

Genetic Variability and Association Analysis of Oat (*Avena sativa* L.) Genotypes for Green Forage Yield and Other Components

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Authors' contributions

This work was carried out in collaboration between both authors. Author MS designed the study and author AT performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Both authors MS and AT managed the analyses of the study. Author AT managed the literature searches. Both authors read and approved the final manuscript.

Article Information

DOI: 10.9734/CJAST/2020/v39i1730762

Editor(s):

(1) Dr. Nhamo Nhamo, Zimbabwe Open University, Zimbabwe.

Reviewers:

(1) Om Prakash Patidar, Central Silk Board, Cooch Behar, West Bengal, India.

(2) M. R. Dhiman, ICAR-Indian Agricultural Research Institute, India.

Complete Peer review History: <http://www.sdiarticle4.com/review-history/57624>

Original Research Article

Received 02 April 2020

Accepted 08 June 2020

Published 04 July 2020

ABSTRACT

Fourteen genotypes of fodder oat (*Avena sativa* L.) were evaluated to assess the genetic variability and association analysis during Rabi 2018-19. The character dry matter yield (q/ha/day) had the highest heritability. GCV and PCV estimate was recorded for the days to 50% flowering. Highest genetic advance was observed for green forage yield (q/ha) were as high as percentage of mean was observed for dry matter yield (q/ha/day). In the present experiment, it is evident for the result that day to 50% flowering has a highly significant negative correlation with green forage yield. The highest positive direct effect contributing to green forage yield (q/ha) was due to low crude protein (q/ha). However indirect effect on improvement in green fodder yield was exerted by most of the traits studied. A direct selection for all these traits will help in the improvement of green fodder yield. Green fodder yield was positively correlated with most of the traits studied except days to 50% flowering and plant height (cm). The study provided the opportunity to identify suitable genotypes to be used in a future breeding programme.

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Keywords: Oats; correlation; path analysis; genetic diversity; green fodder yield; grain yield.

1. INTRODUCTION

The genus *Avena* belongs to the grass family Poaceae. It comprises of about seventy species, although mainly *A. sativa*, *A. nuda* and *A. byzantina* are most commonly cultivated on a commercial scale. Oat (*A. sativa* L.) is an economically important crop and ranks sixth in world cereal production next to wheat, rice, maize, barley and sorghum [1]. It is an important winter forage crop in many parts of the world and is also grown as a multipurpose crop for grain, pasture and forage. It is considered to be one of the best dual purpose cereal crops that fit well into the platter of human and cattle as well. Differing from other cereal grains such as wheat and barley, it is rich in the antioxidants α -tocotrienol, α -tocopherol, and avenanthramides, as well as total dietary fiber including the soluble fiber β -glucan [2]. In recent years, with the advent of exaggerated dairy industry in our country, the oat has fascinated the attention of breeders for its improvement due to its nutritious quality fodder for livestock and its grains as animal feed with high net energy gains [3]. Oats have assumed considerable importance in India as fodder as well as grain for animal feed particularly calves and young stock, horses, poultry and sheep. On dairy farms oat fodder is a must, as it can be fed green and the surplus converted into hay for use during the scarcity period. The oat crop is a heavy yielder and the average yield varies from 45 to 55 tons of green fodder per hectare. Oats can be grown on variety of soils reasonably fertile, well-drained soil is suited if temperature and moisture conditions are favourable; although maximum oat yields are usually not achieved until sufficient lime is added to bring the soil pH up to 5.3-5.7 range. Oat has been shown to tolerate acid soils with a pH of 4.5. It has excellent growth habit, quick regeneration ability after cutting and good quality herbage. Its fodder is palatable, succulent and highly nutritious. In India, oat is grown as fodder crop during *Rabi* season in north western and central parts of the country and is now even extending to eastern region as well. The total area covered under oat cultivation in the country is about 5,00,000 ha. The crop occupies maximum area in Uttar Pradesh (34%), followed by Punjab (20%), Bihar (16%), Haryana (9%) and Madhya Pradesh (6%). Rest of the area is shared by other states viz., Gujarat, Maharashtra, Orissa, Uttaranchal etc. [4]. More nutritious and high yielding fodder varieties are

