



# Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2024.v24.no.2.338>

## APPRAISAL OF CHARACTER ASSOCIATION IN FODDER OAT (*AVENA SATIVA* L.)

Bhautik K. Jani<sup>1\*</sup>, Dipak P. Gohil<sup>2</sup>, Amar A. Sakure<sup>3</sup>, Mukesh P. Patel<sup>4</sup> and Dinesh J. Parmar<sup>5</sup>

<sup>1</sup>Department of Genetics and Plant Breeding, B.A. College of Agriculture, Anand Agricultural University, Anand, Gujarat-388110, India.

<sup>2</sup>Main Forage Research Station, Anand Agricultural University, Anand, Gujarat – 388110, India.

<sup>3</sup>Department of Agricultural Biotechnology, Anand Agricultural University, Anand, Gujarat – 388110, India.

<sup>4</sup>Agricultural and Horticultural Research Station, Anand Agricultural University, Khambholaj, Gujarat, 388 330, India.

<sup>5</sup>Department of Agricultural Statistics, B.A. College of Agriculture, Anand Agricultural University, Anand, Gujarat-388110, India.

\*Corresponding author E-mail: [bhautikjani21@gmail.com](mailto:bhautikjani21@gmail.com)

(Date of Receiving-26-05-2024; Date of Acceptance-12-08-2024)

### ABSTRACT

Countries like India are facing a severe fodder scarcity, require urgent improvement in fodder production to meet the growing demands of livestock sector. Correlation and path analysis guide breeders to improve fodder productivity by identifying key traits influencing yield in selection programs. Therefore, in the present investigation, 72 diverse genotypes of fodder oat (*Avena sativa* L.) were evaluated for character association and path coefficient analysis using thirteen parameters during *Rabi* 2022-23 at Main Forage Research Station, AAU, Anand Gujarat, India. Results revealed that, number of tillers per plant, number of leaves per plant, dry matter yield per plant, plant height, leaf length and days to 50% flowering had a positive direct effect as well as a positive correlation with green fodder yield. Thus, while undertaking genetic improvement for green fodder yield in oat through selection programs, more emphasis should be given to these traits.

**Key words:** fodder oat, correlation, path analysis, selection, green fodder yield

### Introduction

India has only 2.29% of world land area but support approximately 20% of the global livestock population and 17.5% of the human population. It ranked first in global milk production (230.58 million MT in 2022-23), contributing 24.64% at global level (Anon., 2023a). Despite of the largest milk producer in the world, the productivity of Indian cattle is lower than the global average due to insufficient and poor-quality of fodder. Increasing human and livestock population competing each other for arable land, water and other resources for food and fodder production. As a result, land available for green fodder cultivation has remained stable at 5% of the total cropped area (8.4 mha) over the past few decades (Roy *et al.*, 2019).

At present country faces net deficient of 11.24% in

green fodder, 23.4% in dry fodder and 28.9% in concentrated feed ingredients. Total green fodder availability is 734.2 MT against requirement of 827.19 MT (Roy *et al.*, 2019). Expanding land area for fodder cultivation is not feasible thus increasing the productivity of cultivated fodder crops is the only way to meet present and future needs for nutritious fodder. This can be achieved by using appropriate cropping systems, integrating fodder crops into rotations with food and cash crops, cultivating fodder on degraded lands through agroforestry systems and exploring alternative green fodder options.

The oat is a promising fodder crop due to its rapid growth, high nutritional value and salinity tolerance. It is extensively cultivated for its high yield potential, multi-cut nature, excellent palatability, digestibility and rich

soluble carbohydrates. It is used as green fodder crop, hay and silage. Oat straw have more palatability and digestibility than other cereals like wheat and rice. Oat is an important dual purpose winter cereal crop belonging to the genus *Avena* and the family *Poaceae*. The cultivated oat (*Avena sativa* L.) is a natural allohexaploid ( $2n=6x=42$ ) with a genomic constitution of AACCCDD. Oat thrives in temperate and subtropical climates, covering 9.37 million hectares globally with an annual yield of 25.33 million MT (Anon., 2023b). In India, it is grown on about 10 lakh ha, mainly in Uttar Pradesh (34%), Punjab (20%) and Bihar (16%) (Kapoor *et al.*, 2022).

