

GENETIC BEHAVIOUR OF MORPHOLOGICAL AND BIOCHEMICAL TRAITS GOVERNING GREEN FODDER AND SEED YIELD IN OATS (*AVENA SATIVA* L.)

BHOOMIKA, RAVISH PANCHTA, SATYAWAN ARYA AND SACHIN*

Department of Genetics and Plant Breeding
CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India
*(e-mail: sachinvermal105@gmail.com)

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SUMMARY

Oat (*Avena sativa* L.) is an important cereal cum forage crop of the temperate, sub-temperate and tropical climates of the world. It is a cool season crop cultivated in the *Rabi* season. The present investigation was conducted to quantify genetic variability, heritability (broad sense), genetic advance, and to elucidate phenotypic performance of the traits governing green fodder yield in oats. Fifty oat genotypes were evaluated in a randomized complete block design with three replications during *rabi* 2022-23 at CCS Haryana Agricultural University, Hisar. Sixteen morphological and biochemical traits were recorded. Highly significant differences among genotypes were observed for all characters, indicating the presence of substantial genetic variability. High genotypic and phenotypic coefficients of variation were recorded for number of tillers per plant, 100-grain weight and crude protein content. High heritability coupled with high genetic advance (as percentage of mean) was observed for plant height, no. of tillers per plant, leaf: stem, flag leaf length, flag leaf width, panicle length, 100 seed weight and crude protein content, suggesting predominance of additive gene action. Direct selection for such traits is rewarding in green fodder and seed yield improvement in oat.

Key words: Genetic variability and heritability, green forage, seed yield per plant, oat and protein content

Oat (*Avena sativa* L.) is a globally important cereal crop valued for its nutritional quality and utility as both grain and forage. Beside this, it is also used in the form of hay, silage, and concentrate feed grain, and is considered as the most palatable cereal fodder crop suitable for livestock (Satpal *et al.*, 2024). Despite its agronomic importance, oat production is increasingly challenged by abiotic stresses such as drought and low temperature, which significantly restrict growth, development, and yield. Therefore, critical study of yield attributing traits and along with the biochemical traits in breeding programs is essential to sustain the green fodder yield (Ghimire *et al.*, 2024). The global area and output of oat is approximately 27 million hectares and 40 metric tonnes, respectively (Bhoomika *et al.*, 2026). The top five countries for oat production are Russia, Canada, Poland, Finland and Australia (FAO, 2024). As the dairy industry in India expands, oat have captured the interest of breeders for their modernization. This is attributed to their high-quality fodder, nutritional value and increased grain yield, resulting in greater net energy gains (Ruwali *et al.*, 2013). Genetic variability among oat germplasm

remains a critical resource for crop improvement. The extent of genetic variability in the experimental breeding material, as well as the degree to which valuable traits are inherited, determines the success of any targeted breeding program. (Mathavaraj *et al.*, 2025; Sachin *et al.*, 2025 and Ashok *et al.*, 2024).

Germplasm selected from different regions is considered the best natural resources in providing the required variation in traits. Despite these advances, many locally adapted oat cultivars remain poorly characterized with respect to their genetic potential and trait associations. A comprehensive evaluation of phenotypic performance and genetic variability in yield-related and biochemical traits is therefore essential to identify superior genotypes that combine high green-fodder yield with high seed productivity (Sachin *et al.*, 2023). Earlier studies have reported substantial variability for fodder yield and its component traits in oats (Jaipal and Shekhawat, 2016; Poonia *et al.*, 2017; Chauhan and Singh, 2019; Pankaj *et al.*, 2022). The present study was therefore undertaken to assess genetic variability, heritability, genetic advance and to identify key traits influencing green fodder yield and seed yield in oat.

