

Electronic Journal of Plant Breeding



Research Article

Variability, correlation and path co-efficient studies in interspecific crosses (*Avena sativa* × *Avena sterilis*) of oat

Bichewar Nagesh^{1*}, A. K. Mehta¹, Kadthala Bhargava² and S. Ramakrishana¹

¹Department of Genetics and Plant Breeding, College of Agriculture, Jabalpur, JNKVV, Jabalpur-482004, Madhya Pradesh, India.

²Department of Genetics and Plant Breeding, College of Agriculture, Rajendranagar, PJTSAU, Hyderabad-500030, Telangana, India.

*E-Mail: nageshbichewar168@gmail.com

Abstract

Genetic variability, correlation and path coefficients for fifteen agro-morphological traits were studied on 100 oat lines including two checks. Genotypic and phenotypic coefficients of variation were high for leaf number per tiller and weight of panicle. Traits such as tiller number per plant, leaf number per tiller, weight of panicle, stem width, leaf width, individual plant yield, length of internode and thousand seed weight showed high heritability accompanied by high genetic advance indicating that these characters can be enhanced by simple selection. Association studies revealed a positively significant association of individual plant yield with thousand seed weight, floret number per panicle, spikelet number per panicle, weight of panicle, height of plant, length of internode at the phenotypic level. Path analysis disclosed that weight of panicle, width of flag leaf, floret number per panicle, tiller number per plant and length of flag leaf exhibited a positive direct effect on seed yield. Among these characters, weight of panicle, thousand seed weight, height of plant and floret number per panicle possessed positive association and direct effect. So, these traits can be used for creation of plant ideotypes and selecting these traits will be worthwhile for higher yield.

Keywords: Oat, correlation, genetic variability, path Coefficient, heritability, genetic advance and Ideotype.

INTRODUCTION

Oat (*Avena sativa*) is a cereal crop, initially domesticated in the Mediterranean and Middle East origin. It is best suitable for temperate regions due to their winter hardiness (Kumari *et al.*, 2019). The oat was domesticated much later than barley and wheat. Indeed, when barley and wheat were introduced to the European continent as main staple foods, oat and rye were existed as contaminants of weed in Great Britain and East Asia. However, even now oat is one of the oldest crops cultivated by humans. After corn, rice, wheat, barley, sorghum, and millet it is the seventh most economically vital cereal crop (Murphy and Hoffman, 1992). Its area and production in the world are ~27m ha and 40m tonnes respectively with the northern

hemisphere accounting for ~67% of total production. In north western and central parts of India, oat is mainly cultivated as a forage crop in the *rabi* season and is now even expanding to the eastern parts of the country too. Oat is cultivated majorly in Uttar Pradesh having a crop area of 34%, followed by Punjab (20%) Bihar (16%), Haryana (9%) and Madhya Pradesh (6%).

Oat is primarily grown for their edible starchy grains and is mostly grown in temperate climatic regions of the world. The crop has better capacity after rye to withstand poor soil. Even though oat is chiefly cultivated for livestock feed, some part is also used for human consumption,

especially for breakfast food. The plants provide good hay and under favourable agro climatic conditions, furnish excellent grazing and make good silage.

The absence of a sufficient amount of variability is one of the major drawbacks in further progress of oat productivity. In order to get the exact extent of variability present in genotypes, variability is divided into phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV). The extent of genotypic variability to the phenotypic variability detected for quantitative traits can be estimated by heritability. It is also useful in detecting the transmission of traits from parents to offspring. High heritability along with high genetic advance suggests that the heritability is because of polygene effects which can be useful for effective selection and is generally better for predicting the genetic gain due to selection as compared to heritability estimates solitary.

Information on character association, direct and indirect effects contributed by every character to yield can be helpful in hastening the process of selection. Correlation studies and path analysis estimates (Dewey and Lu, 1959) determine the extent of association between yield and yield contributing traits, also it will give a clear picture of the relationship of traits with yield by providing their direct and indirect effects on seed yield. Ultimately, such kind of estimates could help the breeder in formulating the blueprint to increase grain yield. By keeping above fact into consideration the present study was carried out with the objective to evaluate oat genotypes in terms

of their variability and to determine association of yield contributing traits.

MATERIALS AND METHODS

The current study was conducted during the *rabi* season, 2019-20 at Seed Breeding Farm, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur in Randomized Block Design (RBD) including three replications. Hundred (100) oat lines consisting 2 checks were line sown with 100-150 seeds per 3-meter row. **Table 1.** represents the list of oat lines included in the present investigation. In this study, fifteen quantitative traits viz., stem width (cm), leaf width (cm), days to 50% flowering, days to maturity, height of plant (cm), tiller number per plant, leaf number per tiller, length of internode (cm), length of flag leaf (cm), width of flag leaf (cm), weight of panicle (g), spikelet number per panicle, floret number per panicle, thousand seed weight (g) and individual plant yield (g) were considered for recording observation from inner six rows of the plot. The phenotypic and genotypic coefficient of variation in per cent were computed as per Burton (1953). The estimates of PCV and GCV were classified as low (< 10 per cent), moderate (10-20 per cent) and high (> 20 per cent) according to Sivasubramanian and Madhavamenon (1973). Heritability in the broad sense and genetic advance were calculated as per Hanson *et al.* (1956) and according to Johnson *et al.* (1955) it is classified as low (< 30 per cent), moderate (30-60 per cent) and high (> 60 per cent). Using the approach described by Johnson *et al.* (1955) the genetic advance was computed. The genetic advance is generally calculated as a