needed to run an efficient livestock industry on which dependence of increasing population is taking ride. Therefore, fodder cultivars must produce large amounts of highly digestible green fodder for animals, must have high regeneration ability following cuttings [5]. An understanding of the genetic and genomic relationships of extant oat species and cultivars is critical for the further utilization of oat genetic diversity and genomic information in the development of superior cultivars that combine the favourable qualities conditioned by this diverse germplasm because the germplasm collected from different regions serve as the best natural resources in providing the required variation in traits to develop new cultivars. Generally diverse individuals are likely to produce more heterotic effects during the crossing programme and produce desirable segregants.

2. MATERIALS AND METHODS

The field experiment was conducted during the *Rabi* 2018-19 at Department of Genetics & Plant Breeding at Research cum Instructional Farm, Indira Gandhi Krishi Viswavidyalaya, Raipur, C.G. The material was evaluated in (randomized block design) with three replications and row to row spacing of 25cm. fourteen genotypes were evaluated with two standard checks varieties viz., Kent and Oat-6. Recommended package of practices were followed with optimum dose of fertilizers. Observations for all the traits were recorded on five randomly selected plants in each replication. Data was recorded on nine quantitative traits viz., days to 50% flowering, plant height (cm), leaf stem ratio, protein (%), crude protein (q/ha), dry matter yield (q/ha/day), green forage yield (q/ha/day), dry matter yield (q/ha) and green forage yield (q/ha) traits. Data analysis was done using windostat computer software. Windostat was used which uses the following for further detailed analysis. The correlation coefficient at phenotypic and genotypic level was calculated from the variance and covariance according to Johnson et al. [6]. Direct and indirect effect of various contributing traits towards green fodder yield and dry matter yield was calculated using the path coefficients analysis [7]. The data was subjected to statistical analysis and results were described accordingly. Genotypic correlation coefficients were calculated between green fodder yield and its related traits used for the analysis. Green fodder yield was kept as dependent variable and other traits as independent variable as they determine

the basic relationship between path coefficients, were interpreted to estimate the direct and indirect effects.

3. RESULTS AND DISCUSSION

The Analysis of variance worked out for green forage yield and other components in oat indicated that the mean sum of squares due to genotypes were highly significant at both 5 percent and 1 percent level of significance for all the characters.. This is an indication of existence of sufficient amount of variability for the traits among lines in Table 1.

3.1 Characters Wise Range and Mean Performance

Characters wise range and mean performance for green forage yield and other components in oat are presented in Table 2.

1. **Days to 50% flowering:** The character days to 50% flowering varied between 68.00 (Kent) to (HFO-806) 89.33 days with a mean value of 79.19 days.
2. **Plant height (cm):** The plant height ranged from 103.58 (SKO-241) to 141.92 cm (HFO-818) with a mean value plant height of 132.98 cm.
3. **Leaf stem ratio:** The character leaf stem ratio varied between 0.34 (SKO-241) to 0.67 (UPO-18-1) with a mean value of 0.47.
4. **Protein (%):** The character protein (%) varied between 5.33 (OL 1876-1) to 7.47 (HFO-8.6) with a mean value of 6.50%.
5. **Crude protein (q/ha):** The character crude protein varied between 2.53 (SKO-241) to 8.70 (Kent) with a mean value of 7.07 q/ha.
6. **Dry matter yield (q/ha/day):** The dry matter yield ranged from 0.61 (SKO-241) to 1.77 (Kent) with a mean value was recorded 1.38.
7. **Green forage yield (q/ha/day):** The green forage yield ranged between 0.07 (OL-1876-1, JHO 18-1 and RO-11-1) to 0.11 (Kent) with a mean value of 0.08 q/ha/day.
8. **Dry matter yield (q/ha):** The dry matter yield ranged from 42.23 (SKO-241) to 138.70 (OL 1876-1) with a mean value was recorded 109.00 q/ha.
9. **Green forage yield (q/ha):** The green forage yield ranged from 185.19 (SKO-241) to 420.37 (RO-11-1-2) with a mean value was recorded 338.36 q/ha.

