



Correlation and Genetic Divergence Analysis for Seed and Fodder Yield and Its Contributing Character in Oat (*Avena sativa* L.)

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ABSTRACT

A trial was conducted to Studies on heterosis and transgressive segregants for fodder and grain related traits in Oat (*Avena sativa* L.) in a diallel cross set 8 parents, 28 F_1 s and 28 F_2 s oat were evaluated in randomized complete block design with three replications. The aim of correlation coefficient study is to find out the statistical measurement used to find out the degree and direction of the relationship between two or more variables. The characters plant height, tillers per plant, leaves per plant, leaf length, leaf width, dry matter yield, seed per panicle, harvest index, mean groat mass and green area index have positive and significant correlation with grain yield per plant in F_1 generation while in F_2 generation, days to 50 % flowering, days to maturity, plant height, tillers per plant, spike length, leaves per plant, leaf width, seed per panicle, harvest index, hecto lit. grain weight, mean groat mass and groat length have positive and significant correlation with grain yield per plant.

The maximum inter-cluster distance value was recorded between cluster VI and cluster VII in F_1 generation and in F_2 generation maximum inter cluster distance was recorded between cluster I and cluster V. The maximum intra cluster distance was found for cluster VI in F_1 generation while in F_2 generation the maximum intra cluster distance was found for cluster VI. Based on maximum inter cluster distance between cluster VI and cluster VII in F_1 generation while in F_2 generation I and V, superior genotypes of cluster VI may be used as parent with superior genotypes selected from cluster VII in hybridization programme for creation of variability followed by selection for desirable recombination's in segregating generation. As cluster VI had highest intra cluster distance indicated divergence among the genotypes of this cluster. Therefore, genotypes of this cluster might be used for hybridization programme considering the mean performance of genotypes for major yield attributing traits.

Key words: Correlation co-efficient, Genetic divergence.

INTRODUCTION

The oat is grown in several parts of India and abroad. It is mainly grown in *rabi* season mostly for fodder, however, of late, its grain is being used as baby food, breakfast food and

animal feed. Oat is a versatile grain for food, animal feed and non food products due to its unique grain qualities compared to other cereal grains.

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India possesses a large bovine population which includes 200 million cattle and 92 million buffalo. This accounts for 19.5 percent of the global cattle population. Despite this large bovine population, the scenario of milk production and productivity is far below the world average.

The mean values, genotypic and phenotypic variances, correlation coefficients and genetic divergence analysis of the traits are some of the key parameters which determine the efficiency of a breeding program. The phenotypic variance includes total variance among genotypes tested for variance traits. Total genotypic variance explains heritable portion of phenotypic variance. It encompasses the phenotypic variance attributable to genetic causes which have a predictive function in plant breeding leading to permanent genetic improvement. Coefficient of correlations help to measure the level of relationships between the traits. The correlations also give reliable and useful information on nature, extent and direction of selection. The existence of optimum genetic divergence between the parents is an important pre-requisite for success of any crop improvement programs, because crosses between genetically diverse parents have been found to provide superior transgressive segregates in the segregating generations. Thus, genetically diverse parents when crossed can bring together diversity of gene combinations either to exploit heterosis for developing hybrid varieties or obtain superior recombinants for developing pure line varieties. Thus, assessment of genetic diversity existing in the breeding materials is an essential requirement for any breeding programme.