Table 1. List of hundred oat lines including two checks (JO-5 and Kent)

JO (IS) 12-4-1	JO (IS) 12-5-1	JO (IS) 12-6-1	JO (IS) 12-7-3	JO (IS) 12-8-3
JO (IS) 12-4-2	JO (IS) 12-5-2	JO (IS) 12-6-2	JO (IS) 12-7-4	JO (IS) 12-8-4
JO (IS) 12-4-3	JO (IS) 12-5-3	JO (IS) 12-6-3	JO (IS) 12-7-5	JO (IS) 12-8-5
JO (IS) 12-4-4	JO (IS) 12-5-4	JO (IS) 12-6-4	JO (IS) 12-7-6	JO (IS) 12-8-6
JO (IS) 12-4-5	JO (IS) 12-5-5	JO (IS) 12-6-5	JO (IS) 12-7-7	JO (IS) 12-8-7
JO (IS) 12-4-6	JO (IS) 12-5-6	JO (IS) 12-6-6	JO (IS) 12-7-8	JO (IS) 12-8-8
JO (IS) 12-4-7	JO (IS) 12-5-7	JO (IS) 12-6-7	JO (IS) 12-7-9	JO (IS) 12-8-9
JO (IS) 12-4-8	JO (IS) 12-5-8	JO (IS) 12-6-8	JO (IS) 12-7-10	JO (IS) 12-8-10
JO (IS) 12-4-9	JO (IS) 12-5-9	JO (IS) 12-6-9	JO (IS) 12-7-11	JO (IS) 12-8-11
JO (IS) 12-4-10	JO (IS) 12-5-12	JO (IS) 12-6-10	JO (IS) 12-7-12	JO (IS) 12-8-12
JO (IS) 12-4-11	JO (IS) 12-5-13	JO (IS) 12-6-11	JO (IS) 12-7-13	JO (IS) 12-8-13
JO (IS) 12-4-12	JO (IS) 12-5-14	JO (IS) 12-6-12	JO (IS) 12-7-14	JO (IS) 12-8-14
JO (IS) 12-4-13	JO (IS) 12-5-15	JO (IS) 12-6-13	JO (IS) 12-7-15	JO (IS) 12-8-15
JO (IS) 12-4-14	JO (IS) 12-5-16	JO (IS) 12-6-14	JO (IS) 12-7-16	JO (IS) 12-8-16
JO (IS) 12-4-15	JO (IS) 12-5-17	JO (IS) 12-6-15	JO (IS) 12-7-17	JO (IS) 12-8-17
JO (IS) 12-4-16	JO (IS) 12-5-18	JO (IS) 12-6-16	JO (IS) 12-7-18	JO (IS) 12-8-18
JO (IS) 12-4-17	JO (IS) 12-5-19	JO (IS) 12-6-17	JO (IS) 12-7-19	JO (IS) 12-8-19
JO (IS) 12-4-18	JO (IS) 12-5-20	JO (IS) 12-6-18	JO (IS) 12-7-20	JO (IS) 12-8-20
JO (IS) 12-4-19	JO (IS) 12-5-1	JO (IS) 12-6-19	JO (IS) 12-8-1	Kent
JO (IS) 12-4-20	JO (IS) 12-5-2	JO (IS) 12-6-20	JO (IS) 12-8-2	JO 5

percentage of the mean and as per Johnson *et al.* (1955) the range of genetic advance as a percentage of the mean was classified as low (10%), moderate (10 - 20%) and high (> 20%). Correlation co-efficients were assessed by using the procedure given by Pearson (1901) and with the help of simple correlation path coefficient analysis was created to determine the direct and indirect impacts of the yield components on seed yield as suggested by Dewey and Lu (1959) by using statistical software INDOSTAT.

RESULTS AND DISCUSSION

The result of analysis of variance indicated that the mean sum of squares due to advance lines was highly significant for all the traits under study (Table 2). A considerable degree of variability was observed for yield and yield attributing traits. Maximum variability was observed for floret number per panicle followed by the height of plant, days to maturity, spikelet number per panicle, days to 50% flowering, day to flower initiation, tiller number per plant, thousand seed weight, length of panicle, length of flag leaf, leaf number per tiller, individual plant yield, length of internode, length of peduncle, weight of panicle, leaf width, stem width and lowest for width of flag leaf. So these results are in agreement with Bhatia *et al.* (2017) for spikelet number per panicle and thousand seed weight.