Oat have received considerable attention as “Super-grain” due to their superior grain quality, high dietary fiber and wide range of phytochemicals. They are rich in antioxidants, *beta-glucans* and essential vitamins and minerals. *Beta-glucan* in oats help reduce cardiovascular risks, control blood pressure, lower cholesterol, obesity, hypertension and support gastrointestinal health due to their complex structure and delayed glucose release (Rasane *et al.*, 2015). Gluten-free oats benefit coeliac disease patients.

Increasing yield is the ultimate goal of any breeders. In a breeding program, studying genotypic and phenotypic relationships among traits is useful for design, evaluate and development of selection criteria for desirable traits. Polygenic traits such as fodder yield, which are influenced by multiple factors both directly and indirectly through other traits. So, it is crucial to evaluate the contribution of each trait to focus on those which has most significant influence on yield. It creates a complex situation for them to make selections. Therefore, path coefficient analysis could provide a more realistic picture of the interrelationship, as it considers direct as well as indirect effects of the variables by partitioning the correlation coefficient.

## Materials and Methods

The present investigation was carried out at Main Forage Research Station, Anand Agricultural University, Anand, during *Rabi* 2022-23. The experimental materials consisted of 72 fodder oat genotypes obtained from different forage research stations across India were evaluated using a Randomized Complete Block Design with three replications. Each genotype was sown in a single row of 4.5 meters length and keeping row to row distance 30 cm. All recommended package of practices were followed to raise good and healthy crop. Observations were recorded from five randomly selected competitive plants for green fodder yield and yield attributing characters *viz.*, plant height (cm), leaf

**Table 1:** Analysis of variance (mean sum of squares) for different characters in fodder oat.

Sr. No.	Sources of variation	Mean Sum of Squares		
		Replications	Genotypes	Error
	<b>df</b>	<b>02</b>	<b>71</b>	<b>142</b>
1.	Days to 50% flowering	1.59	101.27**	5.94
2.	Plant height	27.07	394.23**	43.37
3.	Leaf length	5.33	86.23**	5.20
4.	Leaf width	0.02	0.23**	0.01
5.	Number of tillers per plant	0.10	4.10**	0.46
6.	Number of leaves per plant	28.44	222.30**	18.87
7.	Leaf: stem ratio	0.01	0.09**	0.01
8.	Green fodder yield per plant	221.40	4391.20**	216.40
9.	Dry matter yield per plant	3.92	229.29**	15.61
10.	Dry matter content	0.28	14.12**	1.77
12.	Crude protein content	0.25	4.65**	0.38
12.	Acid detergent fiber	1.30	6.25**	0.96
13.	Neutral detergent fiber	0.16	6.66**	1.02

Note: \*,\*\* Significant at 5% and 1% level of significance, respectively.

length(cm), leaf width(cm), number of tillers per plant, number of leaves per plant, leaf: stem ratio, dry matter yield per plant (g), dry matter content(%), crude protein content(%), acid detergent fiber (%) and neutral detergent fiber (%). For days to 50% flowering observation was recorded on plot basis.

Samples collected from each genotype were chopped and air-dried for three days, then oven-dried at 100°C until a constant weight was reached and dry matter content was calculated from obtained data. Later, the samples were ground into powder and analyzed using the “FOSS NIR System” (Model: 5000 composite) according to standard analytical protocols to determine quality parameters such as crude protein content (CP), neutral detergent fiber (NDF) and acid detergent fiber (ADF). Genotypic and phenotypic correlation coefficients were estimated as suggested by Hazel (1943). The path coefficient analysis was carried-out according to the method suggested by Wright (1921) and used by Dewey and Lu (1959).

