

CHARACTERIZING VARIATION IN OAT (*AVENA SATIVA* L.) ACCESSIONS FOR GRAIN AND FODDER YIELD DETERMINANTS

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SUMMARY

A comprehensive evaluation of 62 oat accessions was conducted during *Rabi* 2019-2020 at Farm Research Area of Forage section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar (Haryana) to measure and analyze yield-contributing traits. The findings unveiled substantial variability among the oat accessions pertaining to all the scrutinized traits. High heritability along with high genetic advance as percent of mean was observed for all traits except days to 50% flowering and days to maturity. Genotypes namely; OS 403, HFO 1108, GP 781, HFO 1101, HFO 915 and HFO 1104 showed higher seed yield per plant while HFO 1108, HFO 818, HFO 707, HFO 915, HFO 1104 and HFO 529 were found promising for green fodder yield per plant. The discernment of accessions exhibiting coveted trait amalgamations and elevated yield propensity is paramount for oat breeding initiatives. Through the meticulous delineation of variability in these yield attributes, breeders can discerningly concentrate on and assimilate particular traits in their breeding programs. This methodology expedites the progression of refined oat cultivars endowed with augmented yield efficacy and agronomic characteristics.

Keywords: Oat, genetic variability, heritability, fodder, seed yield

Oat cultivation belonging to the Poaceae family, took place subsequent to the cultivation of wheat and barley. The most important commercial oat, *Avena sativa*, is a hexaploid species ($2n = 6x = 42$) with genomic composition as AACDD (Rines *et al.*, 2006). The principal oat species grown for fodder and grain are *Avena sativa* L. and *Avena byzantina* K., usually known as white oat and red oat, respectively. Oat cultivation spans across a global area of 9.4 million hectares, yielding a substantial output of 24.3 million metric tons according to the USDA, 2022. Oats possess remarkable attributes as a forage crop due to their growth characteristics, multi-cut nature, rich nutritional composition and rapid regenerative abilities (Nikolaoudakis, 2016, Chawla *et al.*, 2022). Oats are an indispensable crop due to their nutritional value, health benefits, versatility, role in livestock feed, environmental advantages and

economic importance (De Souza and Bonciu 2022; Dhaliwal *et al.*, 2022). They contribute to a healthy and sustainable food system, benefiting both human health and the environment. The study of crop variability is of paramount importance due to a myriad of reasons (Naresh *et al.*, 2023). It facilitates the identification and preservation of genetic diversity within crops, thereby ensuring the perpetuation of advantageous traits that significantly contribute to agricultural advancement and sustainability (Govindaraj *et al.*, 2015; Jovovic *et al.*, 2020). Moreover, unraveling the intricacies of variability empowers crops to adeptly acclimatize to the ever-changing environmental milieu, including the formidable challenges posed by climate change (Rarieya & Fortun, 2010). This adaptation ensures food security in the face of unpredictable climatic challenges (Poonia *et al.*, 2017).

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Furthermore, crop variability aids in improving yields by selecting and breeding high yielding varieties based on traits related to productivity (Dwivedi *et al.*, 2016; Ahmed *et al.*, 2011). This leads to increased agricultural output and improved efficiency in food production. The genotypic and phenotypic coefficients of variability, heritability and genetic advance are considered as very important parameters for yield improvement (Denton and Nwangburuka, 2011). Consequently, the current investigation was undertaken to evaluate the variability exhibited by 62 oat genotypes with regard to 13 yield contributing attributes, employing diverse genetic parameters for comprehensive analysis.

MATERIALS AND METHODS

The field experiment was performed at the Farm Research Area of Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar (Haryana), during *Rabi* 2019-2020. Sixty-two oat genotypes (Table 1) were evaluated in augmented design for 13 yield related traits. Weather data during the crop season is presented in form of chart (Fig. 1). Five competing plants were chosen randomly for each genotype and the data were recorded on these traits. When the plants reached 50% flowering stage, the data for yield and its attributes were recorded. The data on 62 genotypes, including checks were subjected to analysis of variance (ANOVA) as per augmented design (Federer, 1956). Traits studied were Plant height (cm), Tillers per plant, Number of leaves per plant, Leaf length (cm), Leaf width (cm), Peduncle length (cm), Number of spikelets/panicle, Green fodder yield per plant (g), Dry matter yield per plant (g), Days to 50% flowering, Days to maturity, Seed yield per plant (g), Test weight (1000 seed weight, in g). The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as percent of mean (GAM) was evaluated using R.4.0.3 studio. All the figures were drawn using Excel software, a versatile tool known for its proficiency in data visualization and charting.

