

GENETIC DIVERGENCE ANALYSIS OF MORPHOLOGICAL TRAITS IN OAT (*AVENA SATIVA* L.)

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(Received : 19 October 2019; Accepted : 28 December 2019)

SUMMARY

A total of twenty five genotypes were characterized according to twenty morphological and seed traits. The genotypes differed significantly for most of the traits and relatively wide range of mean for all traits indicated the presence of variation among the tested genotypes. High phenotypic and genotypic coefficient of variation, high heritability coupled with genetic advance as percent of mean based on pooled analysis revealed for seedling dry weight per plant and seed vigour index. Seed yield per plant was showed positive and significant correlation with harvest index, biological yield per plant, dry weight per plant, number of reproductive tillers per plant leaf width, test weight, plant height and number of seeds per main spike, while negative significant with days to flowering and days to maturity at both phenotypic and genotypic levels. High positive direct contribution of biological yield per plant followed by number of leaves per plant, seed germination, spike length, leaf length, harvest index, biomass yield per plant, days to flowering seedling dry weight per plant and number of reproductive tillers per plant simple selection could be effective for these traits. The Cluster with higher number of lines means had low genetic diversity and they are more closely related. Highest intra cluster distance was observed for cluster I and maximum inter cluster distance was observed between cluster I and III indicates that the genotypes included in these clusters are having broad spectrum of genetic diversity and could very well be used in hybridization programme of oat for improving seed yield. Whereas the minimum average inter cluster *D2* value was recorded between cluster III and II. The lowest inter cluster distances indicate that the genotype of these clusters had close relationship and hence, may not be emphasized upon to be used in hybridization programme. The genotypes viz; JHO 03-91, SKO 105, CSAOFSC 14-6, SKO 101, JHO 2007-1, NDO 612 and JHO 851 and cluster III characterized by days to maturity, leaf width, number of nodes per plant number of leaves per plant, biological yield per plant, dry weight per plant and spike length with genotypes namely; CSAOFSC 11-5, CSAOFSC 11-1, CSAOFSC 12-1, UPO 212, CSAOSC 12-1 and OS 403 were expected to exhibited high heterotic performance and are also likely to produce new recombinants with desired characters to get desirable segregates with higher seed yield for developing superior variety of oat.

Key words : Oats, correlation, path analysis, genetic divergence, forage yield

The common oat (*Avena sativa* L.) is a cereal crop grown primarily for its grains. Oats are suitable for human consumption and also used as livestock feed and fodder in forms of green and dry fodder. This crop has three naturally occurring ploidy levels are known within the genus, like diploid ($2n=2x=14$ having A and C genome), tetraploid ($2n=4x=28$ with AB and Ac genome) and hexaploid ($2n=6x=42$ containing ACD genome) and belongs to family poaceae (Loskutov, 2008). Being important feed and fodder crop, it is now gaining importance due to its unique and important quality characteristics, particularly the lipid and protein in grains. Green fodder contains about 10 to 13% crude protein content and 25 to 30% dry

matter. Oat grains are known for rich nutritional profile and well known cereal food for human beings and feed for livestock. In India it is grown in Punjab, Haryana, Jammu & Kashmir, Himachal Pradesh, Uttar Pradesh, Madhya Pradesh, Rajasthan, Maharashtra and West Bengal. The total area covered under oat cultivation 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%) (IGFRI, 2019). Quantitative genetics is important for genetic breeding. Identification, accumulation and perpetuation of favorable genes for quantitative traits may be facilitated if the selection is based on variance

components and genetic parameters. In this way, genetic parameters allow to identify the action nature of involved genes, as well as evaluating the efficiency of different selection methods and strategies, whether from endogamy, cross-breeding or selection (Cruz *et al.*, 2014). Phenotypic traits study makes it possible to estimate genetic parameters from genotypic components, while the magnitude of parameter estimates define the genetic properties of the population (Falconer 1989). Thus, in possession of these data, the breeder has more information for decision-making, increasing selection efficiency.