MATERIALS AND METHODS

The experiment was conducted during *Rabi* 2022-23 at the Forage Research Area, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar (29.14° N, 75.68° E; 228 m AMSL). Fifty oat genotypes (Table 1) were evaluated in a randomized complete block design with three replications. Each entry was grown in paired rows of 3 m length with 30 cm row spacing and 10 cm plant spacing. The 16 observations namely, plant height (cm), days to 50% flowering, days to maturity, no. of tillers per plant, leaf weight per plant (g), stem weight (g), leaf stem ratio, flag leaf length (cm), flag leaf width (cm), internode length (cm), panicle length (cm), 100 seed weight (g), seed yield per plant (g), green fodder yield per plant (g), dry matter yield per plant (g) and crude protein content (%) were recorded in five randomly selected plants of each oat genotype in all three replications and analyzed using appropriate statistical methods. Analysis of variance was carried out as suggested by Fisher (1930). Variability parameters (Range, PCV, GCV, h^2 , GA) were computed according to Hanson *et al.* (1956). Expected genetic advance (GA) was calculated by the method suggested by Johnson *et al.* (1955). R software version 4.4.1 was used for statistical analysis of the recorded data.

RESULTS AND DISCUSSION

The box plot diagrams (Fig.1 to Fig.16) constructed for sixteen quantitative traits provided a visual representation of the extent of phenotypic variability, distribution pattern and presence of

TABLE 2
Analysis of variance for various quantitative traits of Oat (*Avena sativa* L.).

S. No.	Traits	Replication	Genotypes	Error
	DF	2	49	98
1.	PH	372.34	386.45**	5957.11
2.	DFP	6.89	101.96**	5.42
3.	DM	9.25	162.21**	6.21
4.	TPP	1.01	8.93**	0.9
5.	LW	35.95	246.67**	15.08
6.	SW	259.9	178.62**	55.62
7.	L:S	0.01	0.05**	0.01
8.	FLL	8.43	58.24**	2.9
9.	FLW	0.01	0.16**	0.01
10.	IL	0.44	35.32**	3.15
11.	PL	0.83	63.61**	7.99
12.	100 SW	0.1	1.54**	0.17
13.	DMY/PP	0.35	108.44**	7.53
14.	CPC %	0.84	1.28**	0.2
15.	SYPP	18.65	269.33**	13.92
16.	GFYPP	379.56	741.80**	81.57

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

PH = Plant height, DFP = Days to 50% flowering, DM = Days to maturity, TPP = No. of tillers per plant, LW = Leaf weight/plant, SW = Stem weight/plant, L:S = Leaf stem ratio, FLL = Flag leaf length, FLW = Flag leaf width, IL = Internode length, PL = Panicle length, 100 SW = 100 Seed weight, DMYPP = Dry matter yield/plant, CPC% = Crude protein content %, SYPP = Seed yield/plant, GFYPP = Green fodder yield/plant.

extreme genotypes among the oat germplasm. Considerable dispersion of data points beyond the inter-quartile range was observed for most traits, indicating the presence of wide phenotypic variation. Traits such as dry matter yield per plant, green fodder

TABLE 1
The names of oat genotypes used in the experiment

S. No.	Genotypes						
1.	HJ 8	14.	HFO-1009	27.	OL-1949	40.	OL-1944
2.	UPO 212	15.	HFO 1108	28.	RO 19	41.	RO 11-1
3.	OL-1882	16.	HFO 529	29.	HFO 1014	42.	PLP-27
4.	OL-1974	17.	SKO 244	30.	HFO 1208	43.	HFO 1222
5.	HFO 1123	18.	HFO 1209	31.	BAUO-101	44.	HFO 1013
6.	HFO 1204	19.	HFO 611	32.	HFO 904	45.	OL-1960
7.	HFO 1121	20.	OL-1942	33.	JO-07-28	46.	HFO 806
8.	OL-1977	21.	OS 6	34.	UPO-20-2	47.	OS 403
9.	HFO-1016	22.	HFO 707	35.	HFO 917	48.	JO-08-37
10.	JHO 822	23.	HFO 1207	36.	HFO 1221	49.	OS 377
11.	HFO-1003	24.	HFO 1119	37.	HFO 1113	50.	JH 851
12.	Kent	25.	UPO-20-3	38.	HFO 906		
13.	HFO 114	26.	HFO 1217	39.	HFO 915		

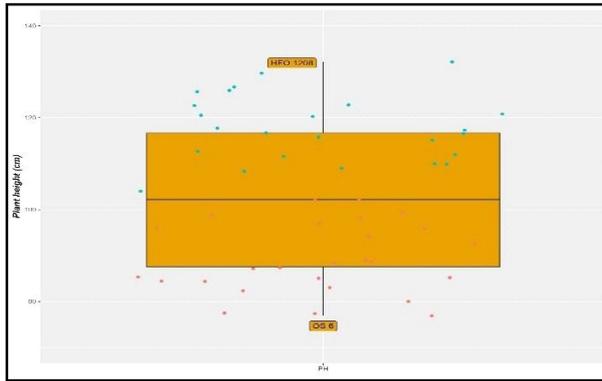


Fig. 1. Plant height (cm).