## Results and Discussion

### Analysis of Variance

The analysis of variance revealed that the mean

**Table 2:** Genotypic and phenotypic correlation coefficient among 13 characters of fodder oat.

Character	DFE	PH	LL	LW	NOT	NOL	LSR	DMY	DMC	CP	ADF	NDF	GFY	
DFE	r <sub>g</sub>	1.000	-0.023	0.375**	0.198	0.112	0.396**	0.175	0.206	-0.223	-0.009	-0.120	0.052	0.387**
	r <sub>p</sub>	1.000	-0.018	0.275**	0.164*	0.068	0.293**	0.169*	0.157*	-0.183**	0.015	-0.125	0.016	0.318**
PH	r <sub>g</sub>		1.000	0.071	0.260**	0.169	0.345**	0.046	0.635**	0.478**	-0.051	0.411**	0.483**	0.527**
	r <sub>p</sub>		1.000	0.083	0.201**	0.133	0.268**	0.057	0.501**	0.346**	-0.021	0.253**	0.322**	0.431**
LL	r <sub>g</sub>			1.000	0.108	0.128	0.319**	-0.106	0.197	-0.197	0.151	-0.254*	0.044	0.358**
	r <sub>p</sub>			1.000	0.098	0.092	0.246**	-0.081	0.181**	-0.148*	0.119	-0.183**	0.014	0.320**
LW	r <sub>g</sub>				1.000	-0.216	0.026	0.082	0.173	0.078	-0.237*	0.099	0.269*	0.143
	r <sub>p</sub>				1.000	-0.170*	0.030	0.088	0.137*	0.034	-0.189**	0.059	0.192**	0.130
NOT	r <sub>g</sub>					1.000	0.805**	0.270*	0.481**	-0.041	0.157	-0.149	-0.253*	0.600**
	r <sub>p</sub>					1.000	0.799**	0.164*	0.498**	0.018	0.114	-0.091	-0.151*	0.608**
NOL	r <sub>g</sub>						1.000	0.257*	0.578**	-0.048	0.122	-0.178	-0.166	0.726**
	r <sub>p</sub>						1.000	0.153*	0.553**	-0.014	0.096	-0.089	-0.105	0.697**
LSR	r <sub>g</sub>							1.000	0.136	-0.057	-0.049	0.044	-0.065	0.155
	r <sub>p</sub>							1.000	0.095	-0.051	-0.022	0.029	-0.018	0.120
DMY	r <sub>g</sub>								1.000	0.586**	-0.021	0.273*	0.313**	0.901**
	r <sub>p</sub>								1.000	0.606**	-0.011	0.189**	0.223**	0.880**
DMC	r <sub>g</sub>									1.000	-0.096	0.369**	0.442**	0.185
	r <sub>p</sub>									1.000	-0.065	0.205**	0.312**	0.170*
CW	r <sub>g</sub>										1.000	-0.167	-0.512**	0.015
	r <sub>p</sub>										1.000	-0.125	-0.391**	0.014
ADF	r <sub>g</sub>											1.000	0.507**	0.144
	r <sub>p</sub>											1.000	0.276**	0.119
NDF	r <sub>g</sub>												1.000	0.168
	r <sub>p</sub>												1.000	0.119
GFY	r <sub>g</sub>													1.000
	r <sub>p</sub>													1.000

Note: \*,\*\* Significant at 5% and 1% level of significance, respectively

DFE - Days to 50% Flowering, PH - Plant Height, LL - Leaf Length, LW - Leaf Width, NOT - Number of tillers per plant, NOL - Number of Leaves per plant, LSR - Leaf: Stem Ratio, GFY - Green Fodder Yield per plant, DMY - Dry Matter Yield per plant, DMC - Dry Matter Content, CP - Crude Protein content, ADF - Acid Detergent Fiber, NDF - Neutral Detergent Fiber

square due to genotypes were highly significant for all the traits under study suggested that the sufficient amount of genetic variability was present among the genotypes which could be exploited in future for improvement of respective traits (Table 1).

### Correlation Analysis

Genotypic and phenotypic correlations for all possible combinations of traits under study are presented in Table 2. Genetic correlations can be due to pleiotropy (a single locus affecting multiple traits), close linkage (association between loci due to physical proximity), linkage disequilibrium (statistical associations between loci due to evolutionary forces) or the relationship with other unrecorded traits. Linkage can be broken through recombination; however, in the case of correlation due to pleiotropy, genetic improvement in one character is not possible without a change in the associated component characters, as it cannot be manipulated by recombination. The results revealed that the estimates of genotypic

correlation coefficients were higher than phenotypic correlation coefficients for most of the characters under study, which indicated a strong inherent association between the characters that might be due to the masking or modifying effects of the environment. It showed that the association was largely due to genetic factors. When two traits are strongly correlated, selecting one trait will automatically result in the selection of another.