MATERIALS AND METHODS

The experiments were carried out at Students Instructional Farm of CSAUA&T, Kanpur over two growing Seasons of *Rabi* (2016-2017 and 2017-18). A total of twenty five genotypes collected from different geographical origins were evaluated in RBD with three replications. Each line was grown in a row of 4 meter length apart 30 cm line-line and plant to plant spacing of 10 cm. Recommended package of practices were followed to raise a good crop. The data was recorded on five randomly selected plants in each plot for twenty traits namely; days to 50% flowering, days to maturity, plant height (cm) numbers of reproductive tillers per plant, biomass yield per plant (g), leaf length (cm), leaf width (cm), number of leaves per plant, number of nodes per plant, spike length (cm), number of grains per spike, grain weight per main spike (g) 100 seed weight (g) biological yield per plant (g), harvest index (%), dry weight per plant (g), germination in percent, seedling length (cm), seedling dry weight (g), seed vigour index and seed yield per plant (g.) For analysis work computer software windostat was used which uses the following for further detailed analysis. Analysis of variance, heritability, GCV and PCV, Genetic advance, correlation, path coefficients and genetic divergence were calculated by formula of Panse and Sukhatme (1985), Fisher (1918), Burton (1952), Johnson *et al.*, (1955), Mahalanobis (1928) and (Dewey and Lu, 1959) Mahalanobis (1936) and Rao (1952) respectively.

RESULTS AND DISCUSSION

Genetic variability

The pooled analysis of variance for randomized completely block design with resopesc

to twenty five genotypes were exhibited significant differences among the genotypes used in the present study for all twenty characters studied, indicating the sufficient genetic variation among the genotypes for all the traits. The magnitude of PCV 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 20 characters studied seed vigour index, and seedling dry weight per plant showed high GCV and PCV. High heritability coupled with high genetic advance as percent of mean was observed for seed vigour index, seedling dry weight per plant, seedling length, test weight, biomass yield per plant and number of reproductive tillers per plant, which revealed that these traits might be under control of additive gene effects and therefore they are more reliable for effective selection Table 1. These results for some or more traits were conformity with the findings of the earlier scientists by Dumlupinar *et al.*, (2012), Krishna *et al.*, (2013), Vaisi *et al.*, (2013), Kumari *et al.*, (2013), Poonia *et al.*, (2017), Wagh *et al.*, (2018) Singh *et al.*, (2018), Pallavi *et al.*, (2018) and Gupta and Mehta (2019).

Character association

Association between various phenotypically traits and seed yield per plant was also worked out and presented in (Table 2). It is clear from the table that the pooled estimates of significant and positive correlation for seed yield per plant was shown by harvest index, biological yield per plant, dry weight per plant, number of reproductive tillers per plant leaf width, test weight, plant height, number of seeds per main spike and leaf length. High positive contribution shown by various traits might have a direct impact on seed yield per plant improvement in oat. While negative significant with days to flowering and days to maturity at both phenotypic and genotypic levels, indicating high degree of inter-relationship between two variables at genotypic and phenotypic levels. Similar results for one or more characters were reported by Dumlupinar *et al.*, (2012), Ahmed *et al.*, (2013), Ahmed and Kamaluddin (2013), Krishna *et al.*, (2013), Vaisi *et al.*, (2013), Poonia *et al.*, (2017), Wagh *et al.*, (2018) Singh *et al.*, (2018), Pallavi *et al.*, (2018) and Gupta and Mehta (2019). However, positive but non-significant correlation was showed by seedling length, seed germination, spike length, seed vigour index, number of leaves per plant and seedling dry weight per plant hence, simple selection

TABLE 1
Estimates of Phenotypic, Genotypic coefficients of variation, heritability and Genetic Advance in oat on based pooled