MATERIAL AND METHODS

Basic material of the trial was taken on the basis of morphological differences for various characters in genotype from the genetic stock of oat. Genetic stock of oat maintained through natural self pollination of section of rabi cereal, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur. Each

parent F_{1s} and F_{2s} treatment was sown in RBD (RANDOMISED BLOCK DESIGN) in single and double rows of 3m length along with row to row and plant to plant spacing of 22.5 cm and 5 cm, respectively. Recommended package of practice was applied to raise healthy crop. The data was recorded for days to 50 % flowering, days to maturity, plant height (cm), number of tillers per plant, spike length (cm), number of leaves per plant, leaf length, leaf width (cm), leaf: stem ratio, total chlorophyll, green fodder yield (g), dry matter yield (g), seed weight per panicle (g), seeds per panicle, harvest index, grain yield per plant (g), test weight (g), crude protein, hecto liter grain weight, grain protein per cent, groat %, ease to dehulling, grain colour brightness, mean groat mass, groat length and width, leaf waxiness, leaf rolling, leaf area index, green area index, pollen viability index, heat susceptible index, membrane stability index mean data were used for statistical analysis.

RESULTS AND DISCUSSION

Correlation and Genetic divergence

The aim of correlation coefficient study is to find out the statistical measurement used to find out the degree and direction of the relationship between two or more variables. The characters plant height, tillers per plant, leaves per plant, leaf length, leaf width, dry matter yield, seed per panicle, harvest index, mean groat mass and green area index have positive and significant correlation with grain yield per plant in F_1 generation while in F_2 generation, days to 50 % flowering, days to maturity, plant height, tillers per plant, spike length, leaves per plant, leaf width, seed per panicle, harvest index, hecto lit. grain weight, mean groat mass and groat length have positive and significant correlation with grain yield per plant. These result were similar to Bibi *et al.*⁵, Tewari and Panday²¹; Krishna *et al.*¹⁴.

The seven cluster formed in divergence analysis contained genotype of F_1 and F_2 generation thereby indicating non-parallelism between genetic diversity. All the parents + F_1

genotypes were grouped into seven distinct non-overlapping clusters. Cluster V had maximum 8 followed by cluster II and III had 7, 7 genotype and parents + F₁ genotypes were also grouped into seven distinct non-overlapping clusters. Cluster VII had maximum 8 followed by cluster II had 7 and parents. The genotypes of a cluster are lesser divergence than the genotypes of other clusters. The maximum inter-cluster distance value was recorded between cluster VI and cluster VII in F₁ generation and in F₂ generation maximum inter cluster distance was recorded between cluster I and cluster V. The maximum intra cluster distance was found for cluster VI in F₁ generation while in F₂ generation the maximum intra cluster distance was found for cluster VI. Based on maximum inter cluster distance between cluster VI and cluster VII in F₁ generation while in F₂ generation I and V, superior genotypes of cluster VI may be used as parent with superior genotypes selected from cluster VII in

hybridization programme for creation of variability followed by selection for desirable recombination's in segregating generation. As cluster VI had highest intra cluster distance indicated divergence among the genotypes of this cluster. Therefore, genotypes of this cluster might be used for hybridization programme considering the mean performance of genotypes for major yield attributing traits. Cluster VII genotypes had maximum mean values for eleven characters in F₁ generation while in F₂ generation cluster VII genotypes had maximum mean values for fourteen characters. The choice of suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographic distances. Murty and Arunchanchalam¹⁶ in sorghum; Nair and Gupta¹⁷ and Sindhu and Mehndiratta¹⁸ in oat, Srivastava *et al.*²⁰ in wheat reported that hybridization between genotype of different clusters can give amount of hybrid vigour.

Estimate phenotypic correlation coefficient for 23 attributes in F1 generation of Oat (*A. sativa*)