### Correlation between yield and yield component traits

The estimates of genotypic correlation coefficient varied between -0.512 (CP vs. NDF) and 0.901 (DMY vs. GFY), whereas the estimates of phenotypic correlation coefficients ranged from -0.391 (CP vs. NDF) to 0.880 (DMY vs. GFY). The green fodder yield per plant exhibited significant and positive correlation with dry matter yield per plant, number of leaves per plant, number of tillers per plant, plant height, leaf length and days to 50% flowering at both genotypic and phenotypic level.

**Table 3:** Genotypic path coefficient analysis showing direct and indirect effects of different characters on green fodder yield in fodder oat.

Cha.	DF	PH	LL	LW	NOT	NOL	LSR	DMC	CP	ADF	NDF	r <sub>g</sub> with 'GFY'
DF	<b>0.2241</b>	-0.0052	0.0728	0.0126	0.0423	0.0959	-0.0083	-0.0263	0.0003	-0.0210	-0.0005	0.3867**
PH	-0.0051	<b>0.2305</b>	0.0138	0.0166	0.0636	0.0837	-0.0022	0.0564	0.0021	0.0718	-0.0044	0.5267**
LL	0.0840	0.0163	<b>0.1942</b>	0.0069	0.0483	0.0775	0.0051	-0.0233	-0.0061	-0.0443	-0.0004	0.3582**
LW	0.0443	0.0600	0.0209	<b>0.0635</b>	-0.0816	0.0063	-0.0039	0.0092	0.0096	0.0172	-0.0025	0.1431
NOT	0.0251	0.0389	0.0248	-0.0137	<b>0.3773</b>	0.1952	-0.0129	-0.0048	-0.0063	-0.0261	0.0023	0.5998**
NOL	0.0886	0.0796	0.0620	0.0017	0.3036	<b>0.2425</b>	-0.0122	-0.0057	-0.0049	-0.0311	0.0015	0.7256**
LSR	0.0392	0.0107	-0.0207	0.0052	0.1019	0.0623	<b>-0.0476</b>	-0.0067	0.0020	0.0078	0.0006	0.1547
DMC	-0.0499	0.1101	-0.0383	0.0050	-0.0153	-0.0118	0.0027	<b>0.1180</b>	0.0039	0.0645	-0.0040	0.1849
CP	-0.0019	-0.0117	0.0293	-0.0151	0.0591	0.0295	0.0023	-0.0113	<b>-0.0403</b>	-0.0292	0.0047	0.0154
ADF	-0.0269	0.0947	-0.0492	0.0063	-0.0564	-0.0432	-0.0021	0.0435	0.0067	<b>0.1747</b>	-0.0046	0.1435
NDF	0.0116	0.1114	0.0085	0.0171	-0.0955	-0.0403	0.0031	0.0522	0.0207	0.0886	<b>-0.0091</b>	0.1683

**Note:** Diagonal values are direct effects, Residual factor = 0.2736, Cha. -Characters, \*, \*\* Significant at 5% and 1% level of significance, respectively.  
 DFF - Days to 50% Flowering, PH - Plant Height, LL - Leaf Length, LW - Leaf Width, NOT - Number of tillers per plant, NOL - Number of Leaves per plant, LSR - Leaf: Stem Ratio, GFY - Green Fodder Yield per plant, DMY - Dry Matter Yield per plant, DMC - Dry Matter Content, CP - Crude Protein content, ADF - Acid Detergent Fiber, NDF - Neutral Detergent Fiber

Whereas, with dry matter content it showed positive correlation at phenotypic level only. The findings suggest that, fodder yield can be improved in these oat genotypes by using these traits as selection criteria in succeeding generations. A multitiller tall plant with more number of leaves having higher length help into increasing the leaf area and improving photosynthetic efficiency which ultimately leads to higher green fodder yield. Therefore, these traits should be given more attention while improving green fodder yield. Positive association of green fodder yield per plant with days to 50% flowering, plant height, leaf length, number of tillers per plant, number of leaves per plant and dry matter yield per plant was also reported by Krishna *et al.*, (2014), Dubey *et al.*, (2015), Wagh *et al.*, (2018) and Negi *et al.*, (2019). Forage quality parameter, crude protein content, acid detergent fiber and neutral detergent fiber along with leaf width and leaf: stem ratio had non-significant positive association with green fodder yield per plant.

