Biological Forum – An International Journal **13(4): 940-945(2021)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Genetic Correlation and Path Analysis for Yield and Quality Attributes in Oat (*Avena sativa* L.)

Rukoo Chawla[1*], Minakshi Jattan[2], D.S. Phogat[3], Nisha Kumari[2], Sandeep Kumar[2] and Atman Poonia[1]
[1]Ph.D. Scholar, Department of Genetics and Plant Breeding,
COA, CCS Haryana Agricultural University, Hisar (Haryana), India.
[2]Assistant Scientist, Department of Genetics and Plant Breeding,
COA, CCS Haryana Agricultural University, Hisar (Haryana), India.
[3]Principal Scientist (Retired), Department of Genetics and Plant Breeding,
COA, CCS Haryana Agricultural University, Hisar (Haryana), India.

(Corresponding author: Rukoo Chawla)*

(Received 29 September 2021, Accepted 18 November, 2021)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Oat (*Avena sativa* L.) is an important winter forage crop suitable for green fodder. Oat has also progressively contributed as a source for human consumption because of its nutritional attributes. Correlation coefficient and path analysis were done to determine the interrelationships and effects among the seventeen yield and quality traits. This will assist in selecting meritorious traits and formulating strategies to accomplish maximum yield potential along with genetic gain for quality attributes. The study was conducted on sixty two oat genotypes in an augmented design during *Rabi* 2019-20 at Research Farm Area of Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The analysis was done using R studio software 4.0.3. Positive and significant correlation of green fodder yield was recorded with dry matter yield, seed yield, test weight, peduncle length, number of leaves per plant, tillers per plant and plant height. Tillers per plant, number of leaves, leaf width, number of spikelets per panicle, green fodder yield, dry matter yield, test weight and days to maturity exhibited positive and significant correlation with seed yield. Path analysis revealed that tillers per plant, number of spikelets per panicle, test weight and plant height had high positive direct effect on seed yield. Number of leaves, green fodder yield, dry matter yield and fodder crude protein via tillers per plant showed high positive indirect effects on seed yield. The residual effect (0.20) indicated that the component traits under study were responsible for around 80% of the variability in seed yield/plant. The study will be helpful in hybridization programmes by including those genotypes possessing a combination of significantly associated traits to maximize fodder or seed yield along with quality.

Keywords: correlation, fodder yield, oat, path analysis, quality traits, seed yield.

INTRODUCTION

Oat (*Avena sativa* L.) is a multipurpose cereal crop grown mainly in temperate and subtropical climates. It is usually considered as a secondary crop as it is derived from a weed of the primary cereal having genome size estimated to be 12.3 Gigabase (Gb**)**. Oat is widely cultivated in the cool and moist climate of Europe, Northern America, Russia, Canada, the United States, Finland, Poland, etc. The global area under oat cultivation covers 10.12 million hectares with a production of 25.56 million metric tons (USDA, April 2021). Earlier oat was dominantly grown by farmers for sole fodder purposes. The grounds for considering oat as an exceptional fodder crop is because of its growth habit, multi-cut nature, high nutritive value and quick regeneration habit. However, with thriving on non-lodging, nitrogen responsive oat cultivars; it has gained value for grain purposes as well. In recent years, oat grain has been used as livestock feed (Nikolaudakis, 2016) for horses, sheep and poultry as it is soft, palatable and rich in fodder crude protein (10-12 percent). Thus devising oat as a salutary crop contributes to both the livestock and agriculture sectors. There are huge benefits of the consumption of oat as it has compounds that help to reduce blood pressure and cholesterol. Oat has beneficial plant compounds called polyphenols and anti-proliferative capacities which are present in its bran (Chen *et al.*, 2018). A special component that makes oat a beneficial healthy substitute is that it contains a large amount of beta-glucan. Beta-glucan is useful in reducing low-density lipoprotein and total cholesterol levels thus reducing the risk of heart diseases **(**Brown *et al.*, 1999).