characters	DF	DM	PH	TPP	SL	LPP	LL	LW	L:S R	TC	GFY	DMY
DF	1.000	0.62**	-0.06	0.51**	0.10	-0.19*	-0.16	0.21*	0.13	-0.18	-0.20*	-0.27**
DM		1.0000	-0.10	0.40**	0.11	-0.11	-0.32**	0.23*	0.09	-0.09	-0.34**	-0.39**
PH			1.0000	0.27**	0.05	0.61**	0.57**	0.45**	-0.08	-0.30**	0.59**	0.73**
TPP				1.0000	0.30**	0.25**	0.08	0.31**	0.17	-0.11	-0.00	-0.03
SL					1.0000	0.11	-0.09	0.27**	0.40**	0.08	-0.09	-0.02
LPP						1.0000	0.52**	0.14	0.03	-0.03	0.40**	0.48**
LL							1.0000	-0.05	-0.05	0.01	0.82**	0.77**
LW								1.0000	-0.01	-0.32**	-0.02	0.08
L:S R									1.0000	-0.00	-0.03	-0.02
TC										1.0000	-0.04	-0.19
GFY											1.0000	0.84**
DMY												1.0000
GYPP	0.13	0.15	0.63	0.43	0.11	0.45	0.25	0.53	-0.04	-0.21	0.19	0.33

characters	SWPP	SPD	HI	CP	HLGW	GP	G	MGM	GL	LAI	GAL
DF	-0.28**	-0.06	0.38**	0.43**	0.25**	0.14	0.16	-0.04	0.59**	-0.01	0.09
DM	-0.28**	0.08	0.29**	0.60**	0.18	0.11	0.04	0.01	0.57**	-0.13	-0.05
PH	-0.05	0.32**	0.07	-0.15	0.36**	0.00	0.32**	0.63**	-0.14	-0.02	-0.06
TPP	-0.23*	0.20*	0.38**	0.30**	0.18	-0.15	0.19*	0.22*	0.26**	-0.14	-0.01
SL	-0.00	0.31**	0.02	0.27**	-0.13	-0.13	-0.18	-0.06	0.20*	0.00	0.01
LPP	0.17	0.33**	0.03	-0.07	0.17	-0.14	0.10	0.37**	-0.07	-0.20*	-0.11
LL	0.27**	-0.11	0.19*	-0.46**	0.42**	0.11	0.41**	0.37**	-0.33**	0.09	0.08
LW	-0.30**	0.54**	0.13	0.24*	-0.00	0.08	-0.00	0.25**	0.14	0.15	0.04
L:S R	0.11	0.11	0.15	0.06	-0.16	0.09	-0.19*	-0.35**	0.27**	0.29**	0.36**
TC	0.54**	-0.25**	-0.13	-0.05	-0.03	-0.23*	0.02	-0.10	-0.01	-0.31**	-0.17
GFY	0.30**	-0.13	0.12	-0.54**	0.47**	0.15	0.38**	0.38**	-0.40**	0.20*	0.16
DMY	0.21*	0.04	0.06	-0.49**	0.35**	0.07	0.27**	0.41**	-0.40**	0.18	0.10
SWPP	1.0000	-0.17	-0.16	-0.26**	-0.06	-0.21*	-0.01	-0.03	-0.16	-0.14	-0.04
SPD		1.0000	0.15	0.11	-0.32**	-0.09	-0.34**	0.12	0.09	-0.04	-0.07
HI			1.0000	-0.06	0.11	0.25**	-0.03	0.00	-0.04	0.15	0.15

CP				1.0000	-0.00	-0.15	-0.00	-0.06	0.61**	-0.22*	-0.22*
HLGW					1.0000	0.16	0.71**	0.48**	0.05	-0.13	-0.11
GP						1.0000	0.02	-0.08	-0.04	0.34**	0.21*
G							1.0000	0.48**	0.01	-0.13	-0.08
MGM								1.0000	-0.12	-0.27**	-0.41**
GL									1.0000	-0.24*	-0.08
LAI										1.0000	0.74**
GAI											1.0000
GYPP	-0.21	0.53	0.23	0.05	0.17	-0.03	0.14	0.40	0.07	-0.22	-0.20

