

Estimation of Genetic Variability, Heritability, Genetic Advance and Character Association in Oat (*Avena sativa* L.) Genotypes for Fodder and Seed Yield Attributing Traits

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Abstract

With increasing population and health-related problems, more emphasis is given to substitutes for generally grown cereal crops. It is widely cultivated for forage purposes because of its high regenerating capability. Oat grain has tremendous health benefits. Therefore the study of variability and correlation among yield contributing traits becomes important. Keeping this in view, in the present research sixteen morphological traits were studied for fifty six diverse oat genotypes. The experiment was conducted in RCBD design during Rabi 2017-2018. Significant variation was seen for all the traits under study. High GCV and PCV were seen for most of the most of traits except plant height, days to 50% flowering, days to maturity. High heritability coupled with high genetic advance was observed for most of the characters viz., flag leaf length, leaf length, leaf width, leaf stem ratio, internode length, number of tillers plant⁻¹, peduncle length, axis length, number of spikelets plant⁻¹, seed yield plant⁻¹, 100-seed weight, green fodder plant⁻¹ and dry fodder plant⁻¹. Genotypes namely HFO-878, HFO-614, HFO-879 and HFO-707 showed good performance for both seed yield as well as green fodder yield. A study of variability, genetic advance, heritability and correlation will provide an opportunity for fruitful selection of the genotypes based on traits with high genetic advance and heritability and showing positive significant correlation with economic yield. Among the different traits which showed positive significant correlation with seed yield and green fodder yield, interestingly tillers plant⁻¹ showed positive significant correlation both.

Key words : Forage, grain, oat, correlation analysis, quality, additive gene action.

Oat is an important cereal crop cultivated for grain, pasture, forage or as a rotation crop. Because of its high fat, protein and mineral contents, oat is used both for human and cattle consumption. Oat is usually considered a secondary crop, i.e., a crop derived from a weed of the primary cereal domesticates wheat and barley (Zhou *et al.*, 1999). Oat originated in Asia Minor (Gibson and Benson, 2002). With increasing emphasis on food, health and nutritional security, oat has emerged as a crucial crop. It is a popular forage crop along with this; oat grain has potential health benefits.

Oat is largely used in cattle feeding and has occurred in the human diet for a long time, mainly as oatmeal and rolled oats. Oats are good source of protein, fibres and minerals. Most of the oat grain worldwide is consumed as animal

feed. Oat fodder, during the fodder deficit period, is also used as silage or hay to feed livestock instead of as green matter (Suttie and Reynolds, 2004). Oats are a fine source of several antioxidants such as vitamin E, phytic acid and phenolic compounds (Collins, 2011 and Poonia *et al.*, 2022). These phenolic compounds are antioxidants in nature which is health beneficial. In the country different types of varieties are being grown by the farmers based on their local environmental conditions. The seed storage proteins of oat are unlike those in wheat, barley and rye and do not contain immune-active fragments that may lead to the development of coeliac disease (CD) in genetically predisposed individuals (Londono *et al.*, 2013). All these benefits make it all the more important to study the variability of these characteristics.

The foremost step in the breeding programme is to assess the amount of variation present in the plant population that is used for crop improvement. Analysis of the genetic variability can be obtained using morphological measurements and phenotypic characterization (Greene *et al.*, 2008). The heritability measurement together with genotypic coefficient of variation would give an accurate idea about the extent of genetic advance that would be expected through simple selection (Burton 1952). High heritability, genetic advance and genotypic coefficient of variation give more precise data on the simple selection that would be valuable for improvement of seed yield per plant in oats genotype (Krishna *et al.*, 2013). Yield is a complex character and it is affected by many factors. Thus, to evaluate the relative importance of the component characters and to start an efficient selection programme, correlation studies are used.