The selection procedure in plant breeding is important to reveal the nature of the association between different traits with the economically important dependent trait. Correlation analysis offers plant breeders to apply indirect selection for complex or quantitative traits which cannot be selected directly like seed yield/green fodder yield. The path coefficient analysis explains that whether the association of each trait with yield is due to its direct effect on yield or it is a consequence of indirect effects via other component traits. In today's epoch of differentia, quality traits are equally consequential as improvement in yield. Therefore, the present study was done to find out the affinity among yield and quality contributing traits in 62 oat genotypes.

MATERIALS AND METHOD

The study was conducted at the Research Farm Area of Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar (Haryana) during *Rabi* 2019-20. The Research Farm Area is situated nearly 3.8 km away from the main campus and at about 29°10′N latitude, 75°44′E longitude and an altitude of 228 m from sea level. Sixty two oat genotypes including three checks (OS 6, JHO 851 and UPO 212) were grown in an augmented design with seven blocks (Table 1). A total of 17 yield and quality traits were studied. The correlation and path analysis was done using R studio software. The graphical representation and diagrams were drawn using R software as well.

Table 1: List of 62 oat genotypes used in the study.

Sr. No.	Genotype	Source	Sr. No.	Genotype	Source
1.	GP 65	CCS HAU, HISAR	32.	HFO 1109	CCS HAU, HISAR
2.	GP 68	CCS HAU, HISAR	33.	HFO 1111	CCS HAU, HISAR
3.	GP 158	CCS HAU, HISAR	34.	HFO 1112	CCS HAU, HISAR
4.	GP 192	CCS HAU, HISAR	35.	HFO 1113	CCS HAU, HISAR
5.	GP 298	CCS HAU, HISAR	36.	HFO 1114	CCS HAU, HISAR
6.	GP 492	CCS HAU, HISAR	37.	HFO 1115	CCS HAU, HISAR
7.	GP 580	CCS HAU, HISAR	38.	HFO 1116	CCS HAU, HISAR
8.	GP 781	CCS HAU, HISAR	39.	HFO 1117	CCS HAU, HISAR
9.	GP 875	CCS HAU, HISAR	40.	HFO 1118	CCS HAU, HISAR
10.	HFO 424	CCS HAU, HISAR	41.	HFO 1121	CCS HAU, HISAR
11.	HFO 529	CCS HAU, HISAR	42.	HFO 1122	CCS HAU, HISAR
12.	HFO 607	CCS HAU, HISAR	43.	HFO 1123	CCS HAU, HISAR
13.	HFO 611	CCS HAU, HISAR	44.	HJ 8	CCS HAU, HISAR
14.	HFO 707	CCS HAU, HISAR	45.	OS403	CCS HAU, HISAR
15.	HFO 806	CCS HAU, HISAR	46.	OL 125	PAU, LUDHIANA
16.	HFO 818	CCS HAU, HISAR	47.	OL 1861	PAU, LUDHIANA
17.	HFO 901	CCS HAU, HISAR	48.	OL 1869-1	PAU, LUDHIANA
18.	HFO 902	CCS HAU, HISAR	49.	OL 1766-2	PAU, LUDHIANA
19.	HFO 903	CCS HAU, HISAR	50.	OL 1874-2	PAU, LUDHIANA
20.	HFO 915	CCS HAU, HISAR	51.	KENT	AUSTRALIA
21.	HFO 917	CCS HAU, HISAR	52.	RO 11-2-2	MPKV, RAHURI
22.	HFO 1003	CCS HAU, HISAR	53.	RO 11-2-6	MPKV, RAHURI
23.	HFO 1005	CCS HAU, HISAR	54.	JHO 822	IGFRI, JHANSI
24.	HFO 1013	CCS HAU, HISAR	55.	JHO 99-1	IGFRI, JHANSI
25.	HFO 1016	CCS HAU, HISAR	56.	JHO 2006-1	IGFRI, JHANSI
26.	HFO 1101	CCS HAU, HISAR	57.	JO 1	JNKVV, JABALPUR
27.	HFO 1104	CCS HAU, HISAR	58.	NDO 1	NDUAT, FAIZABAD
28.	HFO 1105	CCS HAU, HISAR	59.	PLP 1	CSKHPKV, PALAMPUR
29.	HFO 1106	CCS HAU, HISAR	60.	OS 6 (C_1) *	CCSHAU, HISAR,
30.	HFO 1107	CCS HAU, HISAR	61.	JHO 851 (C_2)	IGFRI, JHANSI
31.	HFO 1108	CCS HAU, HISAR	62	UPO 212 (C_3)	GBPUAT, PANTNAGAR