Characters	GCV (%)	PCV (%)	Heritability (%)	GA	GA as % mean
Days to 50% Flowering	1.48	1.53	93.54	2.59	2.95
Days to maturity	1.73	1.77	96.53	4.00	3.51
Biomass yield per plant (g)	11.63	13.22	77.32	34.70	21.06
Number of reproductive tillers per plant	10.23	11.08	85.14	2.34	20.44
Leaf length(cm)	7.11	8.17	75.79	5.02	12.76
Leaf width (cm)	7.69	8.58	80.35	0.25	14.19
Plant Height (cm)	3.75	3.95	90.11	9.23	7.34
Number of nodes per plant	4.57	5.96	58.86	0.38	7.22
Number of leaves per plant	5.12	6.63	59.68	0.45	8.15
Biological yield per plant (g)	4.93	5.16	91.50	1.11	9.72
Number of seeds per main spike	8.51	9.40	81.88	11.78	15.86
Dry weight per plant (g)	5.41	5.95	82.80	0.87	10.14
Test weight (g)	12.38	13.13	88.95	0.97	24.05
Harvest Index (%)	7.78	8.20	90.13	4.66	15.22
Spike Length (cm)	5.25	5.90	79.30	2.80	9.63
Seed germination in percent	1.96	2.02	94.32	3.25	3.92
Seedling length (cm)	15.90	16.60	91.81	6.52	31.39
Seedling dry weight per plant	25.46	27.43	73.20	0.01	41.36
Seed vigour index	25.90	26.39	89.06	0.96	48.41
Seed yield per plant (g)	7.05	7.47	89.07	0.48	13.70

more reliable for these characters. Positive correlation of a particular character with seed yield per plant does not necessarily mean a direct, positive effect of that trait on yield. Similar trend was also recorded from genotypic correlation (Table 3).

Path analysis

To overcome this, Path coefficient analysis measures the direct and indirect influence of a variable on the dependent trait and is an effective tool for selecting meritorious characters to be used in selection programmed to get maximum yield. Therefore, path coefficient analyses which analyses cause & effect relationships and partitions the correlation into direct and indirect effects were carried out. Path coefficient analysis (Table 4) showed that maximum amount of positive direct effect was exerted by biological yield per plant followed by leaves per plant, seed germination in percent, spike length, leaf length, harvest index, biomass yield per plant, seedling dry weight per plant, days to flowering, number of reproductive tillers per plant and test weight showed on seed yield per plant in oat. This positive effect on seed yield per plant as shown by above traits is supplemented further by the indirect affect of other traits. At genotypic level also the estimates of direct and indirect effects were generally similar to those showed at phenotypic level with little variation in magnitudes (Table 5). The magnitudes of residual effects at both genotypic and phenotypic levels were observed to be low at phenotypic and genotypic levels. These results for one or more traits are in agreement

with the earlier findings of Krishna *et al.*, (2013), Vaisi *et al.*, (2013), Poonia *et al.*, (2017), Wagh *et al.*, (2018) Singh *et al.*, (2018), Pallavi *et al.*, (2018) and Gupta and Mehta (2019), Negative direct effect on seed yield per plant was found to be highest in case of seed vigour index followed by days to maturity, seedling length, number of seeds per main spike, number of nodes per plant, leaf width, plant height and dry weight per plant. However there were indirect affect on seed yield per plant which ultimately contributes to direct affect on yield and indirect effect is imposed by biological yield per plant with positive direct effect revealed indirect positive effect for dry weight per plant. Number of seeds per main spike with positive direct effect showed indirect positive effect for test weight. Dry weight per plant with direct effect exhibited indirect positive effect for harvest index. Test weight with direct effect exhibited indirect positive effect for seed vigour index. Harvest index with direct effect exhibited indirect positive effect for seed germination in percent. Spike length with direct effect exhibited indirect positive effect for leaf width. Seed germination in percent with direct effect exhibited indirect positive effect for dry weight per plant. Seedling length with direct effect exhibited indirect positive effect for seed germination in percent. Seedling dry weight per plant with direct effect exhibited indirect positive effect for days to maturity. Seed vigour index with direct effect exhibited indirect positive effect for test weight and seed yield per plant with direct effect exhibited indirect positive effect for harvest index. So a selection for all these traits will helps in improvement of seed yield per plant. Similar results were also reported by