Material and method

The field experiment was performed at the Forage Research Area of the Department of Genetics & Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar (Haryana) during the *Rabi* season of 2017-18. A total of fifty six oat genotypes, including two checks (KENT and UPO212) were investigated in RCBD design (Table 1). In the present research, sixteen morphological traits i.e. Plant height (cm), Number of days to maturity, Days to 50% flowering, Flag leaf length (cm), Leaf length (cm), Leaf width (cm), Leaf stem ratio, Internode length (cm), Number of tillers plant⁻¹, Peduncle length (cm), Axis length (cm), Number of spikelets plant⁻¹, Seed yield plant⁻¹ (g), 100 Seed weight (g), Green fodder plant⁻¹ (g), Dry fodder plant⁻¹ (g) were studied.

Results

The mean of squares due to genotypes were highly significant for all the characters studied as

shown in Table 2. The highest range was observed for green fodder yield followed by number of spikelets per plant, plant height, leaf length and peduncle length. The highest magnitude of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for leaf: stem ratio followed by dry matter yield. Other high category of PCV and GCV was seen for number of tillers plant⁻¹, seed yield plant⁻¹, 100-seed weight plant⁻¹, number of spikelets panicles⁻¹, green fodder yield. Low GCV and PCV were observed for

Table 1. List of fifty six different genotypes of oat used in the experiment

Name of genotype	Source	Name of genotype	Source
HFO809	CCSHAU, Hisar	HFO615	CCSHAU, Hisar
HFO810	CCSHAU, Hisar	HFO619	CCSHAU, Hisar
HFO815	CCSHAU, Hisar	HFO525	CCSHAU, Hisar
HFO816	CCSHAU, Hisar	HFO523	CCSHAU, Hisar
HFO832	CCSHAU, Hisar	HFO505	CCSHAU, Hisar
HFO852	CCSHAU, Hisar	HFO502	CCSHAU, Hisar
HFO862	CCSHAU, Hisar	HFO498	CCSHAU, Hisar
HFO867	CCSHAU, Hisar	HFO488	CCSHAU, Hisar
HFO874	CCSHAU, Hisar	HFO430	CCSHAU, Hisar
HFO876	CCSHAU, Hisar	HFO424	CCSHAU, Hisar
HFO878	CCSHAU, Hisar	HFO419	CCSHAU, Hisar
HFO879	CCSHAU, Hisar	HFO414	CCSHAU, Hisar
HFO883	CCSHAU, Hisar	HFO409	CCSHAU, Hisar
HFO885	CCSHAU, Hisar	OS346	CCSHAU, Hisar
HFO704	CCSHAU, Hisar	HF0503	CCSHAU, Hisar
HFO706	CCSHAU, Hisar	OS403	CCSHAU, Hisar
HFO707	CCSHAU, Hisar	OS377	CCSHAU, Hisar
HFO601	CCSHAU, Hisar	HFO267	CCSHAU, Hisar
HFO602	CCSHAU, Hisar	OS305	CCSHAU, Hisar
HFO603	CCSHAU, Hisar	HFO103	CCSHAU, Hisar
KENT	AUSTRALIA	DUNAV	BULGARIA
UPO212	GBPUAT, Pantnagar	JO-1	JNKVV, Jabalpur
HFO604	CCSHAU, Hisar	RO-19	CCSHAU, Hisar
HFO605	CCSHAU, Hisar	KALOGEN	BULGARIA
HFO607	CCSHAU, Hisar	ALGERIAN	ALGERIA
HFO610	CCSHAU, Hisar	PLP-1	CSKHPAU, Palampur
HFO611	CCSHAU, Hisar	HFO872	CCSHAU, Hisar
HFO614	CCSHAU, Hisar	HFO864	CCSHAU, Hisar

plant height, days to 50% flowering, days to maturity.

