

## INTER-RELATIONSHIP OF GREEN FODDER YIELD WITH YIELD CONTRIBUTING AND QUALITY TRAITS IN *AVENA SATIVA*

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### SUMMARY

The present study was conducted for two years during **Rabi** season of 2010-2011 and 2011-12 with 25 diverse genotypes selected from wide range of germplasm being maintained at forage research farm, Punjab Agricultural University, Ludhiana. The genotypes were analysed with two years pooled data for genetic variability, correlation and path coefficients. High estimates of GCV and PCV were observed in many important traits suggesting that selection based on these characters would facilitate successful isolation of desirable types. High heritability along with high genetic advance (GA) was recorded for number of leaves/plant, leaf width (cm), number of tillers/plant, leaf area index, leaf stem ratio, crude protein (%), dry matter yield/plot (kg) and green fodder yield/plot (kg). Traits like plant height, number of leaves, leaf length, leaf width, number of tillers/plant, stem girth and dry matter yield had positive and significant correlation at genotypic as well as phenotypic level with green fodder yield and the selection based on these traits will result in improving the green fodder yield in oat. Two important quality traits viz; crude protein and *in vitro* dry matter digestibility manifested positive and significant correlation between each other but both were negatively correlated to green fodder as well as dry matter yield. Traits like plant height, number of leaves/plant, leaf width, leaf area index, leaf stem ratio, *in-vitro* dry matter digestibility and dry matter yield showed high direct effect on green fodder yield. Taller plants with more number of leaves and tillers/plant, broader leaves, will be significant for the improvement of green fodder yield in the material under study.

**Key words :** Genetic advance, genotypic coefficient of variation (GCV), heritability, phenotypic coefficient of variation (PCV), Green fodder yield components

In many parts of the world, oat is grown as multipurpose crop for grain, pasture and forage crop. It is considered to be one of the best dual purpose cereal crops that fit well into the platter of human and cattle as well. The great challenge for oat breeders lies in identifying the genetic make-ups that are superior in green fodder yield.

To reach this goal, the basic requirements are to have adequate information on the extent of variability, heritability, expected genetic gain and degree of genetic association among the different characters. Burton and Devane (1953) suggested that genotypic coefficient of variation (GCV) together with heritability estimates would give reliable indication about the expected improvement of a trait under consideration. However, it have reported the importance of using selection strategies, chiefly for quantitative traits, in highly segregating populations. Intensifying artificial selection for low heritability traits of difficult gene action estimation must be practised in advanced generations with reduced frequency of heterozygosity (Allard 1999). The indirect selection through less complex traits with

larger heritability, however, results in larger genetic progress when compared to direct selection. Considerable significance has been devoted to studies involving correlation of traits in breeding programs.

An attempt was, therefore, made to estimate the extent of variability for different green fodder yield contributing traits, magnitude and direction of association among different characters both at genotypic and phenotypic levels and to investigate the direct and indirect effects of yield components on green fodder yield.

The experiment was conducted for two years during **Rabi** season of 2010-11 and 2011-2012 with 25 diverse genotypes selected from wide range of germplasm being maintained at forage research farm, Punjab Agricultural University, Ludhiana. The plant material was grown in a Complete Randomized Block Design (CRBD) with three replications. The experimental plot comprised of ten rows of 5 m length. Row to row spacing was maintained at 30 cm and no plant to plant spacing was maintained as material was to be analysed for fodder related traits. Recommended package of practices to raise a good crop was followed.

Both the years, observations were recorded on five random plants selected from each entry on 14 quantitative variables viz; PH-plant height (cm), NOL-number of leaves/plant, LL-leaf length (cm), LW-leaf width (cm), NOT-number of tillers/plant, SG-stem girth (cm), LAI-leaf area index, LSR-leaf stem ratio, ADF-acid detergent fibre (%), NDF-neutral detergent fibre (%), CP-crude protein (%), IVDMD-*in-vitro* dry matter digestibility (%), DMY-dry matter yield plot<sup>-1</sup>(kg) and GFY-green fodder yield/plot (kg). The pooled data over two years were analysed for variability, divergence, correlation and path coefficient study. Genotypic and phenotypic coefficients of correlation were calculated from genotypic and phenotypic covariances and variances as described by Singh and Chaudhry (1985) and Johnson *et al.* (1955). Direct and indirect effects were calculated by the path coefficient analysis as suggested by Dewey and Lu (1959) at both phenotypic and genotypic levels. Genotypic and phenotypic coefficients were calculated using the formulae as used by Burton and De Vane (1953) and Johnson *et al.* (1955). Heritability in broad sense was estimated as suggested by Burton (1952). The expected genetic advance at 5% selection intensity was calculated by the formula as used by Johnson *et al.* (1955).