RESULTS AND DISCUSSION

Genetic variability

The analysis of variance table exhibited the pronounced significance of the mean sum of squares resulting from treatments across all the observed traits,

signifying the substantial genetic variability among the genotypes. Moreover, the mean sum of squares attributed to blocks was found to be statistically significant for all traits, indicating a relatively lower degree of heterogeneity among the blocks. Additionally, the mean sum of squares pertaining to the checks was deemed significant for all traits, thereby exposing noticeable distinctions among the three checks. The experimental outcomes, expressed through GCV, PCV and ECV have been graphically depicted in Fig. 2 to provide a visual representation. The magnitude of the phenotypic coefficient of variance was slightly higher than the genotypic coefficient of variance for all the characters studied which indicated the lesser influence of environment in the expression of these characters. Comprehending the extent and nature of variability in oat allows breeders to discern and select superior traits for breeding programs (Kumar *et al.*, 2023). By studying the range of variability, breeders can target specific traits such as yield potential, disease resistance, tolerance to environmental stresses and nutritional quality. This erudition plays a pivotal role in the cultivation of enhanced oat cultivars that effectively cater to the ever-changing demands of farmers and consumers.

The highest estimates of GCV and PCV were observed for seed yield per plant (SY) (35.92 & 36.81%), number of leaves per plant (24.49 & 25.72%) and dry matter yield per plant (DMY) (20.49% & 22.63%). However, low GCV and PCV were recorded for traits *viz* days to maturity (DM) (4.10% & 4.26%) and days to 50% flowering (DFF) (3.92% & 3.95%). For these traits having high GCV and PCV, selection would be effective to improve yield in oat cultivars. Jaipal and Shekhawat (2016) and Wani *et al.* (2018) observed similar results in oat.

Heritability and Genetic advance

All the scrutinized characters exhibited substantial heritability (in the broad sense) estimations. The GAM demonstrated high values for all traits, except DM and DFF (Table 2). The combination of high heritability and significant genetic advance indicated the presence of additive genetic effects, suggesting that selection would be influential in enhancing those specific traits. However, relying solely on the study of broad sense heritability is not sufficient for determining the type of gene action at play, as it encompasses both non-additive and additive gene actions. Nevertheless, traits such as days to maturity and days to 50% flowering displayed low genetic