*C_1= Check 1, C_2= Check 2, C_3= Check 3

RESULTS AND DISCUSSION

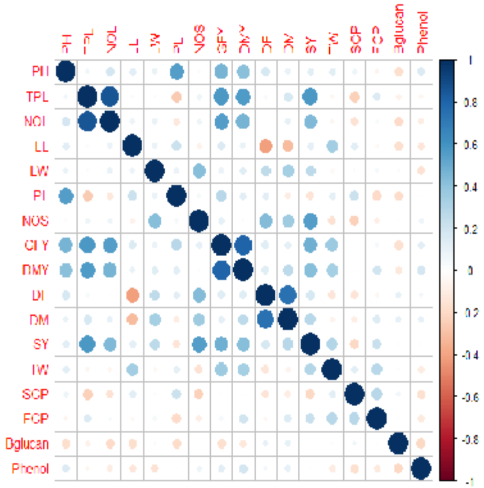
Correlation analysis. Economic traits whether seed yield, green fodder yield or dry matter yield are considered complex quantitative traits. Direct selection for such traits is unsuccessful. Therefore, indirect selection has to be practised in breeding programmes. This can be achieved by incorporating those traits which show a high positive significant correlation with yield. The genotypic correlation coefficients among the 17 traits in 62 oat genotypes are presented in Table 2. Correlation analysis is also illustrated in form of a correlation graph (Fig. 1). The scatter diagram along with frequency distribution is shown in Fig. 2. Results showed that plant height exhibited a positive and significant correlation with peduncle length (0.56), green fodder yield (0.47) and dry matter yield (0.41). Tillers per plant showed a positive and significant correlation with green fodder yield (0.58), seed yield (0.57), dry matter yield (0.57) and number of leaves (0.86) while a negative significant correlation was found with peduncle length (-0.25). Number of leaves per plant exhibited a positive and significant correlation with green fodder yield (0.55), dry matter yield (0.46) and seed yield (0.45). Leaf length showed a positive and significant correlation with test weight (0.35) while a negative significant correlation was found with days to 50% flowering (-0.41) and days to maturity (-0.31). Leaf width exhibited a positive and significant correlation with number of spikelets per panicle (0.42), days to 50% flowering (0.26), days to maturity (0.33) and seed yield (0.27). Negi *et al.*, (2019); Wagh *et al.*, (2018); Poonia *et al*., (2017); Kumar *et al.*, (2016); Krishna *et al*., (2014); Ahmed *et al*. (2013); Kapoor *et al.*, (2011) observed similar results in oat.

Table 2: Genotypic correlation coefficients among 17 traits studied in 62 oat genotypes.

	PH	TPL	NOL	LL	LW	PL	NOS	GFY	DMY	DF	DM	SY	TW	SCP	FCP	βglucan	Phenol%
PH	1	0.06	0.19	0.12	0.09	0.56**	0.03	0.47**	0.41**	0.17	0.10	0.12	0.12	0.08	-0.06	-0.18	0.16
TPL		1	0.86**	-0.03	0.02	-0.25*	0.08	0.58**	0.57**	0.04	0.17	0.57**	-0.06	-0.23	0.15	-0.08	-0.06
NOL			1	0.09	0.09	-0.13	0.08	0.55**	0.46**	0.00	0.10	0.45**	-0.06	-0.15	0.04	-0.19	-0.11
LL				1	0.09	0.22	-0.07	0.16	0.09	-0.41**	-0.31*	0.11	0.35*	0.13	-0.04	-0.17	-0.13
LW					1	0.08	0.42**	0.09	0.14	0.26*	0.33*	0.27*	-0.03	-0.03	0.05	-0.03	-0.15
PL						1	0.05	0.28*	0.13	0.12	-0.10	-0.15	0.11	0.21	-0.20	-0.19	0.00
NOS							1	0.11	-0.02	0.44**	0.35**	0.55**	-0.16	-0.23	-0.10	-0.01	0.08
GFY								1	0.81**	0.14	0.11	0.49**	0.37**	0.00	0.05	-0.17	0.12
DMY									1	0.14	0.27*	0.42**	0.33*	0.01	0.20	-0.13	0.18
DF										1	0.75**	0.17	-0.14	-0.15	-0.04	0.11	0.05
DM											1	0.28*	-0.06	-0.10	0.14	0.10	0.10
SY												1	0.30*	-0.21	0.23	-0.01	-0.01
TW													1	0.13	0.27*	-0.02	-0.11
SCP														1	0.27*	0.06	-0.17
FCP															1	0.01	-0.11
βglucan																1	-0.21
Phenol																	1