For all the characters studied, magnitude of PCV was slightly greater as compared to GCV (Table 3) indicating that trait expression was little influenced by environmental factors.

A high phenotypic coefficient of variation was observed for tiller number per plant followed by leaf number per tiller, stem width, weight of panicle, leaf width and individual plant yield. This indicates that there is a substantial phenotypic variation for these traits. The moderate value of phenotypic coefficient of variation was recorded for length of internode, followed by width of flag leaf, length of flag leaf, thousand seed weight, height of plant, spikelet number per panicle, length of panicle, floret number per panicle, day to flower initiation, days to 50% flowering and length of peduncle. The lowest value of phenotypic coefficient of variation was recorded for days to maturity (Fig. 1). These are in agreement with the findings of Kapoor *et al.* (2011) for length of internode. Surje and De (2014) for individual plant yield. Singh *et al.* (2018) for thousand seed weight. Chakraborty *et al.* (2014) for length of peduncle, spikelet number per panicle and width of flag leaf.

A high amount of genotypic coefficient of variation reveals the presence of greater extent of genetic variability in the population and there is little impact of the environment on the character expression. The high magnitude of genotypic coefficient of variation was recorded for the traits eg. tiller number per plant followed by leaf number per tiller, weight of panicle, stem width and leaf width. This indicated presence of a high magnitude of genetic variance. The moderate estimates of genotypic coefficient of variation were observed in individual plant yield, length of internode, thousand seed weight, width of flag

Table 2. ANOVA for the different traits

Traits	Mean sum of squares	
	Genotype	Error
Stem width(cm)	0.181**	0.061
Leaf width(cm)	0.545**	0.405
Day to flower initiation	109.086**	70.264
Days to 50% flowering	129.149**	97.067
Days to maturity	163.519**	182.756
Height of plant(cm)	345.839**	157.105
Tiller number per plant	58.170**	1.382
Leaf number per tiller	26.523**	1.942
Length of internode(cm)	17.523**	9.055
Length of flag leaf(cm)	27.218**	19.72
Width of flag leaf(cm)	0.158**	0.109
Length of peduncle(cm)	15.428**	11.673
Length of panicle(cm)	27.870**	15.888
Weight of panicle(g)	10.553**	1.849
Spikelet number per panicle	137.195**	59.099
Floret number per panicle	599.064**	277.587
Thousand seed weight(g)	33.511**	16.011
Individual plant yield(g)	26.217**	7.7135

Table 3. Genetic variability parameters for yield and its attributing traits in oat lines

Character	PCV	GCV	Genotypic variance	Phenotypic variance	Heritability (h ²) %	Genetic advance as % of mean
Stem width(cm)	31.98	26.93	0.072	0.102	70.87	46.69
Leaf width(cm)	24.87	20.65	0.311	0.451	68.96	35.33
Day to flower initiation	11.48	9.32	55.149	83.751	65.85	15.58
Days to 50% flowering	10.55	8.48	69.675	107.760	64.66	14.05
Days to maturity	9.23	7.32	97.533	155.418	62.76	11.94
Height of plant(cm)	12.31	9.67	135.902	220.028	61.77	15.66
Tiller number per plant	50.63	48.89	18.930	20.305	93.23	97.24
Leaf number per tiller	41.51	36.17	7.359	9.692	75.93	64.93
Length of internode(cm)	15.52	13.39	8.831	11.876	74.36	23.78
Length of flag leaf(cm)	13.70	11.07	14.498	22.217	65.26	18.42
Width of flag leaf(cm)	14.84	11.76	0.079	0.126	62.73	19.18
Length of peduncle(cm)	10.54	8.93	9.269	12.920	71.75	15.58
Length of panicle(cm)	12.09	9.77	12.991	19.895	65.30	16.26
Weight of panicle(g)	29.45	26.98	3.985	4.750	83.91	50.91
Spikelet number per panicle	12.12	10.43	63.048	85.134	74.06	18.50
Floret number per panicle	11.97	9.94	265.158	384.746	68.92	16.99
Thousand seed weight(g)	12.94	12.02	18.827	21.838	86.21	22.99
Individual plant yield(g)	24.52	9.92	9.171	13.892	66.02	33.35