**Estimates of genetic variability :** It is evident from the range of mean values for different traits among the oat genotypes being evaluated (Table 1) that these had diverse genetic background. The traits like PH (85.1 – 121.8 cm), NOL (46.8 – 120 cm), LL (40.5 – 68.4 cm), NOT (11.2 – 28.9), LAI (7.0 – 27.2), ADF (29.9 – 39.6 %), DMY (13.9 – 32.2 kg) and GFY (38.5 – 92.0 kg) had wide range of mean values.

Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability ( $h^2$ ) and genetic advance as percent of mean (GA) are given in Table 1. Perusal of data revealed that PCV and the GCV were close for most of the traits except ADF (%), NDF (%), indicating primarily the genetic control for these traits rather the environment effect alone. Also high estimates of GCV and PCV were observed in NOL, NOT, SG, LAI, DMY and green GFY, suggesting that selection based on these characters would facilitate successful isolation of desirable types. However, the genetic variability together with heritability estimates would give a better idea on the amount of GA expected from selection (Burton, 1952). High values of GCV were reported for NOL, NOT, LAI, DMY and GFY in accordance with the results of Kapoor *et al.* (2011) and Vaisi *et al.* (2013). PH, LW, SG, LSR, ADF, NDF, CP and IVDMD had low GCV values indicating little scope of

genotypes for improvement in these traits. Surje and De (2014) also reported the low GCV values for traits like plant height, leaf width and stem girth, supporting our results.

High heritability along with high genetic advance (GA) was recorded for NOL, LW, NOT, LAI, LSR, CP, DMY and GFY. Surje and De (2014) also reported similar results for many of these characters. LL, SG, ADF and NDF had lower values of heritability. Traits having high heritability and high genetic advance are supposed to be under control of additive genes, hence, these can be improved by selection based on phenotypic performance (Ghosh and Gulati, 2001). Traits like PH and IVDMD had high  $h^2$  but low values of GA suggesting the involvement of non additive gene action in their inheritance. Traits like NOL, NOT, LAI, DMY and GFY exhibited high heritability coupled with high PCV suggesting greater scope for selection of these traits on phenotypic basis. Our results were also corroborated by the findings of Ahmad *et al.* (2013) and Surje and De (2014).

**Correlation coefficients :** The basic requirement of any selection programme is to ascertain the nature and magnitude of interrelationship between yield and its component traits, and also among the different traits. It was, therefore, considered imperative to carry out correlation studies for various quantitative traits that contributed to green fodder yield along with its quality. Green fodder yield is a complex character controlled by several components which reflect positive and negative effects on this trait. Yield components of fodder yield in cereals like oat consist chiefly of traits like PH, NOL, LL, LW and NOT (Ahmad *et al.* 2013). Thus, for achieving rational improvement in GFY and its components, knowledge of mechanism of association, cause and effect relationship provides a basis for formulating suitable selection methods for the yield components.

Results indicate that PH, NOL, LL, LW, NOT, SG and DMY had positive and significant correlation at genotypic as well as phenotypic level with GFY (Table 2) and the selection based on these traits will result in improving the GFY in oat. Ahmad *et al.* (2013) reported high and positive correlation between GFY and NOT, SG, DMY thus corroborating our findings.

LSR, LAI, CP and IVDMD exhibited a negative and highly significant correlation with GFY whereas ADF showed no correlation with GFY. Traits like PH, NOL, LL, NOT showed positive and highly significant correlation amongst each other except between SG, PH and NOL which showed significant negative correlation amongst each other. This was in accordance to the results obtained by These results

are in accordance with earlier findings of Singh and Singh (2011).

Two important quality traits viz; CP and IVDMD manifested positive and significant correlation between each other but both were negatively correlated to GFY as well as DMY. Another two quality parameters viz; ADF and NDF were found to be positively correlated to GFY as well as DMY. ADF and NDF were also negatively correlated to CP and IVDMD. The results are in agreement to those

obtained by and Sukhchain and Chaudhary (2012).