PH- plant height, TPL- Tillers per plant, NOL- Number of leaves per plant, LL- Leaf length (cm), LW- Leaf width (cm), PL- Peduncle length (cm), NOS- Number of spikelets/panicle, GFY- Green fodder yield per plant (g), DMY- Dry matter yield per plant (g), DF- Days to 50% flowering, DM- Days to maturity, SY- seed yield per plant (g), TW- Test weight (g) (1000 seed weight), (g), SCP- seed crude protein (%), FCP- Fodder crude protein(%), β-glucan- Beta glucan in grains (%), Phenol- Phenols in grains

(** Significant at 1%, * Significant at 5%)



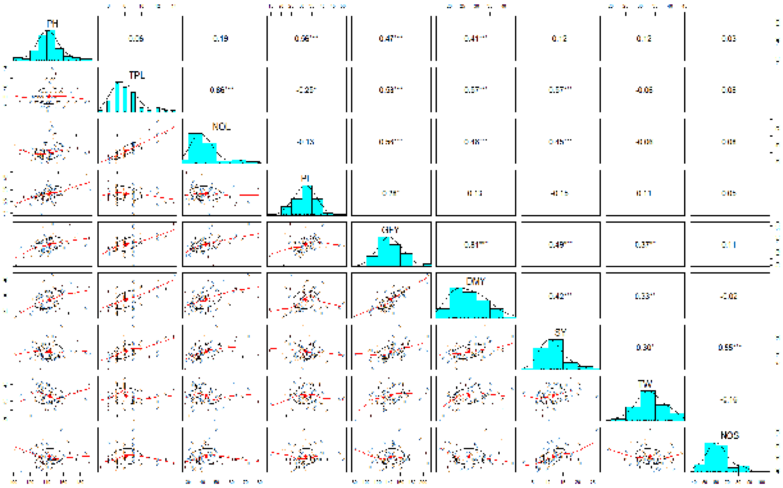
Higher the correlation coefficient value, higher the diameter of the circular shape and darker the intensity of color; red-negative correlation coefficient, blue-positive correlation coefficient

PH- plant height, TPL- Tillers per plant, NOL- Number of leaves per plant, LL- Leaf length (cm), LW- Leaf width (cm), PL- Peduncle length (cm), NOS- Number of spikelets/panicle, GFY- Green fodder yield per plant (g), DMY- Dry matter yield per plant (g), DF- Days to 50% flowering, DM- Days to maturity, SY- seed yield per plant (g), TW- Test weight (g) (1000 seed weight), (g), SCP- seed crude protein (%), FCP- Fodder crude protein(%), Bglucan- Beta glucan in grains (%), Phenol- Phenols % in grains

Fig. 1. Correlation graph: Genotypic correlation among seventeen traits under study.

Peduncle length indicated a positive and significant correlation with green fodder yield (0.28). Poonia *et al.*, (2018) found a similar result in oat. Number of spikelets exhibited a positive and significant correlation with days to 50% flowering (0.44), days to maturity (0.35) and seed yield (0.55). Green fodder yield also exhibited a positive and significant correlation with dry matter yield (0.81), seed yield (0.49) and test weight (0.37). Similarly, a high correlation was found between green fodder yield and seed yield as observed by Ahmed *et al.*, (2013). Dry matter yield also exhibited a positive and significant correlation with days to maturity (0.27), seed yield (0.42) and test weight (0.33). These findings were in agreement with Poonia *et al.*, (2018); Nirmalakumari *et al.* (2013) and Hisir *et al.*, (2012). The positive correlation of green fodder yield per plant with dry matter yield per plant was aligned with the findings of Chaudhary *et al.*, (2020); Jaipal and Shekhawat (2016); Krishna *et al.*, (2014); Mushtaq *et al.*, (2013); Nirmalakumari *et al.*, (2013) in oat.