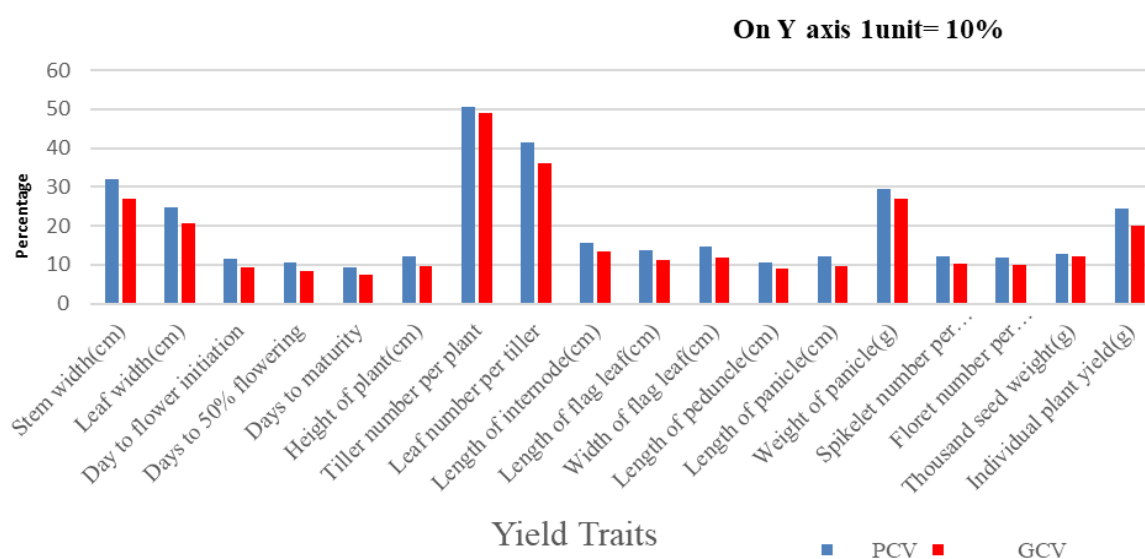


Fig. 1. Histogram of phenotypic coefficient of variation and genotypic coefficient of variation for quantitative traits in oat lines

leaf, length of flag leaf and spikelet number per panicle. The remaining characters exhibited a low magnitude of genotypic coefficient of variation viz., floret number per panicle, length of panicle, height of plant, days to flower initiation, length of peduncle, days to 50% flowering and days to maturity (Fig 1.). These results are in agreement with the findings of Kapoor *et al.* (2011) for individual plant yield and length of internode; Ahmed *et al.* (2013) for days

to 50% flowering and height of plant; Singh *et al.* (2018) for individual plant yield and thousand seed weight; Wani *et al.* (2018) for individual plant yield; Chakraborty *et al.* (2014) for individual plant yield, spikelet number per panicle, width of flag leaf; Krishna *et al.* (2013) for thousand seed weight and spikelet number per panicle. Both PCV and GCV estimates were high for leaf number per tiller, stem width, weight of panicle and leaf width.

The extent of variability can be drawn by GCV and PCV, but the level of variability that is actually transferred to progeny can only be determined by the parameter's heritability and genetic advance.

A high estimate of broad sense heritability was recorded for tiller number per plant, thousand seed weight, weight of panicle, leaf number per tiller, length of internode, spikelet number per panicle, length of peduncle, stem width, leaf width, floret number per panicle, individual plant yield, day to flower initiation, length of panicle, length of flag leaf, days to 50% flowering, width of flag leaf and height of plant. These findings are in proximity with Kapoor *et al.* (2011) for length of internode, tiller number per plant, length of flag leaf, height of plant and individual plant yield; Krishna *et al.* (2013) for length of panicle; Surje and De (2014) for individual plant yield; Wagh *et al.* (2018) for height of plant and leaf width; Wani *et al.* (2018) for individual plant yield; Singh *et al.* (2018) for tiller numbers of per plant, height of plant and individual plant yield.

The estimates of genetic advance expressed as a percentage of mean were high for most of the characters. The high genetic advance as a percentage of mean (at 5% selection intensity) was recorded for tiller number per plant, leaf number per tiller, weight of panicle, stem width, leaf width, individual plant yield, length of internode and thousand seed weight. However, moderate genetic advance as a percentage of mean was recorded for width of flag leaf, spikelet number per panicle, length of flag leaf, floret number per panicle, length of panicle, height of

plant, length of peduncle, day to flower initiation, days to 50% flowering and days to maturity.

These findings are in proximity with Kapoor *et al.* (2011) for the length of internode, tiller number per plant, length of flag leaf, height of plant and individual plant yield; Krishna *et al.* (2013) for thousand seed weight and length of panicle; Surje and De (2014) for individual plant yield; Krishna *et al.* (2013) for spikelet number per panicle, thousand seed weight, length of panicle; Wagh *et al.* (2018) for height of plant and leaf width; Wani *et al.* (2018) for individual plant yield; Singh *et al.* (2018) for tiller numbers per plant, height of plant and individual plant yield.

The high genetic advance along with high heritability was noticed for tiller number per plant, leaf number per tiller, weight of panicle, stem width, leaf width, individual plant yield, length of internode and thousand seed weight (**Table 3**) as shown in **Fig. 2**. suggesting that there is little environmental influence on these character expression of these traits and preponderance of additive gene action, hence suitable for selection. Similar findings were reported by Kapoor *et al.* (2011) for length of internode, tiller number per plant, length of flag leaf, height of plant and individual plant yield, Krishna *et al.* (2013) for length of panicle, Surje and De (2014) for individual plant yield, Wagh *et al.* (2018) for height of plant and leaf width, Singh *et al.* (2018) for numbers of tillers per plant, height of plant and individual plant yield and Toppo and Sahu (2022) for thousand seed weight.