TABLE 1
Sixty-two oat genotypes along with their source

S. No.	Genotypes	Pedigree	Source	S. No.	Genotypes	Pedigree	Source
1	GP 65	HJ 8 X HFO 267	CCS HAU, Hisar	32	HFO 1109	OS 346 X Kent	CCS HAU, Hisar
2	GP 68	Selection from HFO 114	CCS HAU, Hisar	33	HFO 1111	Kent X SKO 148	CCS HAU, Hisar
3	GP 158	OS 6 X UPO 212	CCS HAU, Hisar	34	HFO 1112	HFO 114 X Kent	CCS HAU, Hisar
4	GP 192	Selection from HJ 8	CCS HAU, Hisar	35	HFO 1113	UPO 212 X SKO 148	CCS HAU, Hisar
5	GP 298	Kent X OS 6	CCS HAU, Hisar	36	HFO 1114	HFO 878 X OS 6	CCS HAU, Hisar
6	GP 492	HJ 8 X Kent	CCS HAU, Hisar	37	HFO 1115	HJ 8 X HFO 58	CCS HAU, Hisar
7	GP 580	Selection from OS 7	CCS HAU, Hisar	38	HFO 1116	OS 403 X OS 377	CCS HAU, Hisar
8	GP 781	OS 6 X JHO 851	CCS HAU, Hisar	39	HFO 1117	HJ 8 X OS 346	CCS HAU, Hisar
9	GP 875	Dulo, Introduction from Bulgaria	Bulgaria	40	HFO 1118	HJ 8 X JHO 822	CCS HAU, Hisar
10	HFO 424	HJ 8 X Kent	CCS HAU, Hisar	41	HFO 1121	FOS 1/29 X HJ 8	CCS HAU, Hisar
11	HFO 529	OS 6 X Kent	CCS HAU, Hisar	42	HFO 1122	OS 377 X HJ 8	CCS HAU, Hisar
12	HFO 607	HJ 8 X UPO-04-1	CCS HAU, Hisar	43	HFO 1123	OS 346 X OS 403	CCS HAU, Hisar
13	HFO 611	HJ 8 X UPO 212	CCS HAU, Hisar	44	HJ 8	OS 7 X S3021	CCS HAU, Hisar
14	HFO 707	JHO 822 X NGB 7021	CCS HAU, Hisar	45	OS403	HJ 8 X Algerian	CCS HAU, Hisar
15	HFO 806	OL 125 X UPO 212	CCS HAU, Hisar	46	OL 125	Appler X IPC-63	PAU, Ludhiana
16	HFO 818	JO 1 X HFO 267	CCS HAU, Hisar	47	OL 1861	HJ 8 x OL 1610	PAU, Ludhiana
17	HFO 901	UPO 212 X Kent	CCS HAU, Hisar	48	OL 1869-1	OL 9 X OL 125	PAU, Ludhiana
18	HFO 902	JHO 822 X NGB 6370	CCS HAU, Hisar	49	OL 1766-2	Advance breeding line	PAU, Ludhiana
19	HFO 903	OL 125 X OS 346	CCS HAU, Hisar	50	OL 1874-2	Advance breeding line	PAU, Ludhiana
20	HFO 915	UPO 212 X OS 346	CCS HAU, Hisar	51	Kent	Introduction	USA
21	HFO 917	NGB 6370 X NGB 4871	CCS HAU, Hisar	52	RO 11-2-2	Advance breeding line	MPKV, Rahuri
22	HFO 1003	HFO 878 X OS 6	CCS HAU, Hisar	53	RO 11-2-6	Advance breeding line	MPKV, Rahuri
23	HFO 1005	JHO 822 X NGB 7021	CCS HAU, Hisar	54	JHO 822	IGO 4268 X Indio-6-5-1	IGFRI, Jhansi
24	HFO 1013	UPO 212 X OS 6	CCS HAU, Hisar	55	JHO 99-1	OS 7 X IGO-320-1139-19	IGFRI, Jhansi
25	HFO 1016	UPO 212 X SKO 96	CCS HAU, Hisar	56	JHO 2006-1	Advance breeding line	IGFRI, Jhansi
26	HFO 1101	JHO 2006-1 X HJ 8	CCS HAU, Hisar	57	JO 1	Kent X UPO 50	JNKVV, Jabalpur
27	HFO 1104	HFO 878 X UPO 212	CCS HAU, Hisar	58	NDO 1	Local collection	NDUA&T, Faizabad
28	HFO 1105	UPO 212 X OS 6	CCS HAU, Hisar	59	PLP 1	Selection from Algerian material	CSKHPKV, Palampur
29	HFO 1106	Algerian X OS 6	CCS HAU, Hisar	60	OS 6 (C1)	HFO 10 X HFO 55	CCSHAU, Hisar
30	HFO 1107	HJ 8 X OS 6	CCS HAU, Hisar	61	JHO 851 (C2)	Selection from Huga Kairyokuro	Introduction from Japan
31	HFO 1108	HFO 878 X OS 6	CCS HAU, Hisar	62	UPO 212 (C3)	VS 1492 X Kent	GBPUAT, Pantnagar

TABLE 2

Mean, heritability (Broad sense) %, genetic advance and genetic advance as percent of mean (GAM) for thirteen yield related traits in 62 oat accessions

Traits	Mean	Range		Heritability h ² BS	GA	GAM
		Min	Max			
Plant height	143.1	98.1	190.1	91.3	31.5	22.0
Tillers per plant	8.2	5.2	13.9	76.2	2.8	34.8
Number of leaves per plant	42.3	24.8	75.5	90.7	20.4	48.1
Leaf length	51.0	34.4	63.9	95.2	10.6	20.7
Leaf width	2.3	1.4	4.2	91.8	0.8	34.1
Peduncle length	31.8	14.1	51.5	94.7	11.2	35.0
Number of spikelets/panicle	62.4	40.8	104.0	99.0	25.6	41.0
Green fodder yield per plant	143.1	80.8	207.5	80.2	38.3	26.8
Dry matter yield per plant	27.2	16.1	43.3	82.0	10.4	38.3
Days to 50% flowering	113.2	93.6	121.9	98.5	9.1	8.0
Days to maturity	141.0	117.9	154.5	92.7	11.5	8.2
Seed yield per plant	11.8	1.6	26.4	95.2	8.5	72.3
Test weight	33.2	19.6	43.7	99.2	10.3	31.0