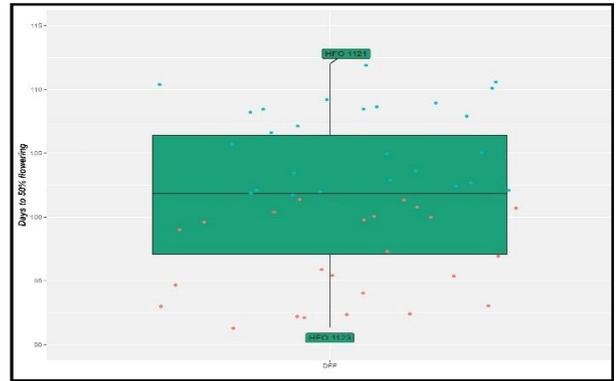


Fig. 2. Days to 50% flowering.

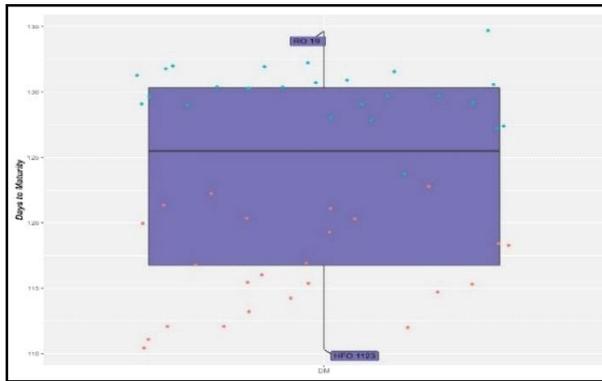


Fig. 3. Days to maturity.

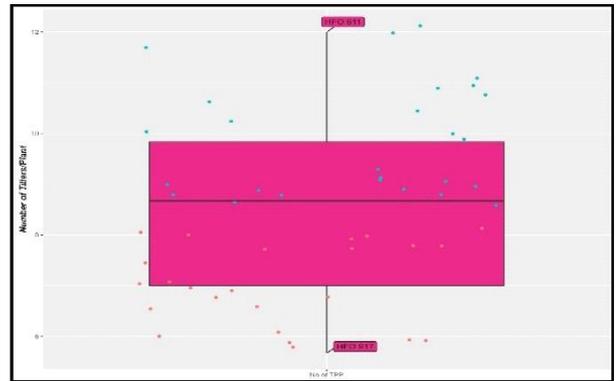


Fig. 4. Numbers of tillers/plant.

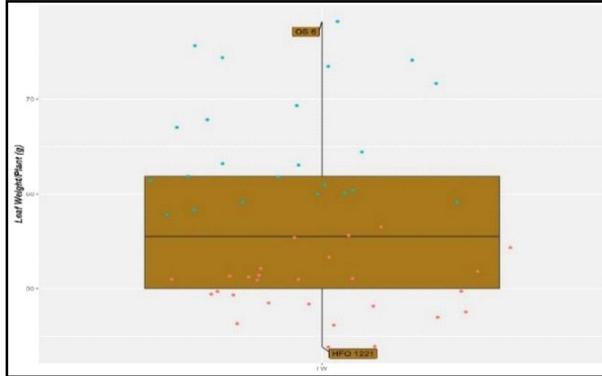


Fig. 5. Leaf weigh/plant (g).

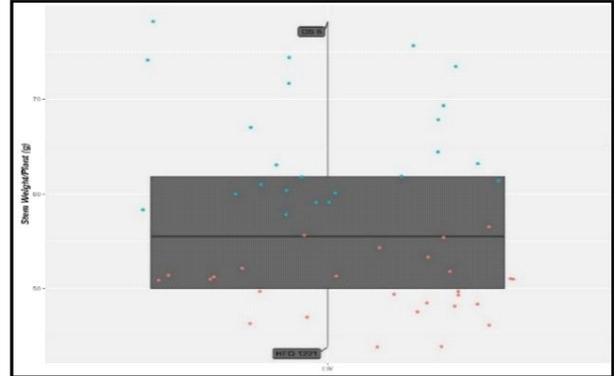


Fig. 6. Stem weight/plant (g).