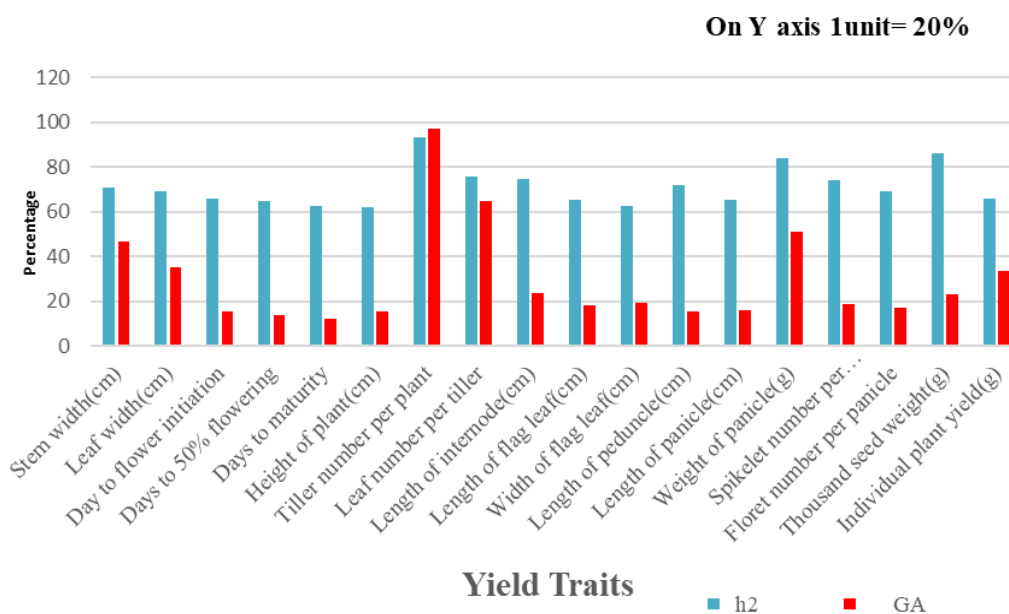


Fig. 2. Histogram of h² (broad sense) and genetic advance as per cent of mean for quantitative traits in oat lines

Table 4 represents the results of the correlation coefficient analysis for various traits. Traits such as, plant height (0.66), thousand seed weight (0.63), floret number per panicle (0.62), spikelet number per panicle (0.62), weight of panicle (0.54) and length of internode (0.44) exhibited positively significant correlation with individual plant yield at the phenotypic level. These results stated that oat lines can be improved by selecting these traits simultaneously. Earlier researchers, Chaudhary *et al.* (2014) and Sangare *et al.* (2017) reported a similar positive association for plant height with seed yield. Surje and De (2014) reported similar findings for spikelet number per panicle and height of plant. Mut *et al.* (2016) observed a positively significant correlation of seed yield with thousand seed weight. Kumar *et al.* (2016) and Bhatia *et al.* (2017) found a significant positive correlation of individual plant yield with thousand seed weights and spikelet number per panicle. Characters such as leaf number per tiller (-0.59) and tiller number per plant (-0.67) exhibited a significantly negative correlation with seed yield. **Table 4.** represents the characters which are positively inter-correlated with each other which can be useful in yield improvement.

Table 5 shows the path coefficient analysis results for yield and yield contributing traits. In the current investigation, individual plant yield was considered as a dependent variable for carrying out path coefficient analysis. It was found that the weight of panicle (1.6082) showed a very high positive direct effect on individual plant yield and characters like width of flag leaf (0.9049), floret number

per panicle (0.6249), tiller number per plant (0.4798), length of flag leaf (0.3184) exhibited a high positive direct effect on individual plant yield (**Fig. 3**). Similar results of the positive direct effect of width of flag leaf on seed yield was reported by Kapoor *et al.* (2011) and Dumlupinar *et al.* (2012) reported the positive direct effect of height of plant on seed yield. In contrast, characters like length of internode (-0.8627), leaf number per tiller (-0.8594), spikelet number per panicle (-0.8055), days to 50% flowering (-0.3738), stem width (-0.335), leaf width (-0.3062) exhibited a very high negative direct effect on individual plant yield and low negative direct effect on individual plant yield was exhibited by thousand seed weight (-0.2455), days to maturity (-0.0415) and height of plant (-0.0046). At phenotypical level the residual effect was 0.2938.

Traits such as weight of panicle, spikelet number per plant, floret number per plant, leaf number per tiller, length of internode and tiller number per plant had a high direct effect and significant positive correlation indicating a true relationship among them. Hence, selection for these traits will be effective. The correlation coefficient of height of plant is high (0.66) but direct effect is negligible (0.0046) hence, indirect selection of characters *viz.*, weight of panicle, spikelet number per plant, floret number per plant, leaf number per tiller, length of internode and tiller number per plant will be rewarding. The width of flag leaf had high direct effect but a negative correlation with seed yield hence, a restricted simultaneous selection should be made.