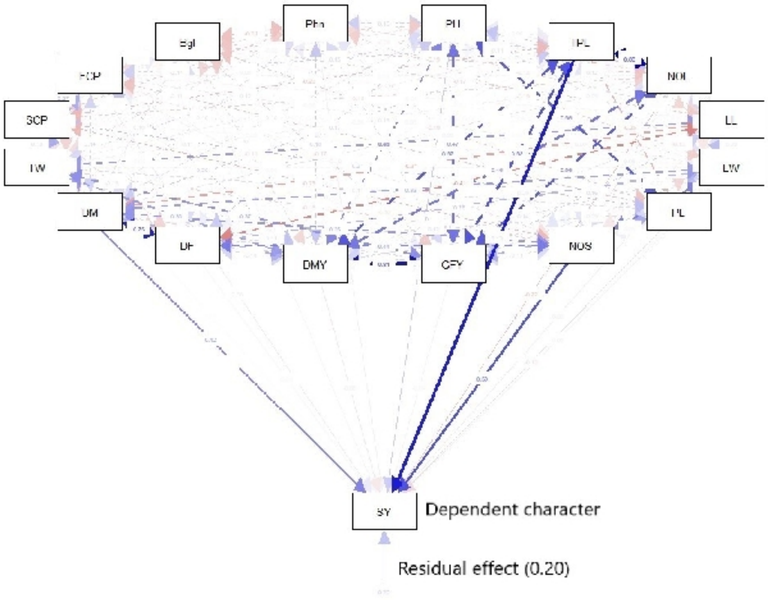
Days to 50% flowering demonstrated a positive and consequentially significant correlation with days to maturity (0.75). A strong correlation between days to 50% flowering and days to maturity, similar to the present study was also observed by Kumar *et al.*, (2016). Days to maturity exhibited a positive and significant correlation with seed yield (0.28). Seed yield exhibited a positive and significant correlation with tillers per plant, leaf width, green fodder yield, number of spikelets per panicle, dry matter yield, number of leaves, days to maturity and test weight (0.30). These results were in agreement to the findings of Bibi *et al.*, (2012), Premkumar *et al.*, (2017); Nirmalakumari *et al.*, (2013) in oat. Ahmed *et al.*, (2013) observed results similar to the present findings for seed yield with leaf width and number of leaves. Test weight also exhibited a positive and significant correlation with fodder crude protein (0.27). Seed crude protein exhibited a positive and significant correlation with fodder crude protein (0.27). Poonia *et al.*, (2018) observed a similar result in oat. Seed crude protein was found to be significantly correlated to fodder crude protein which will help in the selection of parents in crop improvement beneficial for both fodder as well as grain purpose. In the present study, beta-glucan and phenol content were not found to be significantly correlated with yield. The possible justification for this can be residual effect obtained from analysis as there is a scope of studying more traits in the oat crop. Another possible and prominent justification for this can be due to varying environmental conditions from season to season.



PH- plant height, TPL- Tillers per plant, NOL- Number of leaves per plant, PL- Peduncle length (cm), NOS- Number of spikelets/panicle, GFY- Green fodder yield per plant (g), DMY- Dry matter yield per plant (g), SY- seed yield per plant (g), TW- Test weight (g)

Fig. 2. Correlation coefficient, frequency distribution and scatter diagram presenting traits which showed a high significant positive correlation with the economic traits

Path coefficient analysis. Correlation of a particular trait with fodder or seed yield does not necessarily mean a direct and positive effect of that studied trait on fodder or seed yield. Hence, to surmount this, path coefficient analysis was done. It is an effective method of selecting meritorious traits useful in selection programmes of crop improvement. It analyzes cause and effect relationships and partitions the correlation into direct and indirect effects. It provides an estimate of both the magnitude and significance of causal connections between variables. In the present study, path coefficient analysis was done considering seed yield per plant as a dependent character. Partitioning of the total correlation coefficient into direct and indirect effects for seed yield per plant showed a high direct effect on yield contributing traits. Path coefficient values among the 17 traits in 62 oat genotypes are presented in Table 3. Path diagram as shown in Fig. 3 is like a flow chart including different variables which are interconnected with lines describing flow in which the variables under study are related to each other and eventually its effect on dependent character.