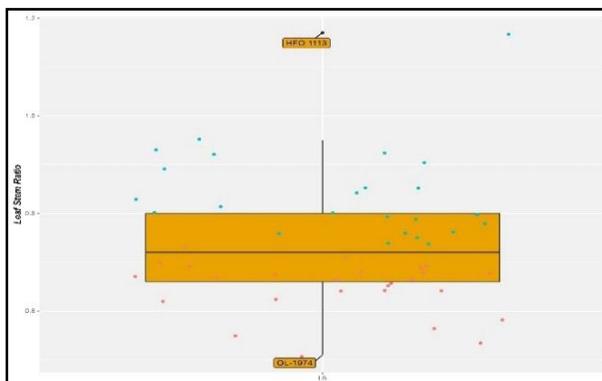


Fig. 7. Leaf stem ratio.

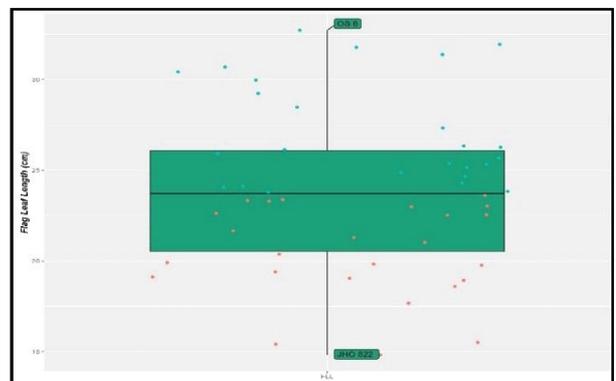


Fig. 8. Flag leaf length (cm).

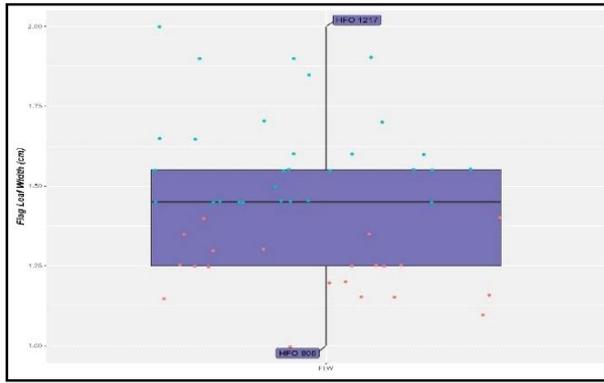


Fig. 9. Flag leaf width (cm).

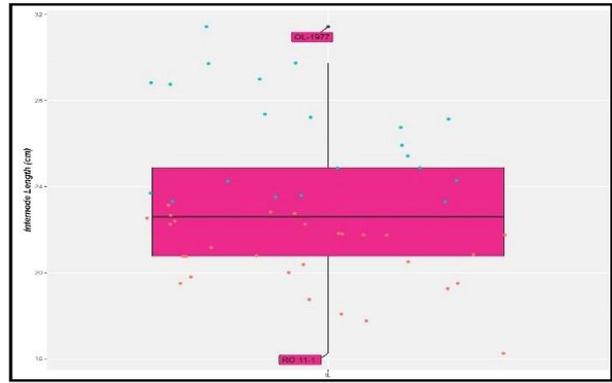


Fig. 10. Internode length (cm).

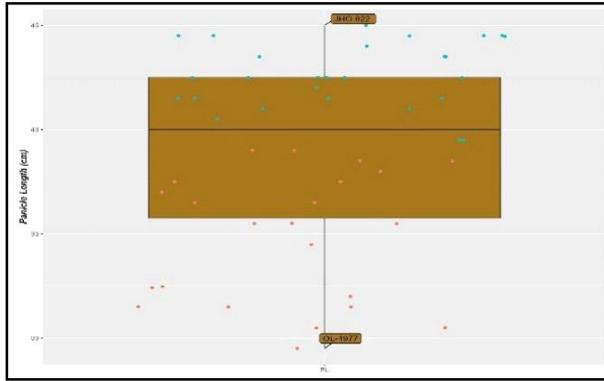


Fig. 11. Panicle length (cm).