Table 4. Correlation coefficient analysis for yield and yield attributing traits in oat lines

Character	LW	DF	DM	PH	NTP	NLT	INL	FLL	FLW	PW	NSP	NFP	1000SW	IPY
SW	0.16	-0.17	-0.31**	0.32**	-0.38**	-0.34**	0.24*	-0.20*	-0.11	0.39**	0.32**	0.35**	0.32**	0.17
LW		-0.13	0.08	0.07	-0.09	-0.05	0.05	0.02	0.10	0.10	0.14	0.15	0.03	0.02
D50%F			0.23*	-0.36**	0.40**	0.42**	-0.27**	0.17	0.15	-0.40**	-0.28**	-0.26**	-0.23*	-0.16
DM				-0.27**	0.29**	0.25**	-0.18	0.21*	0.21*	-0.24*	-0.11	-0.11	-0.11	-0.11
PH					-0.88**	-0.82**	0.60**	-0.13	-0.32**	0.73**	0.72**	0.69**	0.69**	0.66**
NTP						0.90**	-0.68**	0.16	0.39**	-0.86**	-0.74**	-0.72**	-0.77**	-0.67**
NLT							-0.71**	0.14	0.37**	-0.82**	-0.71**	-0.69**	-0.78**	-0.59**
INL								-0.08	-0.29**	0.59**	0.53**	0.53**	0.69**	0.44**
FLL									-0.02	-0.19*	-0.21*	-0.21*	-0.09	-0.17
FLW										-0.33**	-0.20*	-0.23*	-0.15	-0.04
PW											0.70**	0.66**	0.64**	0.54**
NSP												0.91**	0.62**	0.62**
NFP													0.63**	0.62**
1000SW														0.63**

** Significant at 1% level, * Significant at 5% level

SW- Stem width, LW- Leaf width, DF %- Days to 50% flowering; DM- Days to maturity; PH- Height of plant; NTP- Tiller number per plant; NLT- Leaf number per tiller; FLL- Length of flag leaf; INL- Length of internode; FLW- Width of flag leaf; NSP- Spikelet number per panicle; NFP- Floret number per panicle; PW- Weight of panicle; 1000SW- thousand seed weight; IPY- Individual plant yield.

Table 5. Path coefficient analysis for yield and yield attributing traits in oat lines

Character	SW	LW	DF	DM	PH	NTP	NLP	INL	FLL	FLW	PW	NSP	NFP	1000SW	IPY
SW	-0.335	-0.0677	0.1805	-0.0415	-0.0023	-0.2244	0.3947	-0.3919	-0.1606	-0.3172	0.7589	-0.4244	0.3808	-0.1353	0.2006
LW	-0.0668	-0.3062	0.4040	-0.0415	-0.0004	-0.0975	0.1245	-0.1246	0.0599	-0.1211	0.3691	-0.0856	0.0435	-0.0053	0.0932
D50%F	0.1615	0.3311	-0.3738	-0.0415	0.0038	0.3837	-0.7445	0.6147	0.2373	0.6253	-1.3077	0.6595	-0.4838	0.1780	-0.3414
DM	0.3345	0.3062	0.3738	-0.0415	0.0046	-0.4798	0.8594	0.8627	-0.3184	-0.9049	-1.6082	0.8055	-0.6249	0.2455	-1.0000
PH	-0.1676	-0.0260	0.3147	-0.0415	-0.0046	-0.5901	1.0003	-0.8755	-0.0144	-0.8529	1.7293	-0.9854	0.76000	-0.3014	1.0173
NTP	0.1565	0.0622	-0.2989	-0.0415	0.0056	0.4798	-0.8131	0.8610	0.1036	0.6718	-1.5320	0.8141	-0.6401	0.2674	-0.7944
NLP	0.1537	0.0444	-0.3238	-0.0415	0.0053	0.4539	-0.8594	0.9206	0.1077	0.6154	-1.5057	0.7834	-0.6067	0.2813	-0.7515
INL	-0.1520	-0.0442	0.2663	-0.0415	-0.0046	-0.4788	0.9172	-0.8627	-0.0603	-0.8382	1.5253	-0.7771	0.6194	-0.3424	0.6986
FLL	0.1687	-0.0576	-0.2785	-0.0415	0.0002	0.1561	-0.2906	0.1633	0.3184	0.0412	-0.5998	0.4847	-0.3908	0.0297	-0.3634
FLW	0.1173	0.0410	-0.2583	-0.0415	0.0043	0.3562	-0.5845	0.7991	0.0145	0.9049	-1.2014	0.3400	-0.3336	0.1028	-0.1194
PW	-0.1579	-0.0703	0.3039	-0.0415	-0.0049	-0.4570	0.8047	-0.8182	-0.1188	-0.6760	1.6082	-0.8295	0.6441	-0.2370	0.6736
NSP	-0.1763	-0.0326	0.3061	-0.0415	-0.0056	-0.4849	0.8358	-0.8323	-0.1916	-0.3819	1.6562	-0.8055	0.5589	-0.2681	1.0222
NFP	-0.2039	-0.0213	0.2893	-0.0415	-0.0056	-0.4914	0.8343	-0.8550	-0.1991	-0.4831	1.6576	-0.7203	0.6249	-0.2763	1.0258
1000SW	-0.1844	-0.0066	0.2710	-0.0415	-0.0056	-0.5226	0.9849	-1.2032	-0.0385	-0.3789	1.5531	-0.8796	0.7034	-0.2455	1.0621