High heritability was observed for all the

traits under study. The estimates of high heritability coupled with high genetic advance were observed for most of the characters *viz.*, flag leaf length, leaf length, leaf width, leaf stem

Table 2. Analysis of variance for green fodder yield and its component characters

Source of variation	Mean sum of squares							
	Df	Plant height (cm)	Days to maturity	Days to 50% flowering	Flag leaf length (cm)	Leaf length (cm)	Leaf width (cm)	Leaf: Stem ratio
Replicate	2	898.63	3.60	4.86	318.35	220.31	0.61	0.00005
Treatments	55	280.63**	91.44**	50.81**	53.55**	116.43**	0.21**	0.0601**
Error	110	27.63	2.49	1.74	4.81	8.92	0.002	0.00023

Source of variation	Mean sum of squares							
	Df	No. of tillers plant ⁻¹	Peduncle length (cm)	Axis length (cm)	No. of spikelets panicle ⁻¹	Seed yield (g plant ⁻¹)	100-seed weight (g)	Green fodder yield (g plant ⁻¹)
Replicate	2	12.66	16.37	23.75	98.56	5.48	0.03	13.60
Treatments	55	10.17**	153.36**	53.91**	778.04**	79.76**	1.71**	3820.72**
Error	110	1.02	6.67	5.69	9.52	2.25	0.01	128.64

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

Table 3. Mean, range, coefficient of variation (GCV and PCV), heritability and genetic advance as % of mean for various characters in 56 genotypes of oat

Character	Mean	Range		Coefficient of variation (%)		Heritability broad sense (%)	Genetic advance as percent of mean
		Mini-mum	Maxi-mum	Mini-mum	Maxi-mum		
Plant height (cm)	102.84	73.20	123.27	8.93	10.29	75.32	15.97
Days to maturity	117.17	109.67	132.00	4.65	4.84	92.26	9.20
Days to 50% flowering	95.40	86.33	103.00	4.24	4.46	90.37	8.30
Flag leaf length (cm)	26.54	14.73	34.07	15.19	17.29	77.17	27.49
Leaf length (cm)	41.72	22.00	56.00	14.35	16.04	80.06	26.45
Leaf width (cm)	2.23	1.73	2.74	12.00	12.14	97.59	24.41
Leaf: Stem ratio	0.34	0.16	0.86	42.05	42.29	98.85	86.13
Internode length (cm)	23.40	16.00	34.33	13.98	17.40	64.60	23.15
Number of tillers plant ⁻¹	7.11	3.97	11.70	24.56	28.39	74.85	43.78
Peduncle length (cm)	38.77	24.40	56.53	18.04	19.23	87.98	34.85
Axis length (cm)	32.18	21.20	39.60	12.46	14.50	73.84	22.05
Number of spikelets panicle ⁻¹	59.31	33.83	110.67	26.99	27.48	95.41	54.59
Seed yield (g plant ⁻¹)	19.08	10.61	30.20	26.64	27.78	91.98	52.64
100-seed weight (g)	2.80	1.68	4.29	26.96	27.28	97.68	54.88
Green fodder yield(g plant ⁻¹)	149.85	99.00	238.33	23.41	24.61	90.53	45.89
Dry matter yield (g plant ⁻¹)	53.13	31.33	86.33	28.50	30.35	88.19	55.13

Table 4. Genotypic correlation among 16 traits studied for 56 oat genotypes

	TP	NOS	SY	GFY	DMY	AL	SI	DF	PH	DM	FLL	LL	LW	LS ratio	IL	PL
TP	1.00															
NOS	0.02	1.00														
SY	0.37**	0.36*	1.00													
GFY	0.33*	-0.12	0.08	1.00												
DMY	0.05	-0.01	0.08	0.34*	1.00											
AL	0.26	0.19	0.30*	0.18	0.25	1.00										
SI	0.07	0.36*	0.43**	0.00	-0.09	0.11	1.00									
DF	-0.21	-0.19	-0.36**	0.03	-0.12	-0.31*	-0.21	1.00								
PH	0.11	0.14	0.18	0.43**	0.65**	0.18	0.08	-0.17	1.00							
DM	-0.25	-0.04	-0.15	0.02	-0.04	-0.15	0.09	0.50**	0.06	1.00						
FLL	0.21	0.19	0.27*	0.09	0.06	0.27*	0.10	-0.30*	0.17	-0.14	1.00					
LL	0.29*	0.14	0.31*	0.19	0.18	0.31*	0.22	-0.04	0.16	0.12	0.18	1.00				
LW	0.08	0.26	0.21	-0.03	-0.07	0.24	0.03	0.14	-0.05	-0.06	0.07	0.20	1.00			
LS ratio	0.09	0.31*	0.24	-0.14	-0.02	-0.16	0.08	-0.23	0.05	-0.11	0.29*	0.14	0.07	1.00		
IL	0.03	0.12	0.17	0.25	0.09	0.11	0.15	-0.21	0.29*	-0.07	0.17	0.09	0.28*	0.07	1.00	
PL	0.26	0.03	0.13	0.04	0.09	0.41**	0.07	-0.39**	0.12	0.04	0.22	0.10	-0.06	0.18	0.09	1.00