**Path coefficient analysis :** Partitioning of the total correlation coefficient into direct and indirect effects for green fodder yield plant<sup>-1</sup> showed a high direct effect of many yield contributing traits viz; PH, NOL, LL, LAI, LSR, IVDMD and DMY (Table 3). Surje and De (2014), Kakad *et al.* (2017) and Kumar *et al.* (2017) also observed high value of direct effect of these traits on GFY. Negative and high direct effect was

TABLE 1  
Estimates of genetic parameters for different traits in Oat

Characters	h <sup>2</sup> (%)	GA (%)	PCV	GCV	GM	Range	
						Minimum	Maximum
PH	31.91	6.43	9.78	5.53	101.52	85.1	121.8
NOL	92.60	39.90	20.92	20.13	82.69	46.8	120.0
LL	0.77	0.18	11.29	9.22	56.76	40.5	68.4
LW	18.04	5.19	13.96	5.93	2.08	1.6	2.5
NOT	92.72	50.66	26.52	25.54	19.27	11.2	28.9
SG	0.92	0.54	28.32	2.72	0.81	0.5	1.3
LAI	69.32	49.75	34.84	29.01	16.67	7.0	27.2
LSR	58.24	10.39	8.66	6.61	0.65	0.42	1.2
ADF	3.36	0.54	7.76	1.42	35.69	29.9	39.6
NDF	8.31	0.50	2.95	0.85	56.49	52.6	59.0
CP	54.29	10.86	9.71	7.15	9.70	8.6	11.8
IVDMD	56.92	3.75	3.20	2.41	55.18	52.3	57.5
DMY	68.42	25.59	18.16	15.02	25.14	13.9	32.2
GFY	93.95	39.29	20.30	19.68	68.82	38.5	92.0

PH= plant height (cm), NOL= Number of leaves/plant, LL=Leaf length (cm), LW= Leaf width (cm), NOT= Number of tillers/plant, SG= stem girth (cm), LAI= Leaf area index, LSR= Leaf stem ratio, ADF = Acid detergent fibre (%), NDF= Neutral detergent fibre (%), CP= Crude protein (%), IVDMD= In vitro dry matter digestibility (%), DMY= Dry matter yield (q/ha), GFY= Green fodder yield (q/ha). h<sup>2</sup>= heritability (broad sense); PCV= Phenotypic coefficient of variability; CV= Genotypic coefficient of variability; GA (%)= Genetic advance as percentage of mean; GM= grand mean.

TABLE 2  
Genotypic and phenotypic correlation coefficients among various traits of Oat

Characters	PH	NOL	LL	LW	NOT	SG	LAI	LSR	ADF	NDF	CP	IVDMD	DMY
NOL	G	.6064**											
	P	.4255**											
LL	G	.3342*	.4450**										
	P	.0641	-.0585										
LW	G	-.5596**	.3383*	.2202									
	P	-.0181	.1852	.1299									
NOT	G	.3340*	.4458**	0.095	.0313								
	P	.1670	.4204**	.0759	.0132								
SG	G	-.2460	-.7096**	.3230*	.1411	.1846							
	P	.1327	-.0219	.2632*	-.2797*	.1513							
LAI	G	.1102	.6692**	.2845*	.3710**	.5017**	-.6670**						
	P	.2853*	.6325**	.2208	.4319**	.3963**	-.1196						
LSR	G	.3153*	.3739**	.4311**	.5918**	.1256	.3758**	.3135*					
	P	.0836	.2728*	.0263	.0660	.0485	-.0036	.1455					
ADF	G	.4312**	.4641**	.1320	-.7215**	-.5327**	-.2265	-.1468	.3709**				
	P	.2438	.2129	.0843	.1454	-.1525	.2091	.2552	.1549				
NDF	G	.9070**	.3417**	.0121	.1083	-.1060	.7014**	.5934**	.3474**	.9354**			
	P	.1265	.0554	-.0345	-.0764	-.0531	-.0087	.0303	.2864*	.1616			
CP	G	.2467	.1264	.2744	.2092	-.0195	.4876**	-.0777	.4456**	-.1413	-.4941**		
	P	.0718	.0808	.2351	.1820	.0230	.0948	-.0057	.0596	-.1803	-.0878		
IVDMD	G	-.0688	.3837**	.2120	.7549**	.0513	-.9304**	.2071	.4483**	.1689	-.3416**	.7284**	
	P	-.1068	.2317	-.1796	.0843	.0556	-.1325	.0764	.3034*	-.0583	-.0796	.2631*	
DMY	G	-.2574	-.5339**	.1345	-.7298**	-.2492	.6451**	-.4611**	-.3007	.6225**	.0682	-.2325	-.2698*
	P	.0347	-.3683**	.1133	-.1493	-.1415	.1931	-.2085	-.2758*	.0161	.0754	-.0720	-.2243
GFY	G	.3607**	.3847**	.3426**	.6930**	.3691**	.9053**	-.3170*	-.3830**	.0771	.5040**	-.1478	-.3999**
	P	.3175*	.3450**	.2967	.1796	.3563**	.1913	-.2005	-.3486**	.0299	.2071	-.0641	-.3072*