Direct effects are represented in bold value

Residual effect: 0.2938

SW- Stem width, LW- Leaf width, DF %- Days to 50% flowering; DM- Days to maturity; PH- Height of plant; NTP- Tiller number per plant; NLT- Leaf number per tiller; FLL- Length of flag leaf; INL- Length of internode; FLW- Width of flag leaf; NSP- Spikelet number per panicle; NFP- Floret number per panicle; PW- Weight of panicle; 1000SW- thousand seed weight; IPY- Individual plant yield.

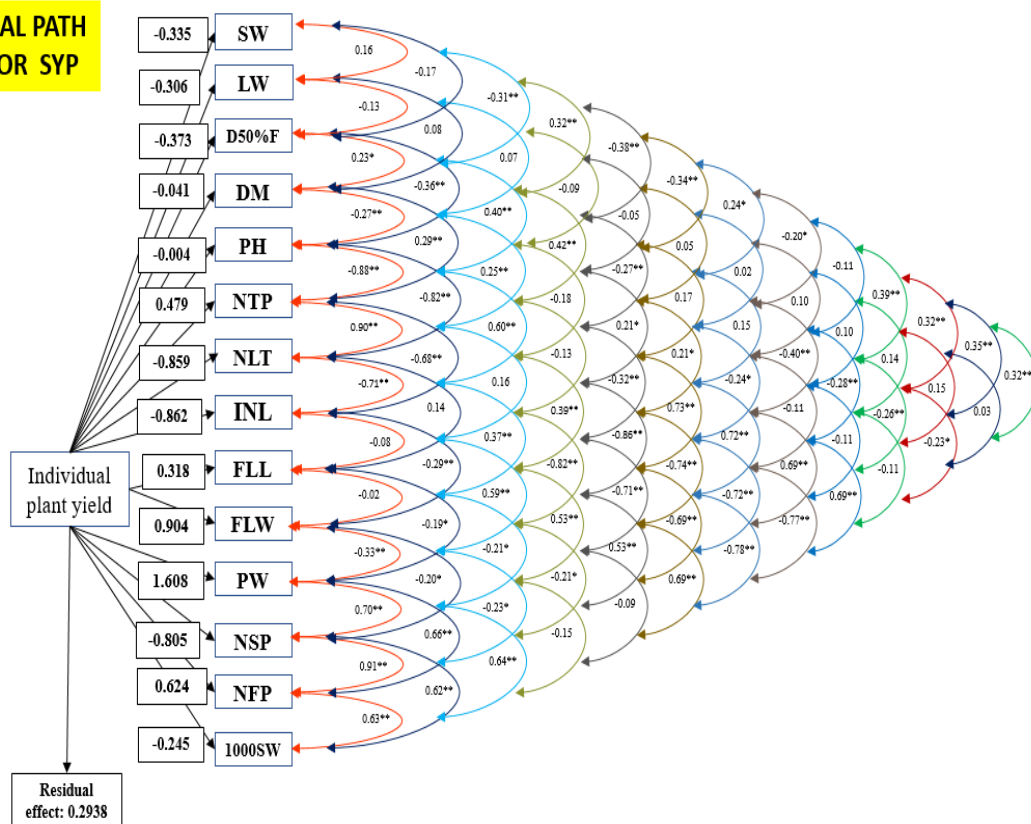
**PHENOTYPICAL PATH
DIAGRAM FOR SYP**


Fig. 3. Phenotypal path diagram for individual plant yield

An overall consideration of the results disclosed that characters such as leaf number per tiller, stem width, weight of panicle and leaf width showed high estimates of PCV and GCV indicating that greater variation is present for these traits, so direct selection of such traits will be fruitful for improvement of the crop. Similarly, association studies showed that individual plant yield could be improved through selection for traits, weight of panicle, thousand seed weight, height of plant and floret number per panicle as they exhibited high positive association and direct effect. So, these traits may be used for the development of plant ideotype and selecting these traits will be worthwhile for higher yield.

ACKNOWLEDGEMENT

The study was supported by ICAR- All India Co-Ordinated Research Project on Forage Crops and Utilization and Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) – 482004

REFERENCES

Ahmed, S., Roy, A.K. and Majumdar, A.B. 2013. Correlation and path coefficient analysis for fodder and grain yield related. *Annals of Biology*, **29**(1):75-8.