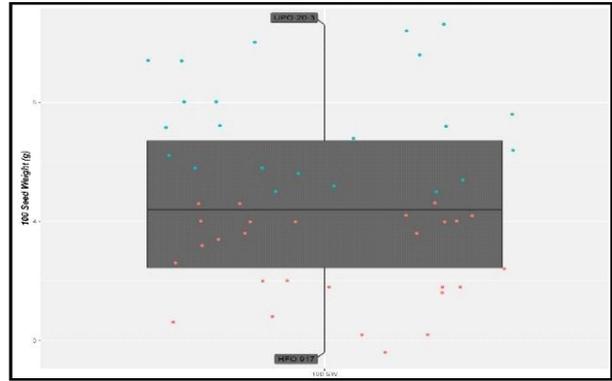


Fig. 12. 100 seed weight (g).

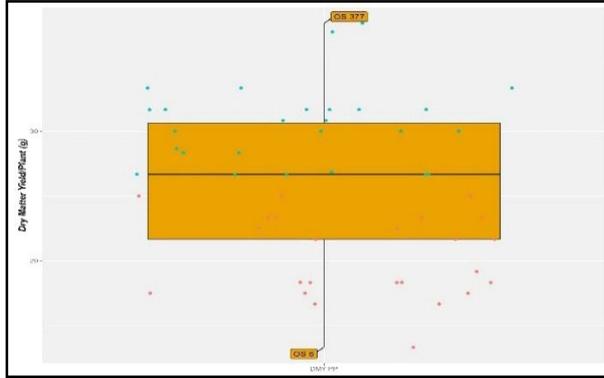


Fig. 13. Dry matter yield/plant (g).

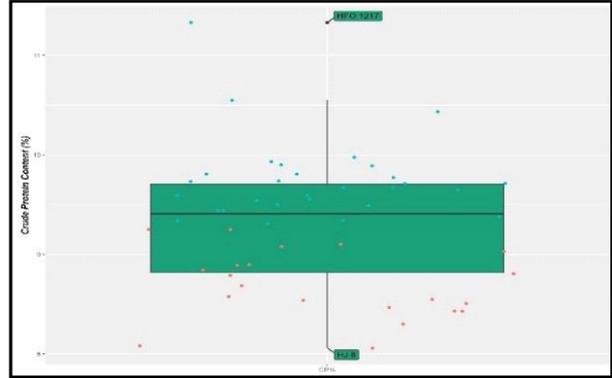


Fig. 14. Crude protein content (%).

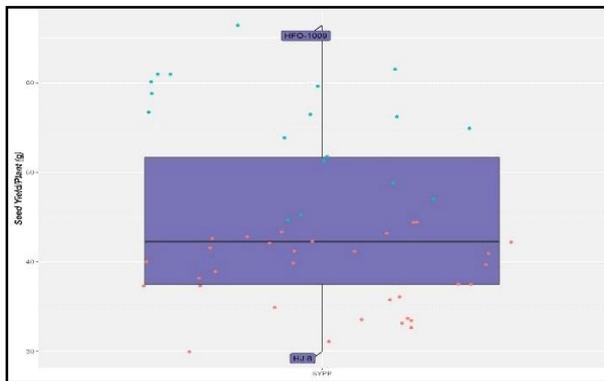


Fig. 15. Seed yield/plant (g).

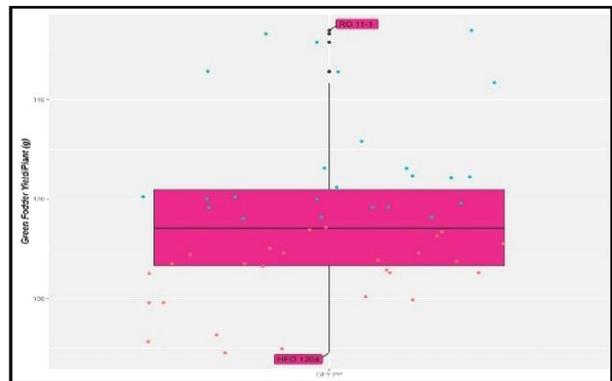


Fig. 16. Green fodder yield/plant (g).

