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Genetic variability and correlation of seed yield and related characters in oat (*Avena sativa* L.)

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Abstract

The present investigation was conducted with 25 genotypes of oats and were grown during rabi 2015-16 to assess the performance, variability, heritability, genetic advance and correlation coefficient analysis using sixteen various yield and yield contributing traits in RCBD with three replications. Variances component method was used to estimate variability and selection parameters using standard approach. The genotypes differed significantly for most of the traits and relatively wide range of the mean for all characters indicated the existence of variation among the tested genotypes. High phenotypes coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for fresh green weight per plant, total number of tillers per plant, number of grains per plant, 100-seed weight and seed yield per plant. High GCV along with high heritability and genetic advance as percent of mean was observed for Fresh green weight per plant, total numbers of tillers per plant, plant height, numbers of grains per plant, 100-seed weight and seed yield per plant. Seed yield per plant was positively and significantly associated plant height, straw weight per plant, harvest index, leaf width, biological yield per plant, and number of grains per plant and 100-seed weight at both phenotypic and genotypic levels. Genotypic path coefficient analysis revealed that number of leaves per plant showed maximum positive direct effect on seed yield and also exhibited positive correlation with seed yield per plant. This study showed that there exists a large genetic variation among oats genotypes for most of the characters which could be exploited for direct selection of high yielding genotypes.

Keywords: Genetic variability, heritability, correlation, path studies, *Avena sativa*

Introduction

Oat (*Avena sativa* L., $2n = 14$) is originated from Mediterranean region and one of the important dual purpose (grain and fodder) crops of the world for edible products of human and animals. In many regions of the World it is grown for used as grain as well as for forage, fodder, straw for bedding, hay, haylase, silage and chaff. Interest in growing oats in India and Uttar Pradesh has quickly increased in recent years because of its high value as grain consumption by human, green fodder and feed for livestock. With the advent of intensified bakeries industries and dairy farming in county, especially with crossbred animals and feeding habits of bakery products by human population, the oat is progressively figuring for its improvement and attracting the attention of breeders. Yield, both grain and forage, are complex and quantitatively inherited traits and highly influenced by environmental factors. The seed yield components are less influenced by environmental variation and thus effective enhancement in seed yield may be brought about by selecting for these component traits. The expected improvement in such traits primarily depends on nature and magnitude of the heritable traits.

Material and Methods

The present study was carried out during *Rabi* season of 2015-16 at the Students Instructional Farm of Chandra shekhar Azad University of Agriculture and Technology, Kanpur. A group of 25 oats genotypes were evaluated under field condition using Randomized Complete Block Design with three replications. Each genotype was sown in 4 rows consisting 3.0 m long and spaced 40 cm apart. The plant to plant distance was maintained 25cm. Observations were recorded on five randomly selected representative plants from each replication leaving the border rows. Observations on sixteen traits were recorded for days to flowering, days to maturity, fresh green weight per plant (g), total number of tillers per plant, plant

height(cm), leaf length(cm), leaf width(cm), number of leaves per plant, number of nodes per plant, biological yield per plant(g), number of grains per plant, 100-seed weight(g), straw weight per plant (g), harvest index(%), panicle length(cm) and seed yield per plant (g). Mean values of these selected five plants were used for statistical analysis. The estimates of variability parameters were worked out according to the method suggested by Lush (1940). Phenotypic and genotypic coefficients of variation were calculated based on the approach cracked by Burton (1952) [7]. Broad sense heritability (h^2) was estimated (Allard, 1960) [2] and expressed in percentage. Genetic advance as percent of mean was calculated by the method advocated by Johnson *et al.*, (1955) [11]. Character association at genotypic, phenotypic levels and path coefficient analysis for seed yield per plant was taken as the dependent variable while the rest of the traits were considered as independent variables simultaneous equations, which expressed the basic relationship between path coefficients were solved to estimate the direct and indirect effects with the formula of suggested by Dewey and Lu (1959) [9].

Result and Discussion

The analysis of variance revealed a significant genetic variance among genotypes for all traits under investigation, indicating the existence of sufficient genetic variability among the genotypes. The mean, range and phenotypic coefficient of variation (PCV) and genotypic coefficients of variation (GCV), heritability in broad sense and genetic advance as per cent of mean are presented in Table 1. Estimates phenotypic coefficient of variation (PCV) were recorded higher than the genotypic coefficient of variation (GCV) for all sixteen traits studied, indicating the minor influence of environment. High estimates of GCV and PCV for fresh green weight per plant (g) total number of tillers per plant, number of grains per plant, 100-seed weight and seed yield per plant, indicated that selection may be effective based on these four traits and their phenotypic expression would be good indication of the genotypic potential. These findings are similar in agreement with earlier reported by Ahmed *et al.*, (2013) [3]; Verma and Yadav, (2013) [8, 20]; Chandan *et al.*, (2013) [8]; Avinash *et al.*, (2014) [4]; Shinde *et al.*, (2015) [18]; Bind *et al.*, (2016) [6]; Jaipal and Shekhawat, (2016) [12]; Revathi, (2016) [16] and Kumar *et al.* (2017) [15].