The measurement of existing variability in genetic material has been the basic requirement of a breeding programme. In the present investigation, a wide range of variability was

observed for nearly all the traits viz., days to 50% flowering, plant height (cm), leaf stem ratio, green forage yield (q/ha/day), dry matter yield (q/ha) and green forage yield (q/ha) in total gene pool, indicating the existence of sufficient variability among the genotypes for the traits. Whereas, little variability has been observed for protein (%), crude protein (q/ha) and dry matter yield (q/ha/day). These results are in general agreement with the previous findings of Ahmed et al. [8].

3.2 Genetic Variability

Genetic parameters of variation for green forage yield ranged and its components in oat are presented in Table 2.

Genotypic and phenotypic coefficients of variation are simple measures of variability; these measures are commonly used for the assessment of variability. The relative values of these types of coefficient gives an idea about the magnitude of variability present in a genetic population. Thus, the components of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed. The phenotypic coefficients of variation were marginally higher than the corresponding genotypic coefficients of variation indicated the influence of environment in the expression of the characters under study.

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are categorized as low (less than 10%), Moderate (10-20%) and high (more than 20%) as suggested by Krishna et al. [9].

The character dry matter yield (q/ha/day) had highest GCV (25.65%) and PCV (27.35%) followed by dry matter yield (q/ha) GCV (23.77%) and PCV (25.84%) and crude protein (q/ha) GCV (22.73%) and PCV (25.89%). Moderate for leaf stem ratio GCV (19.77%) and PCV (23.46%) followed by green forage yield (q/ha) GCV (17.71%) and PCV (20.17%) and green forage yield (q/ha/day) GCV (12.76%) and PCV (14.84%) and low for days to 50% flowering GCV (9.00%) and PCV (9.16%) followed by protein (%) GCV (8.87%) and PCV (10.31%) and plant height (cm) GCV (7.34%) and PCV (8.57%).

The results on genotypic and phenotypic coefficient of variation clearly indicated that the phenotypic coefficients of variation in general were slightly higher than the genotypic coefficients of variation for all the characters

Table 1. Analysis of variance for green forage yield and its components in oat

Source of variation	DF	Mean sum of square								
		Days to 50% flowering	Plant height (cm)	Leaf stem ratio	Protein (%)	Crude protein (q/ha)	Dry matter yield (q/ha/day)	Green forage yield (q/ha/day)	Dry matter yield (q/ha)	Green forage yield (q/ha)
Replication	2	0.16	11.34	70.90	6.25	0.09	0.01	0.16	11.34	840.98
Treatment	13	6082.42**	16992.93**	2.79**	0.0002	0.0001	0.36	6082.42**	16992.93**	101723.90**
Error	26	1.03	19.80	19.30	0.97	0.05	0.05	1.03	19.80	731.99

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

Table 2. Genetic parameters of variation for green forage yield and its components

S. No.	Characters	CV %	CD	Mean	Range		GCV (%)	PCV (%)	H ² (%)	Genetic advance	GA as% of mean
					Min.	Max.					
1	Days to 50% flowering	2.28	2.08	79.19	68.00	89.33	9.00	9.16	96.49	14.42	18.21
2	Plant height (cm)	5.98	9.15	132.98	103.58	141.92	7.34	8.57	73.38	17.23	12.96
3	Leaf stem ratio	18.81	0.10	0.47	0.34	0.67	19.77	23.46	71.04	0.16	34.33
4	Protein (%)	6.88	0.51	6.50	5.33	7.47	8.87	10.31	74.04	1.02	15.73
5	Crude protein (q/ha)	16.88	1.32	7.07	2.53	8.69	22.73	25.89	77.00	2.90	41.08
6	Dry matter yield (q/ha/day)	13.17	0.20	1.38	0.61	1.77	25.65	27.35	87.98	0.69	49.56
7	Green forage yield (q/ha/day)	6.73	0.006	0.08	0.07	0.11	12.76	14.87	73.63	0.02	22.55
8	Dry matter yield (q/ha)	13.30	16.11	109.00	42.23	138.69	23.77	25.81	84.80	49.14	45.09
9	Green forage yield (q/ha)	15.29	55.61	338.36	185.19	420.37	17.71	20.17	77.12	108.41	32.04

indicating the substantial influence of environment in the expression of the characters. The character dry matter yield had the highest GCV and PCV. The moderate GCV and PCV were observed for leaf stem ratio. The GCV and PCV were low for most of the characters viz., days to 50% flowering, protein (%) and plant height. Similar findings were also reported earlier by [8].