Bhatia, D., Joshi, S., Das, A., Vikal, Y., Sahi, G.K., Neelam, K., Kaur, K. and Singh, K. 2017. Introgression of yield component traits in rice (*Oryza sativa* ssp. *indica*) through interspecific hybridization. *Crop Science*, **57**(3):1557-1573. [\[Cross Ref\]](#)

Burton, G.W. and De Vane, E.H. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, **45**: 478-481. [\[Cross Ref\]](#)

Chakraborty, J.A., Arora, R.N., Joshi, U.N. and Chhabra, A.K. 2014. Evaluation of *Avena species* for yield, quality attributes and disease reaction. *Forage Research*, **39**(4):179-84.

Chaudhary, P.K., Vishvakarma, D.N., Singh, P.K. and Kumar, V. 2014. Studies of genotypic and phenotypic correlation coefficient in some quantitative characters in oat (*Avena Sativa* L.). *The Society for Scientific Development in Agriculture and Technology*, **9**:577-583.

Dewey, D.R. and Lu, K. 1959. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy journal*, **51**(9):515-518. [\[Cross Ref\]](#)

- Dumlupinar, Z., Kara, R., Dokuyucu, T. and Akkaya, A. 2012. Correlation and path analysis of grain yield and yield components of some Turkish oat genotypes. *Pakistan Journal of Botany*, **44**(1):321-325.
- Hanson, W.D., Robinson, H.F. and Comstock, R.E. 1956. Biometrical studies of yield segregating population Korean lespandeza. *Agronomy Journal*, **48**: 268-272. [Cross Ref]
- Johnson, H.W., Robinson, H.E. and Comstock, R.F. 1955. Genotypic and phenotypic correlations in soyabeans and their implications in selection. *Agronomy Journal*, **47**: 447-483. [Cross Ref]
- Kapoor, R., Bajaj, R.K., Sidhu, N. and Kaur, S. 2011. Correlation and path coefficient analysis in oat (*Avena sativa* L.). *International Journal of Plant Breeding*, **5**(2):133-136.
- Krishna, A., Ahmed, S., Pandey, H.C. and Bahukhandi, D. 2013. Estimates of genetic variability, heritability and genetic advance of oat (*Avena sativa* L.) genotypes for grain and fodder yield. *Agricultural Science Research Journals*, **3**(2):56-61.
- Kumar, P., Phogat, D.S. and Kumari, P. 2016. Correlation and path coefficient analysis studies in oat (*Avena sativa* L.). *Forage research*, **42**(3):198-200.
- Kumari, T. and Jindal, Y. 2019. Genetic diversity and variability analysis in oats (*Avena sp*) genotypes. *Electronic Journal of Plant Breeding*, **10**(1):1-8. [Cross Ref]
- Murphy, J.P. and Hoffman, L.A. 1992. The origin, history, and production of oat. *Oat science and technology*, **33**:1-28. [Cross Ref]
- Mut, Z., Kose, O.E. and Akay, H. 2016. Grain yield and some quality traits of different oat (*Avena sativa* L.) genotypes. *International Journal of Environmental & Agriculture Research*, **2**(12):83-88.
- Nirmalakumari, A., Sellammal, R., Thamotharan, G., Ezhilarasi, T. and Ravikesavan, R. 2013. Trait association and path analysis for grain yield in oat in the Western Zone of Tamil Nadu. *International Journal of Agricultural Science*, **3**(2):331-338.
- Pearson, K. 1901. Determination of the coefficient of correlation. *Science*, **30**(757):23-25. [Cross Ref]
- Sangare, J.R., Konate, A.K., Cisse, F. and Sanni, A. 2017. Assessment of genetic parameters for yield and yield related-traits in an intraspecific rice (*Oryza sativa* L.) population. *Journal of plant breeding and Genetics*, **5**(2):45-56.
- Singh, A., Vyas, R.P., Kumar, S., Singh, H.C., Deep, A., Malik, P. and Singh, A. 2018. Genetic variability and correlation of seed yield and related characters in oat (*Avena sativa* L.). *International Journal of Current Science*, **6**(1):1532-1537.
- Sivasubramanian, S. and Madhavamenon, P. 1973. Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*, **60**(9-13):1093-6.
- Surje, D.T. and De, D.K. 2014. Correlation coefficient study in oat (*Avena sativa* L.) genotypes for fodder and grain yield characters. *Journal of Agricultural Science and Technology*, **1**(1):89-93.
- Toppo, R. and Sahu, M. 2022. Frequency distribution and genetic variability parameters assessment for forage yield attributing traits in oats (*Avena sativa* L.). *Electronic Journal of Plant Breeding*, **13**(1):92-97. [Cross Ref]
- Wagh, V., Sonone, A. and Damame, S. 2018. Assessment of genetic variability, correlations and path coefficient analysis in forage oat (*Avena sativa* L.). *Forage Research*, **44**(3):172-175.
- Wani, S.A., Habib, M., Bhat, M.A., Dar, Z.A., Lone, A.A., Ansar-ul-Haq, S., Ali, G., Zaffar, G., Bashir, S., Nissa, S. and Khan, A. 2018. Variability and diversity in advanced oat lines under temperate condition. *International journal of pure and applied bioscience*, **6**(3):243-50. [Cross Ref]