yield per plant, number of tillers per plant, leaf:stem ratio and seed yield per plant exhibited broader inter-quartile ranges and longer whiskers, reflecting higher variability and scope for selection. In contrast, relatively narrower boxes were observed for traits such as days to flowering and days to maturity, suggesting comparatively lower variability and greater phenotypic uniformity among genotypes. Several genotypes appeared as outliers above the upper quartile for key yield-contributing traits, indicating the existence of superior genotypes with exceptionally high performance. For instance, a few genotypes recorded markedly higher values for dry matter yield per plant and crude protein content, highlighting their potential as donors for improving fodder productivity and quality. The asymmetrical distribution of data in certain traits, as evidenced by skewed medians and uneven whisker lengths, suggested differential response of genotypes to the growing environment and the influence of non-additive genetic effects. Overall, the box plot analysis complemented the variability parameters by clearly demonstrating the magnitude of dispersion, identifying extreme phenotypes and confirming the presence of exploitable genetic diversity for all the morphological and biochemical traits in the experimental material.

Analysis of variance for the traits are presented in Table 2. Results regarding all the variability parameters *viz.*, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as percent of mean (GAM) for all the sixteen traits have been furnished in Table 3 indicated that there is almost perfect relation between PCV and GCV of each character. In addition to the Table 2 a graph (Fig. 17) depicts the comparative magnitude of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for sixteen traits in oat genotypes, wherein PCV values were consistently higher than the corresponding GCV values for all traits. This pattern indicated the influence of environmental factors on trait expression, although the narrow PCV–GCV differences for several traits suggested substantial genetic control. High genotypic (GCV) and phenotypic coefficient of variance (PCV) were observed for the dry matter yield per plant (22.63 and 25.03%) and seed yield per plant (20.71 and 22.34%) suggesting that these characters were under the influence of genetic control. So, the characters can be relied upon and simple selection can be practiced for further improvement.

While moderate for all the remaining yield attributing traits except days to 50% flowering and

TABLE 3
Estimates for genetic parameters for different traits in Oat (*Avena sativa* L.).

Traits	Mean \pm SE(m)	MAX	Min.	Range	GCV	PCV	Heritability (%)	G A. % of mean
PH	102.82 \pm 4.5	132.15	76.89	55.26	15.14	16.93	79.94	27.88
DFP	101 \pm 1.35	112.00	91.33	20.67	5.59	6.04	85.58	10.65
DM	123 \pm 1.44	134.67	110.33	24.33	5.84	6.17	89.34	11.36
No TPP	8.49 \pm 0.55	12.00	5.67	6.33	19.26	22.26	74.88	34.34
LW	57.18 \pm 2.24	78.21	43.85	34.36	15.37	16.80	83.66	28.96
SW	78.4 \pm 4.31	100.46	62.10	38.37	8.17	12.54	42.44	10.96
L:S	0.74 \pm 0.05	1.17	0.51	0.66	15.34	19.42	62.41	24.96
FLL	23.79 \pm 0.98	32.72	14.82	17.90	18.05	19.42	86.40	34.56
FLW	1.45 \pm 0.06	2.00	1.00	1.00	15.22	16.93	80.82	28.18
INTL	23.13 \pm 1.02	31.43	16.25	15.18	14.16	16.10	77.32	25.64
PL	39.04 \pm 1.63	45.00	29.50	15.50	11.03	13.19	69.88	18.99
100 SW	4.18 \pm 0.24	5.65	2.90	2.76	16.16	18.85	73.48	28.54
DMYPP	25.63 \pm 1.58	38.33	13.33	25.00	22.63	25.03	81.72	42.14
CPC %	9.3 \pm 0.26	11.33	8.06	3.27	6.45	8.03	64.50	10.67
SYPP	44.56 \pm 2.15	66.40	29.95	36.45	20.71	22.34	85.95	39.55
GFYPP	115.9 \pm 5.22	153.92	89.10	64.83	12.79	14.98	72.96	22.51

The present investigation revealed substantial genetic variability among oat genotypes for fodder yield and its component traits. Genotypes RO 11-1, OS 403, HFO 906, HFO 1013 and BAUO-101 were identified as promising donors for green fodder and seed yield improvement.