3.3 Heritability and Genetic Advance

Heritability governs the resemblance between parents and their progeny whereas; the genetic advance provides the knowledge about expected forage for a particular character after selection. Heritability suggests the relative role of genetic factors in expression of phenotypes and also acts as an index of transmissibility of a particular trait to its offspring's. However, the knowledge of heritability alone does not help in formulating concrete breeding programme, genetic advance along with heritability helps to ascertain the possible genetic control for any particular trait. The nature and extent of the inherent ability of a genotype for a character is an important parameter determining the extent of improvement of any crop species. Heritability and genetic advance are the important genetic parameters for selecting a genotype that permit greater effectiveness of selection by separating out environmental influence from total variability.

Heritability estimates along with genetic advance are normally more useful in predicting the gain under selection than that of heritability alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance [6]. An attempt has been made in the present investigation to estimate heritability in broad sense and categorized as low (<50%), moderate (50-70%) and high (>70%) as suggested by Robinson [10].

In present investigation the highest heritability estimate was recorded for the days to 50% flowering (96.49%) followed by dry matter yield (q/ha/day) (87.98%), dry matter yield (q/ha) (84.80%), green forage yield (q/ha) (77.12%), crude protein (q/ha) (77.00), protein (%) (71.04%), green forage yield (q/ha/day) (73.63%), plant height (cm) (73.38) and leaf stemstem ratio (71.04) Table 2. The above findings are in conformity with the earlier reports of Deep et al. [11].

3.4 Genetic Advance

The magnitude of genetic advance was categorized as high (> 20%), moderate (10% -

20%) and low (< 10%) The highest genetic advance was observed for green forage yield (q/ha) (108.41) and dry matter yield (q/ha) (49.14). The plant height (17.23) and days to 50% flowering (14.42) moderate genetic advance. Whereas, the low genetic advance was exhibited for crude protein (q/ha) (2.90), protein (%) (1.02), dry matter yield (q/ha/day) (0.69), leaf stemstem ratio (0.16) and green forage yield (q/ha/day) (0.02).

3.5 Genetic Advance as Percentage of Mean

Among 9 characters studied the highest genetic advance as percentage of mean was reported for dry matter yield (q/ha/day) (49.56) followed by dry matter yield (q/ha) (45.09), crude protein (q/ha) (41.08), leaf stemstem ratio (34.33), green forage yield (q/ha) (32.04), green forage yield (q/ha/day) (22.55), days to 50% flowering (18.21), protein (%) (15.73) and plant height (cm) (12.96). In the present investigation, high heritability coupled with high genetic advance as percentage of mean was found for dry matter yield (q/ha/day), dry matter yield (q/ha) and crude protein (q/ha) which indicated the predominance of additive gene action in the expression of these characters which could be utilized through selection for improvement in these characters. Rest of the traits showed high to moderate heritability estimates coupled with moderate to low genetic advance as percentage of mean indicated the role of non additive genetic variance in their expression. Similar result are also reported by Ahmed et al. [8], Krishna et al. [9], Premkumar et al. [12] and Deep et al. [11].

3.6 Correlation Coefficient Analysis

Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationship between two or more variables. Correlation coefficient analysis measures the mutual relationship between various characters and determines the component characters on which selection can be based for genetic improvement. Knowledge about interrelationship between yield and yield contributing characters facilitates the choice of efficient breeding method to be adopted. To estimate the association between two characters, correlation coefficient at phenotypic, genotypic and environmental levels were worked out in all possible combinations among yield components. Pandey and Gritton [13] have pointed out that no suitable test of significance of genetic correlation is available. Therefore, their primary utility is in strengthening