The success of a breeding plan mainly depends on the extent of additive genetic variance available in the genetic material for related trait. A survey of genetic variability is essentially the first step in crop enhancement and plant breeding is an exercise in the management of variability (Hutchinson, 1958). The broad sense heritability provides an idea about the portion of observed variability attributable to genetic difference. Heritability indicates the accuracy with which a genotype can be identified by its phenotypic performance. Burton (1952) suggested that heritability estimates coupled with genotypic coefficient of variation would be provide an accurate picture about the extent of genetic advance would be expected through simple selection. In the present investigation fresh green weight per plant, total number of tillers per plant, plant height, number of grains per plant, 100- seed weight and seed yield per plant, exhibited high heritability along with high genetic advance as percent of mean, indicates the presence of additive genetic variance for these traits

in the genotypes and the selection of these characters may be helpful for an enhancement of seed yield. These findings were in agreement with Bibi, (2012) [5]; Sangwan *et al.*, (2012) [17]; Ahmed *et al.*, (2013) [3]; Krishna *et al.*, (2013); Shinde *et al.*, (2015) [18]; Bind *et al.*, (2016) [6]; Jaipal and Shekhawat, (2016) [12] and Kumar *et al.*, (2017) [15]. High GCV, heritability and genetic advance provide better information on simple selection that these traits would be useful for an improvement of seed yield per plant in the genotype of oats similar results were also found by Krishna *et al.*, (2013), Shinde *et al.*, (2015) [18]; Bind *et al.*, (2016) [6] and Kumar *et al.*, (2017) [15]. While, all the traits studied except leaves per plant and nodes per plant were found to have high heritability but with a low to moderate magnitude of genetic advance, indicating the preponderance of additive gene effects. Similar results were also observed by Chandan *et al.*, (2013) [8]; Ahmed *et al.*, (2013) [3] and Avinash *et al.*, (2014) [4]. Estimation of phenotypic and genotypic correlation coefficients between each pair of traits is present in Table 3. The result exhibited that genotypic correlation coefficient were higher than the phenotypic correlation coefficients, which is indication of the inherent association among various traits independent of environmental influence. Seed yield per plant showed positive and significant association with plant height, straw weight per plant, harvest index, leaf width, biological yield per plant, number of grains per plant and 100-seed weight at phenotypic and genotypic levels. These results were similar to Bibi *et al.*, (2012) [5]; Tewari and Pandey, (2014) [19]; Krishna *et al.*, (2014) [13] and Kumar, *et al.*, (2017) [15]. While, positive correlation was observed for days to flowering, days to maturity, panicle length, number of nodes per plant and number of leaves per plant is in line with Ahmed *et al.*, (2013) [3], Tewari and Pandey, (2014) [19], Jaipal and Shekhawat, (2016) [12] and Kumar, *et al.*, (2017) [15]. High magnitude and maximum positive direct effects on seed yield per plant was exerted by number of leaves per plant followed by leaf width, plant height, total numbers of tillers per plant, day to flowering, harvest index, 100 seed weight, biological yield per plant and panicle length, indicating the true relationship between these characters as good contributors to seed yield. Similar positive significant observation regarding above result of the present study has also been noted by Ahmed *et al.*, (2013) [3], Tewari and Pandey, (2014) [19]; Jaipal and Shekhawat, (2016) [12] and Kumar, *et al.*, (2017) [15].

The overall results indicate the presence of adequate genetic variability among genotypes for most of the traits in present investigation. High estimates of heritability with high to moderate genetic advance as percent of mean for fresh green weight per plant, total number of tillers per plant, number of grains per plant, 100-seed weight, panicle length, harvest index and seed yield per plant, indicating the preponderance of additive gene effects. Genotypic correlation is higher than phenotypic correlation, indicating less influence of environment in study simple selection could be useful for enhancement of seed yield.

Table 1: Analysis of variance (ANOVA) for sixteen characters of oat (*Avena sativa* L.)

Source of variation	D. F	DF	DM	FGWP	TNP	PH (cm)	LL (cm)	LW (cm)	LPP	NPP	BYPP (g)	GPP	SW	SWP	HI	PL (cm)	SYPP (g)
Replication	2	5.43	8.68	128.87	0.19	67.17	1.95	19.58	13.91	15.74	7.43	25.43	3.80	0.49	15.42	17.45	4.80
Treatment	24	63.40**	16.62**	3392.82**	26.52**	39.58**	2.50**	25.04**	21.45**	31.85**	2.76**	75.37**	2.46**	1.30**	33.05**	30.25**	2.52**
Error	48	0.28	9.46	145.5	12.69	10.58	11.80	011.80	41.48	43.55	3.64	0.81	5.48	68.77	0.52	0.51	76.56