Estimate phenotypic correlation coefficient for 24 attributes in F2 generation of Oat (A. sativa)

characters	DF	DM	PH	TPP	SL	LPP	LL	LW	L:S R	TC	GFY	DMY
DF	1.000	0.60**	-0.00	0.50**	-0.02	-0.00	-0.12	0.12	0.04	-0.25**	-0.34**	0.34**
DM		1.000	-0.03	0.42**	-0.03	-0.03	-0.37**	0.06	0.02	-0.11	-0.44**	-0.45**
PH			1.000	0.29**	0.02	0.59**	0.53**	0.46**	-0.26**	-0.44**	0.42**	0.64**
TPP				1.000	0.29*	0.38*	0.11	0.32**	0.00	-0.15	-0.20*	-0.10
SL					1.000	0.20*	-0.12	0.32**	0.23*	-0.06	-0.22*	-0.13
LPP						1.000	0.49**	0.09	-0.08	-0.01	0.17	0.44**
LL							1.000	0.03	-0.07	-0.11	0.62**	0.76**
LW								1.000	-0.14	-0.57**	0.08	0.14
L:S R									1.000	-0.01	-0.19*	-0.15
TC										1.000	-0.09	-0.19
GFY											1.000	0.76**
DMY												1.000
GYPP	0.277	0.318	0.595	0.495	0.124	0.364	0.181	0.534	-0.230	-0.299	0.071	0.194

characters	SWPP	SPP	HI	CP	HLGW	GP	G	MGM	GL	LAI	GAL
DF	-0.55**	0.04	0.34**	0.40**	0.29**	0.21*	0.10	-0.08	0.56**	0.09	0.12
DM	-0.54**	0.12	0.31**	0.42**	0.16	0.07	-0.00	-0.00	0.55**	-0.05	-0.08
PH	0.08	0.37**	0.12	-0.03	0.49**	0.07	0.46**	0.68**	0.06	-0.01	-0.01
TPP	-0.42**	0.22*	0.36**	0.34**	0.32**	-0.09	0.24*	0.20*	0.37**	-0.18*	-0.05
SL	-0.12	0.26**	-0.12	0.28**	-0.18	-0.19*	-0.18	-0.10	0.27**	-0.07	0.11
LPP	0.13	0.29**	-0.05	0.10	0.25**	-0.34**	0.23*	0.31**	0.13	-0.33**	-0.29**
LL	0.29**	0.03	0.08	-0.38**	0.35**	0.23*	0.38**	0.33**	-0.30**	0.09	0.14
LW	-0.47**	0.52**	0.21*	0.14	0.01	0.05	0.04	0.33**	0.26**	0.17	0.18
L:S R	0.04	0.07	0.05	0.11	-0.33**	0.16	-0.32**	-0.38**	0.23*	0.18	0.23*
TC	0.36**	-0.32**	-0.16	-0.11	-0.08	-0.13	-0.07	-0.18	-0.25**	-0.28**	-0.18
GFY	0.32**	-0.04	0.04	-0.55**	0.24**	0.20*	0.29**	0.30**	-0.45**	0.25**	0.16
DMY	0.37**	0.19*	-0.00	-0.50**	0.23*	0.12	0.29**	0.40**	-0.38**	0.12	0.04
SWPP	1.000	-0.21*	-0.26**	-0.39**	-0.13	-0.09	-0.03	-0.04	-0.49**	-0.11	-0.06
SPD		1.000	0.19*	0.17	-0.21*	-0.04	-0.23*	0.16	0.33**	0.08	0.10
HI			1.000	-0.16	0.21*	0.38**	0.02	0.20*	0.00	0.24*	0.20*
CP				1.000	0.05	-0.17	0.04	-0.05	0.74**	-0.30**	-0.07
HLGW					1.000	0.23*	0.78**	0.53**	-0.01	-0.12	0.03
GP						1.000	0.19*	0.05	-0.02	0.48**	0.53**
G							1.000	0.57**	-0.05	-0.17	-0.05
MGM								1.000	-0.09	-0.18	-0.18
GL									1.000	-0.10	0.03
LAI										1.000	0.58**
GAI											1.000
GYPP	-0.362	0.506	0.424	0.128	0.349	0.072	0.215	0.466	0.294	-0.038	0.016