Table 3. Correlation coefficients for green forage yield and its components

		Days to 50% flowering	Plant height (cm)	Leaf stem ratio	Protein (%)	Crude protein (q/ha)	Dry matter yield (q/ha/day)	Green forage yield (q/ha/day)	Dry matter yield (q/ha)	Green forage yield (q/ha)
Days to 50% flowering	P	1.000	0.258	-0.080	-0.002	0.011	-0.245	-0.638**	0.058	0.147
	G	1.000	0.283	-0.133	0.014	0.008	-0.278	-0.757**	0.052	0.148
Plant height (cm)	P		1.000	0.241	0.145	0.649**	0.581**	0.009	0.640**	0.504**
	G		1.000	0.412**	0.201	0.888**	0.716**	-0.062	0.824**	0.651**
Leaf stem ratio	P			1.000	0.024	0.462**	0.498**	0.109	0.492**	0.391*
	G			1.000	-0.128	0.496**	0.605**	0.024	0.575**	0.642**
Protein (%)	P				1.000	0.288	-0.055	0.718**	-0.119	-0.365*
	G				1.000	0.220	-0.061	0.660**	-0.171	-0.400**
Crude protein (q/ha)	P					1.000	0.893**	0.271	0.912**	0.615**
	G					1.000	0.923**	0.242	0.921**	0.752**
Dry matter yield (q/ha/day)	P						1.000	0.199	0.943**	0.719**
	G						1.000	0.265	0.942**	0.809**
Green forage yield (q/ha/day)	P							1.000	-0.041	-0.280
	G							1.000	-0.058	-0.340*
Dry matter yield (q/ha)	P								1.000	0.798**
	G								1.000	0.915**
Green forage yield (q/ha)	P									1.000
	G									1.000

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

Table 4. Genotypic path coefficient analysis showing direct and indirect effect of different Green forage yield

	Days to 50% flowering	Plant height (cm)	Leaf stem ratio	Protein (%)	Crude protein (q/ha)	Dry matter yield (q/ha/day)	Green forage yield (q/ha/day)	Dry matter yield (q/ha)	Correlation with green forage yield (q/ha) (r)
Days to 50% flowering	3.208	-0.003	-0.166	-0.124	0.149	-0.070	-1.874	-0.972	0.148
Plant height (cm)	0.908	-0.010	0.515	-1.834	16.330	0.179	-0.153	-15.285	0.651**
Leaf stem ratio	-0.426	-0.004	1.252	1.164	9.119	0.152	0.059	-10.673	0.642**
Protein (%)	0.044	-0.002	-0.160	-9.117	4.037	-0.015	1.634	3.180	-0.400**
Crude protein (q/ha)	0.026	-0.009	0.621	-2.002	18.381	0.231	0.600	-17.096	0.752**
Dry matter yield (q/ha/day)	-0.891	-0.007	0.758	0.552	16.966	0.250	0.655	-17.473	0.809**
Green forage yield (q/ha/day)	-2.428	0.001	0.030	-6.017	4.454	0.066	2.476	1.078	-0.340*
Dry matter yield (q/ha)	0.168	-0.008	0.720	1.563	16.935	0.236	-0.144	-18.555	0.915**

Table 5. Mean performance of Green forage yield and its component in oat during Rabi 2018-19

S. No.	Name of genotypes	Days to 50% flowering	Plant height (cm)	Leaf stem ratio	Protein (%)	Crude protein (q/ha)	Dry matter yield (q/ha/day)	Green forage yield (q/ha/day)	Dry matter yield (q/ha)	Green forage yield (q/ha)
1	HFO-806	89.33	128.19	0.55	7.47	6.03	0.90	0.08	80.51	266.67
2	OL 1874-1	89.00	141.14	0.35	7.10	6.98	1.10	0.08	98.16	274.08
3	HFO-818	76.67	141.92	0.55	6.17	7.72	1.63	0.08	125.62	387.04
4	JO-06-23	84.00	141.05	0.40	6.27	8.19	1.56	0.08	130.83	351.85
5	OS-6	71.00	137.53	0.44	7.13	7.80	1.54	0.10	108.93	314.82
6	NDO-1802	72.33	140.57	0.51	7.13	8.58	1.69	0.10	120.39	325.93
7	UPO-18-1	75.33	139.36	0.67	6.07	7.58	1.63	0.08	125.04	388.89
8	Kent	68.00	128.85	0.48	7.23	8.70	1.77	0.11	120.20	344.45
9	OL 1876-1	79.33	133.35	0.54	5.33	7.40	1.73	0.07	138.70	403.70
10	JHO 18-1	82.67	122.85	0.38	6.13	4.87	0.95	0.07	79.21	340.74
11	RO-11-1	83.67	139.86	0.37	6.33	6.36	1.20	0.07	100.70	359.26
12	SKO-241	69.00	103.58	0.34	6.00	2.53	0.61	0.09	42.23	185.19
13	RO-11-1-3	84.00	130.90	0.41	6.30	7.74	1.46	0.08	122.75	374.07
14	RO-11-1-2	84.33	132.60	0.56	6.33	8.44	1.58	0.08	132.77	420.37