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

DF-Days to flowering

PH- Plant Height

NPP- Nodes per plant,

SWP- Straw weight per plant (g)

DM- Days to maturity

LL- Leaf length (cm)

BYPP- Biological Yield per plant (g)

HI- Harvest Index (%)

FGWP- Fresh green weight per plant

LW- Leaf length (cm)

GPP- Grains Per plant

PL - Panicle length (cm)

TNP- Total numbers of tillers per plant

LPP- Leaves per plant

SW- 100 Seed weight (g)

SYPP- seed yield per plant (g)

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

Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (bs)	Genetic Advance	GA as percent of mean
DF	93.81	83.93-101.8	4.92	4.89	98.70	9.39	10.00
DM	127.50	123.80 -131.07	1.86	1.84	98.30	4.80	3.76
FGWP(g)	151.84	82.60-221.60	23.08	21.67	88.10	63.63	41.90
TNP	14.40	8.53-20.13	21.61	20.15	86.90	5.57	38.68
PH(cm)	44.42	35.87-50.07	8.39	8.07	92.40	9.10	35.98
LL(cm)	1.66	1.48-1.77	5.74	5.36	87.10	0.17	10.24
LW(cm)	167.74	154.67-177.93	4.39	4.06	85.40	12.96	7.15
LPP	5.34	5.20-5.47	3.26	3.20	3.30	0.12	0.18
NPP	5.34	5.20-5.60	3.70	3.59	2.60	0.16	0.18
BYPP(g)	14.22	12.53-16.33	6.84	6.71	96.10	1.93	13.57
GPP	95.97	86.40-106.20	25.28	25.19	96.80	26.11	30.53
SW(g)	10.09	8.68-11.72	29.18	28.89	93.60	1.79	27.74
SWP(g)	4.46	3.96-5.35	7.36	7.07	92.40	0.62	13.90
HI(5)	29.68	25.75-37.72	11.35	11.10	95.60	6.63	22.23
PL(cm)	26.69	17.13-29.05	12.57	12.25	95.10	30.32	24.60
SYPP(g)	4.20	3.68-5.34	30.10	29.88	95.80	0.84	30.00

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

Characters		DF	DM	FGWP (g)	TNP	PH (cm)	LL (cm)	LW (cm)	LPP	NPP	BYPP (g)	GPP	SW(g)	SWP (g)	HI (%)	PL (cm)	SYPP (g)
DF	G	-	0.653**	-0.184	-0.214	0.007	0.175	0.069	0.568**	0.513**	0.002	0.070	-0.079	0.153	0.124	0.075	0.134
	P		0.643**	-0.164	-0.193	0.005	0.163	0.053	0.522**	0.490**	-0.002	0.068	-0.080	0.141	0.120	0.070	0.127
DM	G			-0.260	0.409**	-	-0.118	0.418**	0.657**	0.136	0.204	0.447**	0.243	-0.003	-0.106	0.402**	0.052
	P			-0.231	-0.373*	0.015	-0.104	0.389**	0.508**	0.127	0.201	0.482**	0.234	-0.001	-0.101	0.390**	0.054
FGWP(g)	G				0.780**	0.064	0.252	-0.144	-	-	-	-0.196	-	-0.157	0.184	-0.012	-0.118
	P				0.756**	0.059	0.239	-0.135	-	-	-	-0.173	-	-0.135	0.167	-0.013	-0.113
TNP	G					0.007	0.326*	-0.235	-0.226	0.514**	0.500**	-0.164	0.429**	-0.009	0.299	-0.009	-0.002
	P					0.006	0.302*	-0.217	0.151	0.432**	0.452**	-0.154	0.402**	-0.003	0.263	-0.008	-0.026
PH(cm)	G						-0.212	0.786**	0.169	0.578**	-0.047	-0.037	0.418**	0.560**	0.417**	0.064	0.471**
	P						-0.174	0.652**	0.168	0.523**	-0.041	-0.036	-0.364	0.533**	0.393**	0.086	0.464**
LL(cm)	G							0.094	0.384**	0.230	0.412**	0.458**	-0.239	-0.212	0.125	-0.018	-0.181
	P							0.115	0.359*	0.223	-0.373*	0.397**	-0.195	-0.170	0.096	-0.009	-0.166
LW(cm)	G								-0.100	-0.091	0.206	0.151	0.597**	-	-	0.084	0.562**
	P								-0.047	-0.049	0.196	0.146	0.583**	0.528**	0.543**	0.089	0.482**
LPP	G									0.875**	-0.180	-0.012	-0.098	0.147	0.039**	0.315*	0.068
	P									0.749**	-0.150	-0.042	-0.055	0.096	0.033	0.225*	0.067
NPP	G										-0.124	0.018	-0.054	0.095	0.056	0.237	0.001
	P										-0.116	-0.010	-0.042	0.066	0.041	0.194	0.021
BYPP(g)	G											0.357*	0.795**	0.055	-	0.115	0.325*
	P											0.351*	0.752**	0.058	-	0.110	0.324*

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