** Significant at 1%, * Significant at 5%. (TP- Number of tillers plant⁻¹, NOS- Number of spikelets panicle⁻¹, SY-Seed yield (g plant⁻¹), GFY-Green fodder yield (g plant⁻¹), DMY- Dry matter yield (g plant⁻¹), AL- Axis length (cm), SI-100-seed weight (g), DF- Days to 50% flowering, PH-Plant height (cm), DM- Days to maturity, FLL- Flag leaf length (cm), LL- Leaf length (cm), LW- Leaf width (cm), LS ratio- Leaf:Stem ratio, IL- Internode length (cm), PL- Peduncle length (cm))

ratio, internode length, number of tillers plant⁻¹, peduncle length, axis length, number of spikelets plant⁻¹, seed yield plant⁻¹, 100-seed weight, green fodder plant⁻¹ and dry fodder plant⁻¹. However low genetic advance over percent mean was seen for traits including plant height, number of days to maturity and days to 50% flowering (Table 3).

Correlation coefficient analysis showed that traits namely 100-seed weight (0.43), number of tillers plant⁻¹ (0.37), number of spikelets plant⁻¹ (0.36), leaf length (0.31), axis length (0.30) and flag leaf length (0.27) had positive and significant correlation with seed yield. While days to 50% flowering (-0.36) had negative significant correlation with seed yield. (Table 4). It was further seen that green fodder yield was found significantly positive correlated with plant height (0.43), dry matter yield plant⁻¹ (0.34) and tillers plant⁻¹ (0.33). For dry matter yield high positive

significant correlation was with plant height (0.65). Other traits showing negative significant correlation was between axis length and days to 50% flowering (-0.31), days to 50% flowering and flag leaf length (-0.30), days to 50% flowering and peduncle length (-0.39). Graphical representation of scatter diagram, correlation coefficients and frequency distribution is depicted in Fig. 1 and 2.

Discussion

The study of analysis of variance clearly indicates that all the oat genotypes studied showed high variability for fodder yield and its component traits. The genotypes reveal a vast range of variation that is to be used for the selection of superior and desirable genotypes for further improvement and utilized through selection, hybridization, heterosis and combination breeding. The previously

researchers Shehzad *et al.* (2011); Cattivelli *et al.* (2011); Ahmed *et al.* (2011); Arora (2013); Krishna *et al.* (2013); Bind *et al.* (2016); Premkumar *et al.* (2017) and Singh *et al.* (2018) also reported a huge and usable variation in oat germplasm.

The phenotypic coefficient of variation (PCV) estimates was found higher than the genotypic coefficients of variation (GCV) for all the characters studied showing the effects of the environment on the expression of these characters. GCV along with heritability and genetic advance was significant as good estimates of genetic gain to be expected from the selection on a phenotypic basis. The plant selections based on phenotypic performance are showing high heritability and high genetic advance and signify the usefulness of the trait. Similar results for high GCV and PCV of traits were also reported by Singh and Singh (2011); Govindaraj *et al.* (2011) and Shekhawat and Jaipal (2016) for one or more characters.

The results for the characters having high heritability along with high genetic advance over mean underlines the scope for improvement through selection and signifies the presence of additive gene action. Shekhawat and Jaipal (2016) and Premkumar *et al.* (2017) reported high heritability with high genetic advance for various traits of green fodder yield and its component.