Table 1: Pooled clusters means for 29 characters in parents +F1 hybrids

Cluster	DF	DM	PH	TPP	SL	LPP	LL	LW	L: S R	TC	GFY	DMY	SWPP	SPP
I	89.503	133.056	137.411	4.270	30.503	22.233	56.122	1.566	0.313	41.356	205.007	66.892	36.960	87.411
II	91.080	130.508	151.125	3.652	30.430	21.747	57.778	1.675	0.354	37.425	251.103	95.677	35.822	88.567
III	93.910	136.900	159.619	4.429	32.790	24.376	54.420	1.828	0.328	35.684	187.347	80.357	32.167	104.271
IV	111.694	145.617	145.867	4.425	30.105	19.155	52.503	1.731	0.319	35.175	146.745	47.446	28.475	91.950
V	113.117	143.083	147.908	4.717	32.892	20.442	56.300	1.773	0.334	37.333	223.307	76.412	36.388	92.483
VI	101.764	138.778	137.689	4.229	32.022	20.488	53.323	1.668	0.363	37.672	157.694	55.495	33.352	96.667
VII	98.858	136.858	164.567	4.492	31.004	25.507	60.602	1.721	0.327	36.105	291.400	114.718	34.931	96.587

HI	GYPP	TW	CP	HLGW	GP	G%	MGM	GL	GW	LAI	GAI	PVT	HIS	MSI
40.988	6.361	36.960	11.168	48.700	13.244	53.522	25.811	7.400	2.467	5.219	5.808	81.600	0.858	37.778
39.013	6.130	35.927	10.519	49.350	14.608	51.592	24.092	7.547	2.493	6.020	7.163	81.175	0.747	35.217
39.804	8.703	32.161	12.205	45.671	13.424	47.733	26.905	7.679	2.647	5.395	6.007	85.510	0.973	33.381
41.728	7.811	28.475	13.161	53.383	14.867	54.833	26.550	8.087	2.622	5.349	6.014	88.450	1.058	35.558
42.463	7.563	35.638	12.339	52.300	14.150	55.767	25.600	7.902	2.569	5.547	6.543	88.008	1.006	36.433
43.103	7.257	33.352	11.830	41.806	14.300	41.583	22.878	7.855	2.612	5.503	6.335	84.889	1.007	33.261
44.135	9.229	34.931	10.693	54.479	14.708	53.688	27.671	7.615	2.759	5.402	6.052	90.079	1.446	38.096

Table 2: Pooled clusters means for 29 characters in parents +F₂ hybrids

Cluster	DF	DM	PH	TPP	SL	LPP	LL	LW	L: S R	TC	GFY	DMY	SWPP	SPP
I	107.807	140.353	143.273	4.747	30.831	21.691	53.467	1.677	0.339	33.924	140.411	50.448	25.733	95.193
II	104.214	140.767	146.422	4.356	29.462	18.740	53.214	1.662	0.286	34.433	167.289	50.829	25.077	84.811
III	91.867	134.117	142.467	3.622	29.875	22.938	54.405	1.531	0.333	37.742	174.288	68.924	34.965	93.033
IV	95.447	133.852	137.967	3.846	29.590	18.076	54.028	1.620	0.319	35.353	189.625	62.133	30.037	92.093
V	88.166	128.033	145.444	3.884	28.766	21.340	56.926	1.563	0.312	37.633	247.252	86.832	35.473	81.489
VI	94.100	134.233	157.447	4.272	30.317	22.980	55.811	1.717	0.297	33.599	201.232	82.137	30.023	98.237
VII	96.500	132.950	162.800	4.267	28.283	24.577	59.193	1.668	0.298	33.688	304.293	119.333	33.727	95.317