PH- plant height, TPL- Tillers per plant, NOL- Number of leaves per plant, LL- Leaf length (cm), LW- Leaf width (cm), PL- Peduncle length (cm), NOS- Number of spikelets/panicle, GFY- Green fodder yield per plant (g), DMY- Dry matter yield per plant (g), DF- Days to 50% flowering, DM- Days to maturity, SY- seed yield per plant (g), TW- Test weight (g) (1000 seed weight), (g), SCP- seed crude protein (%), FCP- Fodder crude protein(%), Bgl- Beta glucan in grains (%), Phn- Phenols% in grains

Fig. 3. Path diagram. Direct, indirect and residual effects considering seed yield as dependent character. Positive and negative effects are shown by blue and red color respectively; color intensity proportional to value of its respective coefficient

Table 3: Path coefficient analysis of 17 traits studied in 62 oat genotypes.

	PH	TPL	NOL	LL	LW	PL	NOS	GFY	DMY	DF	DM	TW	SCP	FCP	βglucan	Phenol%
PH	**0.167**	0.048	-0.042	0.008	0.005	-0.070	0.016	-0.022	-0.032	-0.005	-0.001	0.050	0.001	-0.004	-0.006	0.008
TPL	0.010	**0.771**	-0.191	-0.002	0.001	0.032	0.045	-0.026	-0.044	-0.001	-0.002	-0.024	-0.003	0.010	-0.002	-0.003
NOL	0.031	0.662	**-0.222**	0.006	0.005	0.016	0.047	-0.026	-0.036	0.000	-0.001	-0.023	-0.002	0.003	-0.006	-0.005
LL	0.020	-0.021	-0.019	**0.064**	0.005	-0.027	-0.044	-0.007	-0.007	0.013	0.003	0.145	0.002	-0.003	-0.005	-0.006
LW	0.015	0.019	-0.020	0.006	**0.052**	-0.011	0.248	-0.004	-0.010	-0.008	-0.003	-0.015	0.000	0.003	-0.001	-0.006
PL	0.093	-0.194	0.028	0.014	0.004	**-0.126**	0.029	-0.013	-0.010	-0.004	0.001	0.046	0.003	-0.013	-0.006	0.000
NOS	0.005	0.059	-0.018	-0.005	0.022	-0.006	**0.590**	-0.005	0.002	-0.014	-0.004	-0.066	-0.003	-0.006	0.000	0.004
GFY	0.078	0.444	-0.124	0.010	0.004	-0.035	0.065	**-0.046**	-0.063	-0.004	-0.001	0.155	0.000	0.003	-0.005	0.005
DMY	0.069	0.437	-0.103	0.006	0.007	-0.016	-0.011	-0.037	**-0.078**	-0.004	-0.003	0.138	0.000	0.013	-0.004	0.009
DF	0.029	0.028	0.001	-0.026	0.013	-0.016	0.258	-0.006	-0.011	**-0.032**	-0.007	-0.057	-0.002	-0.003	0.003	0.003
DM	0.017	0.134	-0.022	-0.020	0.017	0.013	0.209	-0.005	-0.021	-0.024	**-0.010**	-0.027	-0.001	0.009	0.003	0.005
TW	0.020	-0.045	0.012	0.022	-0.002	-0.014	-0.094	-0.017	-0.026	0.004	0.001	**0.418**	0.002	0.018	-0.001	-0.005
SCP	0.013	-0.180	0.034	0.008	-0.001	-0.027	-0.136	0.000	-0.001	0.005	0.001	0.052	**0.015**	0.018	0.002	-0.007
FCP	-0.010	0.118	-0.008	-0.003	0.003	0.025	-0.058	-0.002	-0.015	0.001	-0.001	0.114	0.004	**0.065**	0.000	-0.005
βglucan	-0.030	-0.059	0.043	-0.011	-0.002	0.024	-0.004	0.008	0.010	-0.003	-0.001	-0.008	0.001	0.001	**0.032**	-0.009
Phenol	0.028	-0.049	0.025	-0.008	-0.006	0.001	0.050	-0.005	-0.015	-0.002	-0.001	-0.043	-0.002	-0.007	-0.007	**0.046**

