03	0.48**	0.45**
	P				1.00	0.32**	0.24**	0.04	0.26**	-0.05	0.49**	0.46**
No. of tillers per plant	G					1.00	0.43**	0.08	0.41**	0.02	-0.02	0.12
	P					1.00	0.44**	0.09	0.48**	0.03	-0.02	0.13
Stem girth (mm)	G						1.00	0.30**	0.30**	0.01	0.17	0.51**
	P						1.00	0.33**	0.39**	0.01	0.17	0.53**
No. of green pods per spike	G							1.00	0.49**	0.27**	0.05	-0.04
	P							1.00	0.51**	0.29**	0.01	-0.05
Length of spike (cm)	G								1.00	0.30**	0.04	0.12
	P								1.00	0.36**	0.08	0.19
Leaf stem ratio	G									1.00	0.37**	-0.02
	P									1.00	0.39**	-0.03
Dry fodder yield per plant (g)	G										1.00	0.39**
	P										1.00	0.40**
Green fodder yield per plant (g)	G											1.00
	P											1.00

\*,\*\*significant at 5% and 1% level, respectively

correlation the green fodder yield/plant showed positive and significant correlation with plant height (0.36), flag leaf area (0.45), stem girth (0.51) and dry fodder yield/plant (0.39), while exhibited negative but non-significance correlation of green fodder yield/plant with days to 50% flowering (-0.04), number of green pods/spike (-0.04) and leaf stem ratio (-0.02) and revealed positive but non-significant correlation of green fodder yield/plant with number of leaves/plant (0.05), number of tillers/plant (0.12) and length of spike (0.12).

### Studies on genetic divergence

The major task before the plant breeder lies in the selection of suitable parents to obtain superior heterotic combinations. However, it would be important to select the most suitable and genetically diverse parents, unless it has been provided with necessary information with respect to genetic variability and genetic divergence present in the base population. In the hybridization programme, diversity of the parental material is emphasized, because crosses between genetically divergent parents would be more suitable for obtaining appreciable improvement, as they are likely to yield desirable recombinants in the segregating generations. Generally, phenotypic or geographic diversity is considered as a measure of genotypic diversity. This being an inferential criterion may not be so effective in differentiating between populations occupying ecological marginal habitats. Multivariate analysis by means of Mahalanobis (1936) and as described by Rao (1952),  $D^2$  statistics is a powerful tool in quantifying the degree of divergence among biological population. The importance of Mahalanobis  $D^2$  analyses, to assess the genetic diversity, has been recognized by various workers in different crops. In the present study the group constellation and cluster formation analysis was given by Ward (1963). Comparison of these methods with large number of character revealed the superiority and consistency of  $D^2$  analysis, canonical and factor analysis

which are complementary to each other. However, usefulness of  $D^2$  measure of genetic diversity depends on the degree of its stability over different environment. It has been found that geographical distribution and genetic diversity as estimated by the  $D^2$  statistics could be directly related in the number of crop plant with different breeding system. In the present study thirty-eight genotypes of oat were subjected to  $D^2$  analysis using eleven component characters. Consequently eight clusters were formed. From the pattern of clustering it could be inferred that sufficient divergence was present to enable the formation of individual clusters. The clustering pattern is suggestive of the fact that geographic diversity is not efficient index of genetic diversity. Therefore, Mahalanobis  $D^2$  analysis of quantitative traits is a powerful tool for measuring genetic divergence among the material selected even from the same geographic region. The per cent contribution of green fodder yield per plant have maximum contribution to divergence followed by days to 50% flowering, plant height, dry fodder yield per plant, number of leaves per plant, number of tillers per plant and length of spike contributed most towards genetic divergence. Remaining characters contributed very little or did not contribute at all towards genetic divergence. Out of the 8 clusters, cluster I had 7 genotypes, cluster II had 7 genotype, cluster III had 8 genotypes, cluster IV had 5 genotype, cluster V had 4 genotype, cluster VI had 1 genotype, cluster VII had 1 genotype and cluster VIII had 5 genotypes. Based on present investigation, it was concluded that in general, there was parallelism between genetic and geographic diversity.

The intra-cluster distance among various clusters exhibited maximum intra-cluster distance for cluster III (7.04) and lowest intra-cluster distance was recorded for cluster I (2.69). Hence, the entries of cluster III (NDO-1, Kent, OS 7, JHO-2001-1, UPO 272, AOS 1-1, UPO 268 and JHO-2002-6) with high intra-cluster distance may be used for

making crosses with each other to get the better recombinants and superior hybrids for the green fodder yield improvement in oats. The maximum intra-cluster distance was because of wide genetic diversity among its genotypes. The chance of developing good segregates by crossing the genotypes of the same cluster showing low value for intra-cluster distance are very low. Therefore, it would be logical to attempt crosses between the genotypes of clusters separated by larger inter cluster distances. The little diversity and selection of parents within the cluster having higher mean for a particular character may also be useful for further developing high yielding oat varieties.