advance as percentage of mean, despite their high heritability. Similar outcomes, with low genetic advance relative to the mean, were observed in the studies conducted by Wani *et al.* (2018) and Chaudhary *et al.* (2020) for days to 50% flowering. These findings, characterized by low genetic advance alongside high heritability, indicate the presence of non-additive gene action. Consequently, simple selection procedures would prove ineffective in identifying desired traits through simple selection alone.

Best Performing Genotypes

The genotype HFO 1108 displayed the highest green fodder yield reaching 207.5 g/plant. Remarkably, genotypes HFO 1108, HFO 818, HFO 707, HFO 915, HFO 1104 and HFO 529 exhibited superiority in terms of green fodder yield. The genotype HFO 1108,

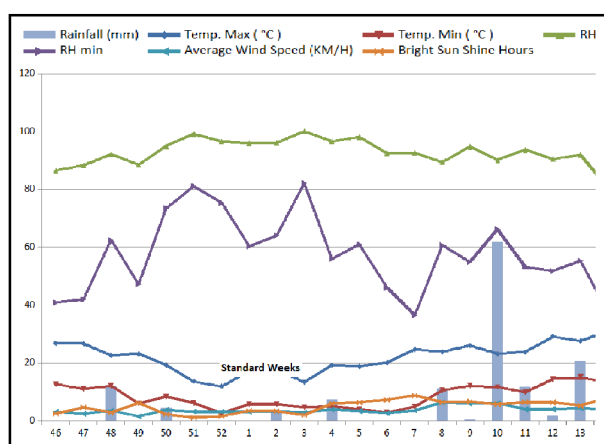


Fig. 1. Weather chart of Rabi 2019-2020.

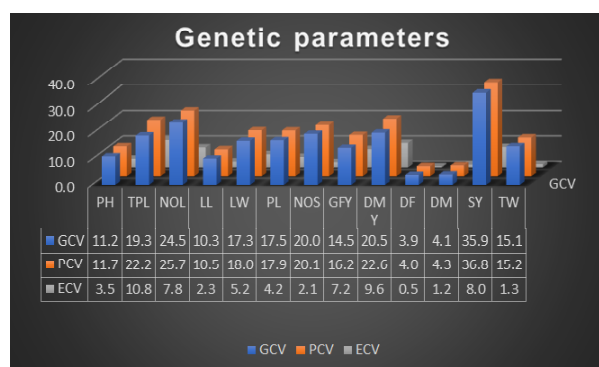


Fig. 2. Graph illustrating GCV, PCV, ECV for 13 yield related traits clearly depicting PCV> GCV.

showcased the highest dry matter yield i.e., 43.3 g/ plant. Promising genotypes for dry matter yield included GP 68, HFO 707, HFO 818, GP 158 and HFO 806. Achieving higher fodder yield in oat brings multiple advantages, including improved livestock nutrition, cost efficiency, farm sustainability, enhanced animal health and welfare and flexibility in feed management. The highest seed yield per plant was observed in the genotype OS 403, amounting to 26.4 g/plant. Additionally, genotypes HFO 1108, GP 781, HFO 1101, HFO 915 and HFO 1104 demonstrated commendable yield and were considered superior. Furthermore, promising genotypes for yield attributed traits with high positive correlation can be used for indirect selection (Chawla *et al.*, 2021).

CONCLUSION

The mean sum of squares associated with genotypes exhibited a significant statistical relevance

across all examined characteristics, indicating the presence of substantial genetic variability among the genotypes under study. The majority of traits displayed a range of high to moderate GCV and PCV, except for the traits, days to 50% flowering and days to maturity which exhibited lower GCV and PCV values. Based on yield attributes, genotypes such as **HFO 1108** (exhibiting high seed yield, green fodder yield and dry matter yield), **HFO 707** (displaying high green fodder yield and dry matter yield), **HFO 915** (demonstrating high seed yield, green fodder yield and seed yield) and **HFO 1104** (showcasing high seed yield and green fodder yield) exhibited promising characteristics.

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