interpretations based on phenotypic correlation and in better predicting correlated responses to selection. Hence, important findings based on phenotypic correlation are discussed here. In the present investigation correlation coefficients at genotypic, phenotypic and environmental level have been worked out among green forage yield and its components are presented in Table 3.

The character days to flowering initiation exhibited highly significant positive correlation with days to 50% flowering at both genotypic and phenotypic levels.

It is evident for the result that days to 50% flowering has a highly significant negative correlation (-0.757 and -0.638) with green forage yield (q/ha) at genotypic and phenotypic level respectively. Whereas plant height (cm) is shows a highly positive correlation with crude protein (q/ha) (0.888 and 0.649), dry matter yield per day (q/ha/day) (0.716 and 0.581), dry matter yield (q/ha) (0.824 and 0.640) and green forage yield (q/ha) (0.651 and 0.504) at genotypic and phenotypic level respectively. Leaf stem ratio on the other hand had a highly significant positive correlation with crude protein (q/ha) (0.496 and 0.462), dry matter yield (q/ha/day) (0.605 and 0.498), dry matter yield (q/ha) (0.575 and 0.492) and green forage yield (q/ha) (0.642 and 0.391). Protein (%) exhibited and highly significant correlation in positive direction with green forage yield (q/ha/day) (0.660 and 0.718) at genotypic and phenotypic level respectively and while a highly significant negative correlation with green forage yield (q/ha) (-0.400 and -0.365) at genotypic and phenotypic level respectively. Crude protein (q/ha) exhibited a highly significant correlation in positive direction with dry matter yield (q/ha/day) (0.923 and 0.893), dry matter yield (q/ha) (0.921 and 0.912) and green forage yield (q/ha) (0.752 and 0.615) at genotypic and phenotypic level respectively. From the result of the present experiment a highly significant positive correlation of dry matter yield (q/ha/day) with dry matter yield (q/ha) (0.942 and 0.943) at genotypic and phenotypic level respectively and green forage yield (q/ha) (0.809 and 0.719) at genotypic and phenotypic level respectively was clearly evident. Whereas, dry matter yield (q/ha) exhibited a highly significant positive correlation with green forage yield (q/ha) (0.915 and 0.798) at genotypic and phenotypic level respectively. The findings were in general agreement with the findings of Ahmed *et al.*, [8] and Deep *et al.* [11].

3.7 Path Coefficient Analysis

Path coefficient analysis measures the direct and indirect contribution of various independent characters on a dependent character. Path coefficient analysis given by Dewey and Lu [7] has been used to estimate the magnitude and direction of direct and indirect effects of various yield contributing characters. Correlation coefficients along with path coefficients together provide more reliable information which can be effectively predicted in crop improvement programme. If the correlation between yield and a character is due to direct effect of a character, it reveals true relationship between them and direct selection for this trait will be rewarding for yield improvement. However, if the correlation coefficient is mainly due to indirect effects of the character through another component trait, indirect selection through such trait will be effective for yield improvement. Genotypic correlation coefficients of various yield attributing characters for seed yield per plant were further partitioned into direct and indirect effects and are given in Table 4 respectively.

The highest positive direct effect contributing towards green forage yield (q/ha) was observed due crude protein (q/ha) (18.381) followed by days to 50% flowering (3.208), green forage yield (q/ha/day) (2.476), leaf stemstem ratio (1.252), dry matter yield (q/ha/day) (0.250), plant height (cm) (-0.010), protein (%) (-9.117) and dry matter yield (q/ha) (-18.555).