TABLE 2
Estimates of Phenotypic correlation coefficients in oat (*Avena sativa* L.) on based pooled

[illegible]

TABLE 3
Estimates of genotypic correlation coefficients in oat (*Avena sativa* L) on based pooled

[illegible]

TABLE 4
Estimation of Phenotypic path with seed yield per plant in oat based on pooled

Traits	DF	DM	FYTPP	NRTTP	LL	LW	PH	NNPP	NLPP	BYPP	NSPMS	DWPP	TW	HI	SL	SG	SLL	SLDWPP	SVI	SYPP
DF	0.024	0.034	0.001	-0.002	0.000	-0.002	0.000	0.004	-0.009	0.037	0.000	-0.002	-0.002	-0.022	-0.002	0.001	-0.001	-0.008	0.018	-0.227*
DM	0.012	-0.166	-0.001	-0.002	-0.001	0.002	0.000	0.016	-0.024	0.313	0.000	-0.006	-0.016	-0.214	0.005	0.012	0.000	0.022	-0.018	-0.268*
BYPP(g)	0.001	-0.005	0.112	0.000	0.000	0.001	0.001	-0.003	0.005	-0.093	0.000	-0.001	0.004	-0.092	-0.007	0.009	0.000	-0.002	0.007	-0.166
NRTTP	0.005	0.016	0.004	-0.008	-0.002	0.005	0.000	0.000	0.008	-0.027	0.000	-0.003	-0.003	-0.157	-0.007	-0.003	0.000	0.012	-0.011	0.372**
LL(cm)	0.001	-0.008	0.000	0.002	0.019	-0.013	0.003	-0.006	0.011	0.092	0.000	-0.002	0.001	0.021	0.014	0.009	0.000	-0.005	-0.004	0.324**
LW(cm)	0.001	-0.004	0.000	0.001	0.003	-0.037	0.000	-0.003	0.002	-0.040	0.000	0.000	0.004	0.127	0.020	-0.004	0.001	-0.017	0.015	0.364**
PH(cm)	-0.001	-0.001	0.001	0.001	0.004	-0.002	0.016	0.014	-0.015	-0.006	0.000	-0.002	-0.009	-0.176	0.009	0.014	0.000	0.009	-0.015	0.344**
NNPP	0.003	0.028	-0.001	0.000	-0.001	0.003	0.002	0.041	-0.054	0.161	0.000	-0.004	-0.007	-0.199	0.006	0.019	0.000	0.001	0.000	-0.003
NLPP	0.004	0.027	-0.001	0.001	-0.002	0.001	0.001	0.035	-0.063	0.081	0.000	-0.001	-0.008	-0.124	0.004	0.017	0.000	-0.001	0.003	0.025
NSPMS	-0.005	-0.007	-0.001	0.001	0.004	-0.015	0.003	-0.006	0.006	-0.095	-0.001	0.001	-0.004	0.097	0.014	0.000	0.000	0.011	-0.020	0.315**
DWPP	0.003	0.026	0.000	-0.001	0.001	-0.001	0.001	0.010	-0.004	0.402	0.000	-0.017	-0.012	-0.825	0.013	0.028	0.000	0.011	-0.012	0.379**
TW	-0.001	-0.027	0.001	0.001	0.000	-0.003	-0.001	-0.007	0.013	-0.126	0.000	0.005	0.043	0.284	0.003	-0.024	0.001	-0.056	0.065	0.368**
HI	0.000	-0.013	-0.001	0.001	0.000	-0.004	-0.001	-0.007	0.007	-0.276	0.000	0.013	0.011	0.110	-0.004	-0.022	0.000	-0.004	0.006	0.815**
SL(c)	-0.001	0.009	-0.002	0.000	0.003	-0.018	0.001	0.007	-0.006	0.107	0.000	-0.005	0.003	-0.099	0.040	-0.054	0.000	-0.024	0.024	0.048
SG(%)	0.000	-0.016	-0.002	0.000	-0.002	-0.003	-0.002	-0.014	0.020	-0.227	0.000	0.009	0.019	0.462	-0.007	-0.054	0.002	-0.026	0.036	0.195
SLL(cm)	-0.004	-0.002	0.001	0.001	0.001	-0.006	0.000	0.001	0.003	0.095	0.000	0.001	0.008	0.120	-0.004	-0.020	0.014	-0.009	0.010	0.199
SLDW(g)	0.002	-0.016	0.000	0.001	0.000	-0.007	-0.001	0.000	-0.001	-0.037	0.000	0.002	0.024	0.046	0.010	-0.015	0.000	-0.094	0.090	0.07
SVI	0.005	-0.013	0.001	0.001	0.000	-0.005	-0.001	0.000	-0.002	-0.054	0.000	0.002	0.027	0.071	0.010	-0.020	0.000	-0.086	0.098	0.034