PH- plant height, TPL- Tillers per plant, NOL- Number of leaves per plant, LL- Leaf length (cm), LW- Leaf width (cm), PL- Peduncle length (cm), NOS- Number of spikelets/panicle, GFY- Green fodder yield per plant (g), DMY- Dry matter yield per plant (g), DF- Days to 50% flowering, DM- Days to maturity, SY- seed yield per plant (g), TW- Test weight (g) (1000 seed weight), (g), SCP- seed crude protein (%), FCP- Fodder crude protein(%), β-glucan- Beta glucan in grains (%), Phenol- Phenols% in grains

Direct effect. The path coefficient analysis exhibited high direct and positive effects of tillers per plant (0.771), number of spikelets per plant (0.590), test weight (0.418), plant height (0.167) which depicted the importance of association of these traits with seed yield while number of leaves (-0.222), peduncle length (-0.126), green fodder yield (-0.046), dry matter yield (-0.078) days to 50% flowering (-0.032) and days to maturity (-0.010) had negative direct effect on seed yield.

Indirect effect. Leaf length (0.145), green fodder yield (0.155), dry matter yield (0.138), fodder crude protein (0.114) via test weight; leaf width (0.248), days to 50% flowering (0.258), days to maturity (0.209) via number of spikelets; number of leaves (0.662), green fodder yield (0.444), dry matter yield (0.437) and fodder crude protein (0.118) via tillers per plant had high indirect positive effect on seed yield. However, seed crude protein (-0.136) via number of spikelets; tillers per plant (-0.191), green fodder yield (-0.124) and dry matter yield (-0.103) via number of leaves; peduncle length (-0.194) and seed crude protein (-0.180) via tillers per plant had high negative indirect effect on seed yield.

Residual effect. The residual effect calculated was 0.20. This indicated that a considerable magnitude of variation was present for the association of seed yield with dependent traits. The residual effect indicated that the component traits under study were responsible for about 80% of the variability in seed yield/plant.

Partitioning of genotypic correlation between seed yield per plant and its component traits revealed that the direct effects were, in general, of higher magnitude than those of their indirect effects for all the traits. Kumar *et al.* (2016) observed a high value of the direct effect of number of spikelets per panicle, test weight and plant height on seed yield and a negative direct effect of peduncle length on seed yield. Similarly, Nirmalakumari *et al.*, (2013) observed a high value of the direct effect of test weight on seed yield in oat.

CONCLUSION

In the present study, it was observed that traits *viz.*, plant height, tillers per plant, number of leaves, seed yield and test weight exhibited a positive and significant correlation with green fodder as well as with dry matter yield. Tillers per plant, leaf width, green fodder yield, number of spikelets per panicle, dry matter yield, number of leaves, days to maturity and test weight exhibited a positive and significant correlation with seed yield and need to be given more selection pressure for improving seed yield. The path coefficient analysis exhibited high direct and positive effects of tillers per plant, number of spikelets per plant, test weight and plant height which depicted the importance of association of these traits with seed yield. Therefore, breeders should formulate a selection criterion at the morphological level because some of the component traits discussed above have affected the seed yield directly.

FUTURE SCOPE

The findings suggest that traits associated positively and significantly with complex yield trait will be helpful in indirect selection for improving yield traits in oat and formulating model plant type in plant breeding programmes.

Acknowledgement. The research was financially supported by the Director of Research, CCS Haryana Agricultural University, Hisar (Haryana), The completion of this undertaking could not have been possible without the assistance of so many people whose names may not be enumerated and facilities provided for the research by the university.

Conflict of Interest. None.

REFERENCES

Ahmed, S., Roy, A. K. and Majumdar, A. B. (2013). Correlation and path coefficient analysis for fodder and grain yield related traits in oats (*Avena sativa* L.). *Annals of Biology, 29*(1): 75-78.

Bibi, A., Shahzad, A. N., Sadaqat, H. A., Tahir, M. H. and Fatima, B. (2012). Genetic characterization and inheritance studies of oats (*Avena sativa* L.) for green fodder yield. *International journal of Biology, Pharmacy and Allied Sciences, 1*(4): 450-460.