Treatments given in Table 1.

TABLE 3  
Path coefficient analysis for direct (diagonal and bold) and indirect effects on green fodder yield (kg/plot) in Oat

Traits	PH	NOL	LL	LW	NOT	SG	LAI	LSR	ADF	NDF	CP	IVDMD	DMY	Genotypic correlation with GFY
PH	.2379	.0078	.0137	-.3342	-.4207	.0064	.1312	.648	-.4160	-.2574	-.1236	-.0207	-.8363	.3607**
NOL	.2964	.2129	.0178	.2020	-.5615	.0185	.7969	.769	-.4477	-.0967	-.0633	.1155	-.7346	.3847**
LL	.0704	-.2333	.0434	0614	-.0416	-.0588	.0734	.1143	-.0927	.0173	.0318	.0394	.0261	.3426**
LW	-.1964	.0044	.0124	.5972	-0.394	-.0037	.4418	.1216	.6608	-.0307	-.1048	.2272	-.3711	.6930**
NOT	.7140	.0058	.0165	.0187	-.2595	-.0309	.5975	.0258	.5139	.0301	.0097	.154	-.8096	.3691**
SG	-.5259	-.0092	.0153	-.0843	-.4920	-.0261	-.7943	.2417	.0775	-.4698	-.2459	-.2800	.3450	.9053**
LAI	.2355	.0087	.0336	.2215	-.6319	.0174	.1909	.0644	.1417	-.1684	.0389	.0623	-.4980	-.3170*
LSR	.6740	.0048	.0169	.3534	-.1582	-.0307	.3733	.2055	-.3578	-.3824	-.2232	.1349	-.9769	-.3830**
ADF	.9219	.0060	.0179	-.0280	.6709	.1102	-.1749	.0762	-.9648	-.6847	.0708	.0508	.0226	.0771
NDF	.9390	.0044	.0066	.0647	.1335	-.2270	.7067	.2769	-.7263	-.2838	.2475	-.1023	.4708	.5040**
CP	.5274	.0016	.0118	.1249	.0245	-.0649	-.0925	.0916	.1363	.1403	-.5008	.2192	-.7554	-.1478
IVDMD	-.1471	.0050	.0093	.4508	-.0646	.0243	.2466	.0921	-.1629	.0965	-.3648	.3009	-.8767	-.3999**
DMY	-.5503	-.0069	.0105	-.4358	.3139	-.0429	-.5491	-.0618	-.6006	-.3032	.1164	-.0812	.2491	.9477**

Treatments given in Table 1.

contributed by traits like NOT, ADF, NDF and CP, however, deluded the positive and direct effect of earlier traits on GFY.

The positive indirect effects were contributed through most of the traits except SG, ADF, NDF, CP and dmy exerting negative impact on the GFY. Ahmad *et al.* (2013) also reported negative indirect effect of above mentioned quality traits on GFY. High and significant genotypic correlation values of traits like PH (.3607\*\*), NOL (.3847\*\*) and LW (.6930\*\*), with GFY and their high direct effect values on GFY i.e. .2379, .2129, and .5972 respectively, indicated a true picture of association between these traits.

**CONCLUSION**

Selection for taller plants with more NOL, broader leaves, will be significant for the improvement of GFY in the material under study. At the same time progress in breeding for enhanced GFY may be adversely affected by selection for traits like LAI, LSR and IVDMD due to a strong negative association of these traits with green fodder yield.

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