HI	GYPP	TW	CP	HLGW	GP	G %	MGM	GL	GW	LAI	GAI	PVT	HIS	MSI
40.917	7.625	25.733	12.633	44.860	13.393	45.433	23.340	8.050	2.629	5.165	6.033	85.607	1.052	32.507
39.263	7.171	25.077	11.742	53.189	14.033	56.967	26.211	7.839	2.510	5.196	5.900	85.256	0.924	35.789
35.857	5.884	34.965	11.484	42.325	12.442	44.608	23.200	7.687	2.577	4.920	5.464	83.017	1.188	33.258
40.365	6.407	30.020	10.109	43.330	14.067	43.315	23.211	7.489	2.534	5.506	6.196	81.600	0.723	33.541
37.642	5.923	35.407	10.269	50.689	14.222	54.778	24.722	7.257	2.390	5.309	6.268	79.122	0.648	35.633
40.083	7.968	30.026	10.533	47.107	13.113	49.060	26.583	7.565	2.613	5.126	5.789	83.997	0.986	34.610
41.983	8.167	33.728	9.178	53.517	14.600	56.433	27.050	7.460	2.818	5.457	5.920	87.550	1.217	36.933

Table 3: Pooled average intra- and inter-cluster distance for 29 characters in F₁ generation

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	103.298	241.065	302.847	326.561	266.394	314.460	537.462
Cluster II		109.496	261.66	510.797	266.529	414.260	407.832
Cluster III			102.191	345.985	252.46	421.589	314.720
Cluster IV				87.102	250.998	306.364	708.531
Cluster V					170.404	362.185	412.406
Cluster VI						213.144	851.538
Cluster VII							82.621

Table 4: Pooled average intra- and inter-cluster distance for 29 characters in F₂ generation

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	118.54	216.753	261.495	312.202	622.581	330.277	666.552
Cluster II		114.43	288.039	302.614	404.579	283.936	533.232
Cluster III			144.221	244.352	338.814	260.359	449.186
Cluster IV				151.251	295.5	325.182	576.471
Cluster V					173.525	395.778	412.461
Cluster VI						176.799	304.333
Cluster VII							176.471

Clustering pattern of F₁ generation

Cluster Number	No. of Genotype	Genotype
1	3	UPO94*RO19,RO19,RO19*JHO851,
2	7	NDO*ROO19,UP94*NDO1,NDO1*JHO851
3	7	UPO94*SKO90,RO19*SKO90, NDO1*SKO90,JHO822*SKO,JHO851*SKO90,KENT*SKO90
4	3	UPO94,KENT, KENT*JHO851,JHO822*KENT, KENT
5	8	NDO*JHO822,NDO1*KENT, JHO822*RO19,RO19*KENT
5	4	UPO94*JHO851,UPO94,JHO851,JHO822*JHO851,JHO822
6	4	UPO94*JHO2001-3,RO19*JHO2001-3,KENT*JHO2001-3,JHO2001-3,JHO2001-3,SKO90*JHO2001-3,NDO*JHO2001-3,JHO*2001-3

Clustering pattern of F₂ generation

Cluster Number	No. of Genotype	Genotype
1.	3	UPO94*JHO851,NDO1*JHO851,JHO81
2.	7	UPO94*KENT,UPO94*SKO90,NDO1*JHO822,NDO1*KENT,JHO822*RO19, JHO822*JHO851,RO19*KENT
3.	5	UPO94*JHO822,JHO822*KENT, JHO822*SKO99,JHO822, KENT
4.	6	UPO94*RO19,UPO94*RO19,RO19*JHO851, KENT*JHO851, JHO851*SKO90,UPO94
5.	4	JHO822*JHO2001-1,KENT*SKO90,KENT*JHO2001-3, SKO90
6.	3	NDO*RO19, NDO1, RO19
7.	8	UPO94*JHO2001-3.NDO1*JHO2001-3,RO19*SKO90,RO19*JHO2001-3, JHO851*JHO2001-3,SKO90*JHO2001-3,JHO2001-3

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