These results provide a strong quantitative basis for trait-based selection and breeding of high-yielding, nutritionally superior oat varieties.

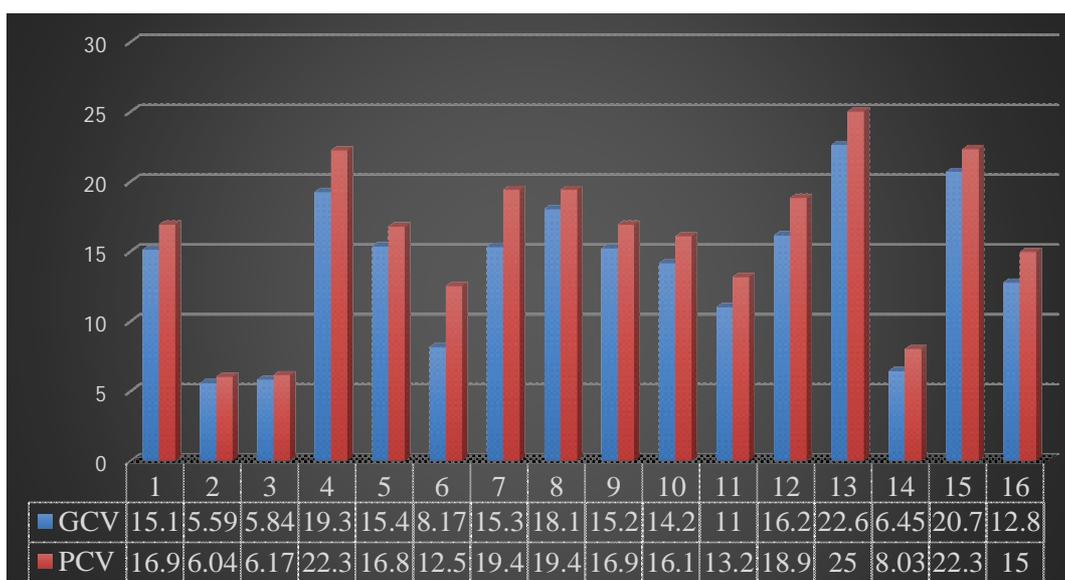


Fig. 17. Comparison between PCV and GCV.

days to maturity where these were low. Heritability refers to how much genetic variation contributes to phenotypic variability. Estimates of broad sense heritability was recorded almost high for all the traits and it ranged from 42.44 percent (stem weight per plant) to 89.34 percent (days to maturity) indicating less effect of environment on these traits. However, selection for the traits showing high heritability is not significant because broad sense heritability is calculated from total genetic variance which include additive, dominant and epistatic variances. A high value of genetic advance show that the trait is regulated by additive gene action. Thus, the effective selection came from the combination of traits having high heritability coupled with high genetic advance. High heritability coupled with high genetic advance (as percentage of mean) was observed for plant height (cm), no. of tiller per plant, leaf: stem, flag leaf length (cm), flag leaf width (cm), panicle length (cm), 100 seed weight (g) and crude protein content (%). These revealed that additive gene action played a predominant role in governing these traits and further it also indicated the suitability of selection of these traits for further improvement among genotypes under studied. Similar results were reported by Shankar et al. (2002), Pundir et al. (2003) and Wagh *et al.* (2018) while working on oat for the same traits evaluated in the present investigation. The consistency of these findings supports the reliability of the observed genetic variability.

CONCLUSION

The mean squares attributed to genotypes (treatments) were highly significant for all characters, demonstrating substantial genetic variability among the genotypes studied. High GCV and PCV were observed for dry matter yield per plant and seed yield per plant which means that these traits had more variability. Additive gene action played a predominant role in governing the studied traits and further indicated the suitability of selection of these traits for improvement among genotypes. Based on phenotypic performance and genetic behavior of the genotypes HFO 1009 followed by HFO 1108, HFO 1014, JO-08-37 and HFO 611 demonstrated good seed yields and were found to be superior. On the other hand, Genotypes RO 11-1, OS 403, HFO 906, HFO 1013 and BAUO-101 were found to be superior in green fodder yield per plant. Thus, to increase the yield, these genotypes can be applied in oat breeding programs.

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