Residual = 0.043.

TABLE 5
Estimation of genotypic path with seed yield per plant in oat based on pooled

Traits	DF	DM	FYTPP	NRTTP	LL	LW	PH	NNPP	NLPP	BYPP	NSPMS	DWPP	TW	HI	SL	SG	SLL	SLDWPP	SVI	SYPP
DF	0.074	-0.083	0.011	0.017	0.000	-0.001	0.002	-0.012	0.055	0.067	0.023	-0.001	-0.004	-0.006	-0.007	-0.003	0.025	0.007	-0.058	-0.304**
DM	0.040	-0.156	-0.015	0.015	-0.020	0.008	0.001	-0.058	0.168	0.459	0.013	-0.003	-0.023	-0.233	0.022	-0.067	0.004	-0.021	0.053	-0.386**
BYPP(g)	0.006	0.016	0.138	0.020	-0.013	0.012	-0.009	0.002	-0.006	-0.155	0.012	-0.001	0.007	-0.124	-0.042	-0.053	-0.014	0.000	-0.019	-0.177
NRTTP	0.020	-0.037	0.044	0.061	-0.033	0.013	0.004	0.011	-0.076	-0.056	0.014	-0.002	-0.003	-0.207	-0.033	0.014	0.017	-0.014	0.033	0.378**
LL(cm)	0.000	0.021	-0.012	-0.014	0.148	-0.042	-0.041	0.005	-0.045	0.145	-0.058	-0.001	0.001	0.038	0.072	-0.054	-0.021	0.001	0.022	0.382**
LW(cm)	0.001	0.014	-0.017	-0.008	0.067	-0.094	-0.007	0.002	0.024	-0.060	-0.052	-0.001	0.006	0.130	0.108	0.026	-0.026	0.019	-0.052	0.374**
PH(cm)	-0.002	0.002	0.001	-0.003	0.082	-0.009	-0.074	-0.042	0.085	0.001	-0.054	-0.001	-0.012	-0.196	0.045	-0.077	0.014	-0.007	0.053	0.354**
NNPP	0.009	-0.092	-0.003	-0.007	-0.007	0.001	-0.032	-0.099	0.289	0.374	0.019	-0.003	-0.012	-0.320	0.057	-0.139	-0.007	0.000	0.001	0.031
NLPP	0.013	-0.086	-0.003	-0.015	-0.022	-0.007	-0.021	-0.094	0.303	0.218	0.014	-0.001	-0.014	-0.189	0.050	-0.130	0.002	0.009	-0.014	0.026
BYPP	0.006	-0.090	-0.027	-0.004	0.027	0.007	0.000	-0.047	0.084	0.790	0.016	-0.006	-0.014	-0.589	0.030	-0.119	-0.024	-0.009	0.031	0.394**
NSPMS	-0.017	0.020	-0.016	-0.009	0.086	-0.048	-0.040	0.018	-0.043	-0.122	-0.101	0.000	-0.005	0.122	0.068	0.004	0.009	-0.008	0.068	0.325**
DWPP	0.012	-0.064	0.011	0.014	0.027	-0.009	-0.010	-0.035	0.046	0.625	0.006	-0.008	-0.018	-0.967	0.054	-0.157	0.012	-0.011	0.036	0.435**
TW	-0.005	0.065	0.018	-0.003	0.002	-0.010	0.017	0.021	-0.078	-0.203	0.010	0.002	0.055	0.362	0.013	0.138	-0.029	0.054	-0.215	0.373**
HI	0.000	0.032	-0.015	-0.011	0.005	-0.011	0.013	0.028	-0.050	-0.406	-0.041	0.006	0.017	0.147	-0.015	0.130	-0.019	0.006	-0.026	0.820**
SL(c)	-0.003	-0.020	-0.035	-0.012	0.064	-0.061	-0.020	-0.034	0.091	0.141	-0.041	-0.003	0.004	-0.101	0.166	-0.057	0.021	0.026	-0.084	0.068
SG(%)	-0.001	0.038	-0.026	0.003	-0.029	-0.009	0.020	0.049	-0.142	-0.337	-0.002	0.004	0.027	0.535	-0.034	-0.278	-0.055	0.026	-0.114	0.233*
SLL(cm)	-0.013	0.005	0.014	-0.007	0.022	-0.017	0.007	-0.005	-0.005	0.133	0.007	0.001	0.011	0.152	-0.024	0.109	-0.141	0.011	-0.035	0.224*
SLDW(g)	0.006	0.042	0.000	-0.011	0.002	-0.022	0.006	0.000	0.033	-0.091	0.010	0.001	0.037	0.089	0.055	0.092	-0.019	0.079	-0.287	0.036
SVI	0.015	0.028	0.009	-0.007	-0.011	-0.017	0.014	0.000	0.015	-0.084	0.024	0.001	0.040	0.104	0.048	0.109	-0.017	0.078	-0.291	0.057