In the present study, the maximum inter-cluster distance was revealed between cluster III and II (10.66) followed by cluster IV and III (8.67), cluster VII and VI (8.51), cluster VI and V (7.88), cluster V and IV (7.70), cluster VIII and VII (7.67) and cluster V and cluster III (7.32). This indicates that the genotypes included in this clusters are having broad spectrum of genetic diversity and could very well be used in hybridization programme of oat for improving fodder yield. The least inter-cluster distance was between clusters II and I (0.02) followed by cluster III and I (0.07) and cluster VI and I (1.64). The lowest inter-cluster distances indicated that the genotype of these clusters had close relationship and hence, may not be emphasized upon to be used in hybridization programme.

Crosses suggesting parents belonging to most divergent clusters would be expected to manifest maximum heterosis and also wide variability of genetic architecture. Thus the crosses between the genetically diverse genotypes of cluster VII characterized by higher number of tillers per plant, stem girth and green fodder yield per plant with genotype EC-2676176 and cluster VI characterized by higher plant height, number of leaves/plant, flag leaf area, number of tillers/plant, leaf stem ratio, dry fodder/plant and green fodder yield/plant with genotype like EC-246128

is expected to exhibit high heterosis and are also likely to produce new combinants with desired traits. Similarly UPO-2005-1, EC-1176404, JHO-581 and EC-246198 genotypes constituting cluster V which exhibited excellence for days to 50% flowering, stem girth, number of green pods/spike and length of spike could be crossed with EC-246128 and EC-2676176 may be rewarding and effective in the oat improvement programme. Hence, the above genotypes can be utilized in further breeding programme in which the characters number of tillers per plant and green fodder yield/plant will be considered for selection to achieve the best result of the breeding programme. Based on the genetic diversity and superiority with respect to any of the traits the genotypes may be identified and may be involved in crossing for obtaining high heterotic population, segregants and also may be exploited for development of hybrids in oats.

### SUMMARY

The analysis of genetic divergence

through Mahalanobis  $D^2$  statistics showed considerable genetic diversity among genotypes. The thirty-eight genotypes were grouped into 8 clusters. The III (8 genotypes), I (7 genotypes) and II (7 genotypes) cluster having the maximum number of genotypes. This envisaged that the genotypes grouped within a particular cluster were more or less genetically similar to each other and apparent wide diversity was mainly due to the remaining genotypes distributed over rest of the other clusters.

Per cent contribution and expression of characters towards the genetic divergence play an important role in selecting the superior genotypes among diverse genotypes. Green fodder yield per plant had maximum contribution towards the genetic divergence followed by days to 50% flowering, plant height, dry fodder yield per plant, number of leaves per plant, number of tillers per plant and length of spike. Remaining traits showed very low contribution per cent towards the genetic divergence. Maximum intra-cluster distance was recorded in III indicating

greater genetic divergence between the genotypes belongs to these clusters and crosses involving genotypes viz., NDO-1, Kent, OS 7, JHO-2001-1, UPO 272, AOS 1-1, UPO 268 and JHO-2002-6 are suggested. Crosses in the above combinations are expected to provide enough genetic variability to select high green fodder yielding and stable segregates in the segregating generations. Genetic divergence study suggested that crosses between the genotypes of cluster VI (EC-246128), cluster VII (EC-2676176) and genotypes of cluster V (UPO-2005-1, EC-1176404, JHO-851 and EC-246198) for getting better hybrid vigour in  $F_1$  or better hybrids and also for good recombinants in segregating population.

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## Attracting and Retaining Youth in Agriculture (ARYA)

Realizing the importance of rural youth in agricultural development especially from the point of view of food security of the country, ICAR has initiated a program on "Attracting and Retaining Youth in Agriculture.

The objectives of ARYA project are:

- (i) To attract and empower the youth in rural areas to take various agriculture, allied and service sector enterprises for sustainable income and gainful employment in selected district;
- (ii) To enable the farm youth to establish net work groups to take up resource and capital intensive activities like processing, value addition and marketing; and
- (iii) To demonstrate functional linkage with different institutions and stakeholders for convergence of opportunities available under various schemes/program for sustainable of youth.

ARYA project will be implemented in 25 states through KVKs, one district, 200-300 rural youth will be identified for their skill development in entrepreneurial activities and establishment of related micro-enterprise units in the area of Apiary, Mushroom, Seed processing, Soil testing, Poultry, Dairy, Goatry, Carp-hatchery, Vermi-compost etc. KVKs will involve the Agricultural Universities and ICAR Institutes as technology partners. At KVKs also one or two enterprise units will be established so that they serve as entrepreneurial training units for farmers. The purpose is to establish economic models for youth in the villages so that youths get attracted in agriculture and overall rural situation is improved.

The trained youth groups will function as role model for other youths and will demonstrate the potentiality of the agri-based enterprises which will help in improving their confidence levels and encourage them to pursue farming as profession, generate additional employment opportunities to absorb under employed and unemployed rural in secondary agriculture and service related activities in rural areas.