As the trait crude protein (q/ha) exhibited the positive correlation with green forage yield (q/ha). Although, character dry matter yield (q/ha/day) exhibited the positive correlation with green forage yield (q/ha) but its direct effect on green forage yield (q/ha) was negative which is mainly due to nullifying effects *via* crude protein (q/ha), dry matter yield (q/ha/day) and dry matter yield (q/ha). Hence, direct selection for these traits could be practiced for developing high dry matter yield and green forage yield oat genotypes. The findings were in general agreement with the findings of Ahmed *et al.* [8] and Premkumar *et al.* [12].

4. CONCLUSION

The study helps in determining the positive and negative correlations among different traits and traits which can utilized directly for selection of best performing genotypes for high green fodder yield. Path coefficient analysis measures the direct and indirect influence of variables on the

green fodder yield and helps in selecting meritorious characters to be used in selection programme to get maximum yield. The relationships must be taken into consideration as a change on one during selection might lead to change in other performing traits. This study also helps in selection and improvement of desirable traits to be used or transferred during crossing program.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. FAO. *Production statistics*; Food and Agriculture Organisation, Rome. Oliver RE, Jellen EN, Ladizinsky G, Korol AB, Kilian A, Beard JL, Dumlupinar Z, Wisniewski-Morehead NH, Svedin E, Coon M, Redman RR, Maughan PJ, Obert DE, Jackson EW. New Diversity Arrays Technology (DArT) markers for tetraploid oat (*Avena magna* Murphy et Terrell) provide the first complete oat linkage map and markers linked to domestication genes from hexaploid *A. sativa* L. *Theor Appl Genet.* 2011;123:1159-71.
2. Oliver RE, Obert DE, Hu G, Bonman JM, Jackson EW. Development of oat based markers from barley and wheat microsatellites. *Genome.* 2010;6:458-71.
3. Ruwali Y, Verma JS, Kumar L. Comparative genetic diversity analysis of oat (*Avena sativa* L.) by microsatellite markers and morphological rainfed expressions. *African Journal of Biotechnology.* 2013;12(22):3414-24.
4. Anonymous. Directorate of economics and statistics. Economic survey report, Government of Chhattisgarh. Raipur. 2012;60-62.
5. Stevens EJ, Armstrong KW, Bezar HJ, Griffin WB, Hampton JB. Fodder oats: an over view. In *Fodder oats: A world over view*, JM Suttie, SG Reynolds, Eds. Plant Production and Protection series No 33, FAO Rome Italy. 2004;11-18.
6. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlation in soybeans and their implication in selection. *Agron J.* 1955;47:477-482.
7. Dewey DR, Lu KH. A correlation and path analysis of components of crested grass seed production. *Agron. J.* 1959;51:515-518.
8. Ahmed S, Roy AK, Majumdar AB. Correlation and path coefficient analysis for fodder and grain yield related traits in oats (*Avena sativa* L.). *Annals of Biology.* 2013;29:75-78.
9. Krishna A, Ahmed S, Pandey HC, Kumar V. Correlation, path and diversity analysis of Oat (*Avena sativa* L.) genotypes for grain and fodder yield. *J Plant Sci Res.* 2014;1(2):110-116.
10. Robinson HF. Quantitative genetics in relation to breeding on centennial of Mendelism. *Indian J. Genet.* 1966;26(A):171-187.
11. Deep A, Singh S, Singh M, Yadav L, Malik P. Correlation and genetic divergence analysis for seed and fodder yield and its contributing character in Oat (*Avena sativa* L.). *Int. J. Pure App. Biosci.* 2019;7(3):471-477.
12. Premkumar R, Nirmalakumari A, Anandakumar CR. Studies on genetic variability and character association among yield and yield attributing traits in oats (*Avena sativa* L.). *Int. J. Curr. Microbiol. App. Sci.* 2017;6(11):4075-4083.
13. Pandey S, Griton ET. Genotypic and phenotypic variances and correlation in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Crop Science.* 1975;15:353-356.

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