Residual = 0.0056.

Krishna *et al.*, (2013), Vaisi *et al.*, (2013), Poonia *et al.*, (2017), Wagh *et al.*, (2018) Singh *et al.*, (2018), Pallavi *et al.*, (2018) and Gupta and Mehta (2019).

(d) Gene Divergence

The importance of genetic divergence for improving yield potential through hybridization has been emphasized and reviewed by Frey (1971). Although, it has been appreciated by breeders, the basic difficulty has always been reliable estimation of such diversity without making actual crosses Bhatt (1970). Ahmed *et al.*, (2011) studied clustering pattern in five germplasm lines of oat for yield and contributing traits using D² analyses. The D² analysis on morphological traits grouped the twenty five genotypes into four clusters based on distance ranges for the tree shown in Table 6. Days to 50% flowering showed highest mean for cluster number IV and lowest mean for cluster number II. Days to maturity exhibited highest mean for cluster number III and lowest mean for cluster number I. Biomass yield per plant exhibited higher mean for cluster number IV and lower mean for cluster number I. Number of reproductive tillers per plant exhibited highest mean for cluster number IV and lowest mean for cluster number II. Leaf length exhibited highest mean for cluster number II and lowest mean for cluster number IV. Leaf width exhibited highest mean for cluster number III and lowest mean for cluster number IV. Plant height exhibited highest mean for cluster number II and lowest mean for cluster number III. Number of nodes per plant exhibited highest mean for cluster number III and lowest mean for cluster number IV. Number of leaves per plant exhibited highest mean for cluster number III and lowest mean for cluster number IV. Biological yield per plant exhibited highest mean for cluster number III and lowest mean for cluster number I. Number of seeds per main spike exhibited highest mean for cluster number II and lowest mean for cluster number IV. Dry weight per plant exhibited highest mean for cluster number III and lowest mean for cluster number I. Test weight exhibited highest mean for cluster number I and lowest mean for cluster number III. Harvest index exhibited highest mean for cluster number I and lowest mean for cluster number III. Seed germination in percent exhibited highest mean for cluster number I and lowest mean for cluster number III. Seedling length exhibited highest mean for cluster number I and lowest mean for cluster number VI.