Brown, L., Rosner, B., Willett, W. W. and Sacks, F. M. (1999). Cholesterol-lowering effects of dietary fiber: a meta-analysis. *The American journal of clinical nutrition, 69*(1): 30-42.

Chaudhary, M., Singh, S. K., Kumar, M., Chand, P. and Kumar, M. (2020). Genetic variability, heritability and character association among yield and yield attributing traits in oats (*Avena sativa* L). *International Journal of Chemical Studies*, *8*(5): 1295-1301.

Chen, C., Wang, L., Wang, R., Luo, X., Li, Y., Li, J. and Chen, Z. (2018). Phenolic contents, cellular antioxidant activity and antiproliferative capacity of different varieties of oats. *Food Chemistry, 239*: 260–267.

Hisir, Y., Kara, R. and Dokuyucu, T. (2012). Evaluation of oat (*Avena sativa* L.) genotypes for grain yield and physiological traits. *Agriculture, 99*(1): 55-60.

Kapoor, R., Bajaj, R. K., Sidhu, N. and Kaur, S. (2011). Correlation and path coefficient analysis in oat. *International Journal of Plant Breeding*, *5*: 133-137.

Krishna, A., Ahmed, S., Pandey, H. C. and Kumar, V. (2014). Correlation, path and diversity analysis of oat (*Avena sativa* L.) genotypes for grain and fodder yield. *Journal of Plant Science and Research, 1*: 1-9.

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.

Mushtaq, A., Gul Zaffar, S. D., Mir, Z. A., Dar, S. H., Dar, S. I. and Bukhari, G. H. K. (2013). Estimation of correlation coefficient in oats (*Avena sativa* L.) for forage yield, grain yield and their contributing traits. *Journal of Plant Breeding and Genetics*, *7*: 188- 191.

Negi, H., Prasad, B., Kumar, A. and Kumar, S. (2019). Simple correlation and phenotypic path coefficient analysis in oat germplasm. *International Journal of Chemical Studies, 7*(3): 1174-1178.

Nikoloudakis, N., Bladenopoulos, K. and Katsiotis, A. (2016). Structural patterns and genetic diversity among oat (*Avena sativa*) landraces assessed by microsatellite markers and morphological analysis. *Genetic Resources and Crop Evolution*, *63*: 801–811.

Nirmalakumari, A., Sellammal, R., Thamodharan, G., Ezhilarasi, T. and Balasubramanian, T. (2013). Qualitative characterization and assessment of variability in oat genotypes. *Green Farming*, *6*: 749-752.

Poonia, A., Phogat, D. S., Bhuker, A. and Chhavikant (2018). Study of character association and path coefficient analysis for quantitative and qualitative traits in multi-cut oat. *Journal of Pharmacognosy and Phytochemistry, 7*(4): 77-83.

Poonia, A., Phogat, D. S., Pahuja, S. K., Bhuker, A. and Khatri, R. S. (2017). Variability, character association and path coefficient analysis in fodder oat for yield and quality traits. *Forage Research*, *43*(3): 239-243.

Premkumar, R., Nirmalakumari, A. and Anandakumar, C. R. (2017). Germplasm characterization for biochemical parameters in oats (*Avena sativa* L.). *International Journal of Pure and Applied Biosciences, 5*(4): 68–72.

Shekhawat, S. S. and Jaipal. (2016). Genetic variability and divergence studies in oats (*Avena sativa* L.) for green fodder and grain yield. *Forage Research*, *42*(1): 51-55.

USDA, Foreign Agriculture Service. (April, 2021). World agriculture production, Circular Series.

Wagh, V. R., Sonone, A. H. and Damame, S. V. (2018). Assessment of genetic variability, correlations and path coefficient analysis in forage oat (*Avena sativa* L.). *Forage Research*, *44*(3): 172-175.

How to cite this article: Chawla, R.; Jattan, M.; Phogat, D.S.; Kumari, N.; Kumar, S. and Poonia, A. (2021). Genetic Correlation and Path Analysis for Yield and Quality Attributes in Oat (*Avena sativa* L.). *Biological Forum – An International Journal, 13*(4): 940-945.