#### Inter- correlation among Yield Component traits

Plant height had significant and positive association with number of leaves per plant, leaf width, green fodder yield per plant, dry matter yield per plant, dry matter content, acid detergent fiber and neutral detergent fiber at both genotypic and phenotypic levels. Which inferred that increase in plant height leads to simultaneous improvement in the above mention traits. These results are in close agreement with the reports of Wagh *et al.*, (2018) for the number of leaves per plant, leaf width and green fodder yield per plant; Kapoor (2018) for acid detergent fiber and neutral detergent fiber. Number of tillers per plant exhibited significant and positive

correlation with number of leaves per plant, leaf: stem ratio, dry matter yield per plant and green fodder yield per plant, while it showed negatively significant correlation with neutral detergent fiber at both genotypic and phenotypic levels. It indicated that selection for more tiller numbers may lead to lower NDF content, potentially improving fodder quality. Our findings are in agreement with the results of Devi *et al.*, (2018) regarding positive and significant correlation of number of tillers per plant with number of leaves per plant, dry matter yield per plant and green fodder yield per plant; Negi *et al.*, (2019) for leaf: stem ratio, dry matter yield per plant and green fodder yield per plant. The present finding are in agreement with the results of Devi *et al.*, (2018) and Negi *et al.*, (2019) for leaf: stem ratio, number of tillers per plant with number of leaves per plant, dry matter yield per plant and green fodder yield per plant. Number of leaves per plant exhibited significantly positive genotypic and phenotypic correlation with days to 50% flowering, plant height, leaf length, number of tillers per plant, leaf: stem ratio, dry matter yield per plant, green fodder yield per plant at both genotypic and phenotypic levels. Similar results were found by Ahmed *et al.*, (2013) and Dubey *et al.*, (2015) for days to 50% flowering, plant height, leaf: stem ratio and number of tillers per plant. Days to 50% flowering had significant and positive correlation with leaf width, leaf: stem ratio and dry matter yield while negative association with dry matter content at phenotypic level only. Late maturing genotypes had wider leaves and higher leaf: stem ratio and dry matter yield. Krishna *et al.*, (2014) reported positive and significant correlations for days to 50% flowering with

leaf width and leaf: stem ratio. The positive correlation between ADF and NDF indicated that, as the indigestible fraction (ADF) increases, the overall fiber content (NDF) also rises, reducing forage digestibility. Therefore, selection of genotypes with low ADF and NDF is crucial for improving digestibility and nutritional value of forage. Similar correlation was also reported by Kapoor (2018). The negative correlation of acid detergent fiber with crude protein content and leaf length indicated that, simultaneous improvement of these traits may not be possible. Therefore, it is necessary to consider hybridization followed by selection to overcome this challenge.

### Path coefficient analysis

The association of characters as determined by the simple correlation coefficient may not provide an exact representation of the relationship between yield and yield attributes. In contrast, path coefficient analysis divide the correlation coefficients into direct and indirect effects, elucidate causal relationships among traits that cannot be explained by correlation studies.

In this investigation, green fodder yield per plant was considered as the dependent variable and the remaining eleven yield contributing characters were taken as independent (causal) variables. The results of path coefficient analysis at genotypic level showing direct (diagonal values) and indirect effects of different contributing traits on fodder yield per plant of fodder oat was mentioned in Tables 3. According to the results of genotypic path analysis, the number of tillers per plant had the highest direct effect on green fodder yield per plant (0.3773), followed by number of leaves per plant (0.2425), plant height (0.2305), days to 50% flowering (0.2241) and leaf length (0.1942), acid detergent fiber (0.1747), dry matter content (0.1180) and leaf width (0.0635). These traits can be considered primary selection criteria in breeding programs for improvement of green fodder yield in fodder oat. Remaining characters, *viz.*, neutral detergent fiber (-0.0091), crude protein (-0.0404) and leaf: stem ratio (-0.0476) exerted negative and negligible direct effect on green fodder yield per plant. These results are in close agreement with the findings of Negi *et al.*, (2019) and Swati (2023) for the number of tillers per plant. Dubey *et al.*, (2015) and Kapoor (2018) reported positive direct effects for the number of leaves per plant. Shekhawat and Jaypal (2016), Kapoor (2018), and Swati (2023) reported positive and moderate direct effects of plant height on green fodder yield per plant. Positive direct effects of days to 50% flowering on green fodder yield per plant were also reported by Krishna *et al.*, (2014) and Negi *et al.*, (2019). Maximum positive indirect effects on fodder yield were observed in number

of tillers per plant *via* number of leaves per plant followed by number of leaves per plant *via* number of tiller per plant, plant height *via* dry matter content and plant height *via* NDF. The residual effect of 0.2736 indicated that the characters included in the path analysis explained 73% of the variability in fodder yield at the genetic level.