TABLE 6
Estimation of genetic divergence for twenty five genotypes in oat based on pooled Cluster mean

Clusters	DF	DM	FYTPP	NRTPP	LL	LW	PH	NNPP	NLPP	BYPP	NSPMS	DWPP	TW	HI	SL	SG	SLL	SLLDWPP	SVI	SYPP
I Mean	87.83	112.98	160.52	11.85	38.61	1.81	123.27	5.23	5.45	11.14	72.60	8.24	4.47	32.62	28.85	84.81	23.20	0.03	2.40	3.64
±SE	0.99	1.78	14.92	1.36	1.57	0.12	3.90	0.17	0.18	0.65	7.29	0.36	0.49	2.81	1.32	0.94	3.37	0.01	0.58	0.34
II Mean	87.40	113.58	164.26	10.67	42.89	1.76	132.67	5.33	5.60	11.40	82.37	8.41	3.92	31.42	29.32	82.30	21.09	0.02	1.84	3.58
±SE	2.03	2.52	23.37	1.43	2.83	0.17	1.06	0.27	0.35	0.37	7.44	0.36	0.51	1.81	0.99	1.31	2.91	0.00	0.34	0.20
III Mean	87.82	115.68	162.92	12.28	38.97	1.82	127.09	5.61	5.84	11.88	74.16	9.06	3.69	28.93	30.44	81.46	20.30	0.02	1.87	3.44
±SE	1.08	1.12	22.81	1.01	2.22	0.10	4.07	0.10	0.12	0.56	3.61	0.31	0.39	1.59	1.40	1.16	3.84	0.01	0.62	0.18
IV Mean	88.03	113.90	170.03	12.73	38.39	1.65	123.47	5.08	5.24	11.43	71.80	8.72	3.98	29.71	28.11	82.69	18.85	0.02	1.79	3.39
±SE	1.53	1.91	23.06	0.78	3.42	0.13	3.58	0.20	0.24	0.47	4.60	0.46	0.41	1.56	1.61	1.04	2.07	0.00	0.15	0.19

DF= Days to flowering DM= Days to maturity BYPP= Biomass yield per plant (g) NRTPP= Number of Reproductive Tillers per plant LL= Leaf length (cm) LW= Leaf width (cm) PH= Plant height (cm), NNPP= Number of Nodes per plant NLPP= Number of Leaves per plant BYPP= Biological yield per plant (g) NSPMS= Number of seeds per main spike DWPP= Dry weight per plant TW= Test Weight HI= Harvest Index (%) SL= Spike Length (cm) SG= Seed Germination (%) SLL= Seedling length (cm) SDWPP= Seedling dry weight SVI= Seed Vigour Index SYPP= Seed Yield per Plant (g).

TABLE 7
Distribution of twenty five genotypes in each clusters of oat based on pooled

SL.	Number of genotypes	Genotypes
I	7	JHO03-91, SKO105, CSAOFSC14-6, SKO101, JHO2007-1, NDO612, and JHO851
II	4	ANDO2, NDO25, OS6, JHO99-2
III	6	CSAOFSC11-5, CSAOFSC11-1, CSAOFSC12-1, UPO212 CSAOFSC12-1 and OS403
IV	8	CSAOFSC12-1, Kent, CSAOFSC11-4, ANDO1, OS344, OS1, JHO2007-2 and JHO03-93