The highest positive significant correlation was seen between dry matter yield and plant height. Significant positive correlation was seen between dry matter yield and green fodder yield & between number of days to maturity and days to 50% flowering (Kumar *et al.*, 2016). Correlation coefficient analysis will help in knowing the association between the complex yield trait i.e. grain yield, green fodder yield and dry matter yield with other traits under study. These results will help in selection of genotypes

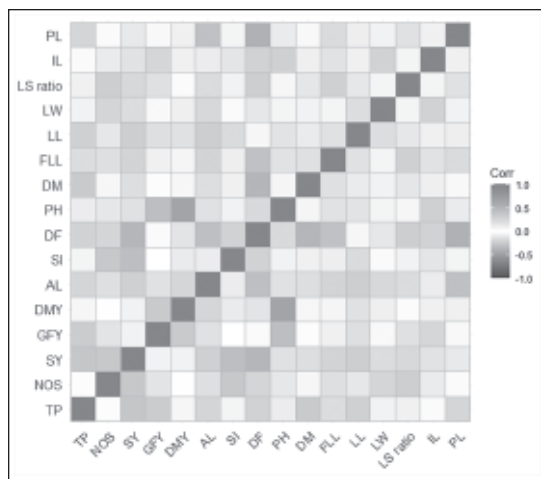


Fig. 1. Correlation plot depicting colour intensity proportional to significance of correlation coefficient among 16 traits

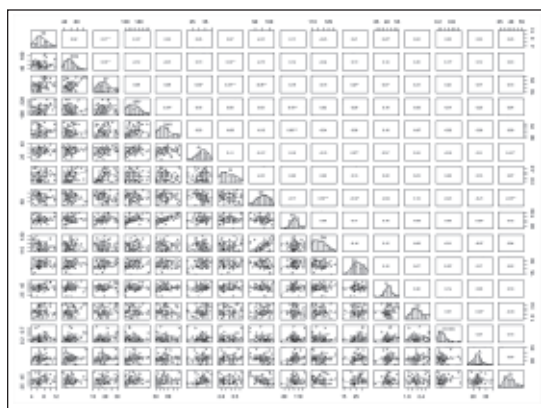


Fig. 2. Plot depicting correlation coefficient above the diagonal along with frequency distribution on diagonal and scatter diagrams below the plot among 16 traits for 56 oat genotypes

based on traits showing significant correlation with the economic yield trait. The results as shown above for the grain yield, green fodder yield and dry matter yield having significant positive correlation were seen in agreement with Chawla *et al.* (2021), Poonia *et al.* (2018), Premkumar *et al.* (2017), Poonia *et al.* (2017) and Nirmalakumari *et al.* (2013).

Best performing oat genotypes for yield trait : In single cut, the genotypes HFO-707, HFO-879, HFO-488, JO-I, KALOGEN, HFO-815, HFO-878, HFO-883, HFO-878, HFO-615, HFO-267, RO-19 and HFO-614 were recognized as valuable genotypes for green fodder yield while HFO-614, HFO-502, HFO-605, HFO-603, JO-I, RO-19, HFO-879, HFO-607, HFO-832, OS-377, and HFO-267, had high dry matter yield. The highest mean for seed yield (g plant⁻¹) was observed in the case of genotype, HFO-498. Genotypes namely HFO-878, HFO-614, HFO-879 and HFO-707 showed good performance for both seed yield as well as green fodder yield. Therefore these genotypes play significant role in oat crop improvement programmes to increase the yield for both seed and fodder.

Conclusion

The parameters such as heritability, PCV, GCV and genetic advance help in deciding the method of selection to improve a certain population for a specific trait. Significant variability among genotypes for all traits and high PCV and GCV signifies great diversity among the genotypes taken for study. Selection will be effective for all the traits except plant height, number of days to maturity and days to 50 per cent flowering. Among the different traits studied interestingly, tillers plant⁻¹ showed positive significant correlation with seed yield and green fodder yield both.

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