The path coefficient analysis revealed that number of tillers per plant, number of leaves per plant, plant height and leaf length could be considered as major yield components and should be given due weightage / special attention while exercising selection for improvement in terms of green fodder yield as they had high positive direct effect as well as positive correlation with green fodder yield.

### Conclusion

The traits *viz.*, days to 50% flowering, plant height, leaf length, number of tillers per plant, number of leaves per plant and dry matter yield per plant exhibited positive and significant association with green fodder yield per plant. The results of genotypic path coefficient analysis revealed that, number of tillers per plant, number of leaves per plant, plant height, days to 50% flowering, leaf length, acid detergent fiber, dry matter content and leaf width exhibited positive direct effect on green fodder yield per plant.

Based on the above studies it can be concluded that, while doing genetic improvement for green fodder yield in oat through selection programme more emphasis should be given on number of tillers per plant, number of leaves per plant, dry matter yield per plant, plant height and leaf length as they had positive direct effect as well as positive correlation with green fodder yield. The selection of genotypes having more plant height and tillers, bearing numerous leaves with significant length would be rewarding as it shows direct as well as positive association with the green fodder yield.

### 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**(2), 75-78.
- Anonymous (2023a). Year End Review 2023: Achievement of the Department of Animal Husbandry and Dairying (Ministry of Fisheries, Animal Husbandry and Dairying, Government of India). Retrieved from <https://pib.gov.in>
- Anonymous (2023b). USDA FAS (2022/23). Circular Series, World Agricultural Production. Retrieved from <https://apps.fas.usda.gov/psdonline/circulars/production>
- Dewey, D.R. and Lu K. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, **51**(9), 515-518.

- Devi, P., Sood V.K. and Devi R. (2018). Evaluation of morphological and genetic determinants of fodder yield as a selection criterion in  $F_2$ ,  $F_3$  and  $F_4$  generations of oat (*Avena sativa* L.). *Forage Research*, **44(1)**, 1-7.
- Dubey, N., Avinash H.A., Jaiwar S., Chichkhede L. and Mehta A.K. (2015). Character association and path analysis study in fodder oat (*Avena sativa* L.). *Environment & Ecology*, **33(2A)**, 844-848.
- Hazel, L.N. (1943). The genetic bases for constructions selection of indices. *Genetics*, **28(6)**, 476-490.
- Kapoor, R. (2018). Inter-relationship of green fodder yield with yield contributing and quality traits in *Avena sativa* L. *Forage Research*, **43(1)**, 330-333.
- Kapoor, R., Deep A. and Hilli H.J. (2022). OL 15: A high yielding, single cut variety of fodder oat developed for Punjab state. *Electronic Journal of Plant Breeding*, **13(1)**, 125-131.
- 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 & Research*, **1(2)**, 1-9.
- 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.
- Rasane, P., Jha A., Sabikhi L., Kumar A. and Unnikrishnan V.S. (2015). Nutritional advantages of oats and opportunities for its processing as value added foods. *Journal of Food Science and Technology*, **52(2)**, 662-675.
- Roy, A.K., Agrawal R.K., Bhardwaj N.R., Mishra A.K. and Mahanta S.K. (2019). Revisiting national forage demand and availability scenario. Indian forage scenario: Redefining state wise status. ICAR-AICRP on Forage Crops and Utilization, Jhansi, India, 1-21.
- Shekhawat, S.S. and Jaipal P.S. (2016). Character association studies in oats (*Avena sativa* L.) for green fodder and grain yield. *Forage Research*, **42(1)**, 24-29.
- Swati (2023). *Genetic diversity studies in oat (Avena sativa L.) for forage yield and quality parameters* (M.Sc. Agri. Thesis, Birsa Agricultural University, Kanke, Ranchi, Jharkhand). Retrieved from <https://krishikosh.egranth.ac.in/items/ec00bcac-feb7-4ecd-95b3-36c6b614651b>
- 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.
- Wright, S. (1921). Correlation and causation. *Indian Journal of Agricultural Research*, **20(7)**, 557-585.