Seedling dry weight per plant exhibited highest mean for cluster number I and lowest mean for cluster number IV. Seed vigour index exhibited highest mean for cluster number I and lowest mean for cluster number IV. Seed yield per plant exhibited highest mean for cluster number I and lowest mean for cluster number IV. Such clustering helps in selecting desirable individuals with specific traits for crossing programme. Similar results are in agreement with the earlier findings of Ahmed *et al.*, (2011), Poonia *et al.*, (2017), Wagh *et al.*, (2018) Singh *et al.*, (2018), Pallavi *et al.*, (2018) and Gupta and Mehta (2019). The D² analysis on morphological traits grouped the twenty genotypes into four clusters based on distance ranges. Cluster IV includes eight numbers of genotypes, Cluster I had seven, III six and II four genotypes Table 7. 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 I characterized by, biological yield per plant, test weight, harvest index seed germination, seedling length, seedling dry weight per plant, seed vigour index and seed yield per plant with genotypes *viz*; JHO 03-91, SKO 105, CSAOFSC 14-6, SKO 101, JHO 2007-1, NDO 612, and JHO 851 and cluster III characterized by days to maturity, leaf width, number of nodes per plant number of leaves per plant, biological yield per plant, dry weight per plant and spike length with genotypes namely; CSAOFSC 11-5, CSAOFSC 11-1, CSAOFSC 12-1, UPO 212, CSAOSC 12-1 and OS 403 were expected to exhibited high heterotic performance and are also likely to produce new recombinants with desired characters to get desirable segregates with higher seed yield for developing superior variety of oat. A crossing within this cluster will be of less use in improvement programme. Results of cluster analysis indicated that the highest intra cluster distance was observed for cluster I followed by cluster II, cluster IV and cluster III, indicating that genotypes in these cluster are relatively more diverse among themselves. The maximum inter cluster distance observed was between cluster I and III followed by cluster IV and II, cluster

I and II, cluster III and IV, cluster II and III and II and IV suggesting significant diversity among lines of these clusters. The inter cluster distances were higher than intra cluster distances suggesting presence of high genetic diversity between the genotypes of any two cluster than the genotypes present within the cluster (Table 8). So crossing between genotypes belonging to these clusters may result into high heterosis, which could be exploited in oat improvement. Studied the D² analyses in 25 oat genotypes and grouped into four clusters. Cluster IV was the largest and contained eight genotypes. The contribution of various characters towards the expression of genetic divergence is given in Table 9. It is clear from the table that days to 50%

TABLE 8
Estimation of inter and intra clusters distance for twenty five genotypes of oat (*Avena sativa* L) based on pooled

SL.	I	II	III	IV
I	3.842			
II	4.019	3.752		
III	4.866	3.776	3.400	
IV	3.775	4.149	3.956	3.454

TABLE 9
Contribution in percent of different characters in creating diversity in oat based on Mahalanobis's D₂ analysis

S. No.	Characters	% contribution
1.	Days to 50% Flowering	4.82
2.	Days to maturity	3.51
3.	Biomass yield per plant (g)	6.44
4.	Number of reproductive tillers per plant	6.02
5.	Leaf length(cm)	6.22
6.	Leaf width (cm)	4.23
7.	Plant Height (cm)	4.96
8.	Number of nodes per plant	5.07
9.	Number of leaves per plant	7.98
10.	Biological yield per plant (g)	2.83
11.	Number of seeds per main spike	5.52
12.	Dry weight per plant (g)	5.42
13.	Test weight (g)	5.04
14.	Harvest Index (%)	4.60
15.	Spike Length (cm)	5.70
16.	Seed germination in percent	3.50
17.	Seedling length (cm)	4.39
18.	Seedling dry weight per plant	6.20
19.	Seed vigour index	3.33
20.	Seed yield per plant (g)	4.21

flowering, days to maturity, biomass yield per plant, number reproductive tillers of per plant, leaf length, leaf width, plant height, number of nodes per plant, number of leaves per plant, biological yield per plant, number of seeds per main spike, dry weight per plant, test weight harvest index, spike length, germination in percent, seed ling length, seed ling dry weight per plant, seed vigour index and seed yield per plant have contribution more towards divergence, so the direct selection for these traits would be helpful.

CONCLUSION

Through agro-morphological techniques, valuable diversity was found among the genotypes for the traits of forage yield in most of the traits studied. the present study was found to be highly significant which shows that there was a great potential in these studied genotypes for the said traits, which can be used in future breeding programmes for selecting the promising genotypes.

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