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STUDY OF GENETIC DIVERSITY AMONG OAT (*AVENA SATIVA* L.) GENOTYPES FOR GREEN FODDER YIELD AND QUALITY TRAITS

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ABSTRACT

An experiment was conducted to evaluate the genetic diversity among thirty-four oat (*Avena sativa* L.) genotypes for green fodder yield and quality traits during Rabi season of 2024–25 at Birsa Agricultural University, Ranchi, India. The experiment was laid out in a Randomized Block Design with three replications, each genotype grown in four rows with 25/ cm spacing. Observations were recorded at both plot and plant levels for phenological, morphological, yield and quality traits, including crude protein content, neutral detergent fiber, acid detergent fiber and in vitro dry matter digestibility. Analysis of variance revealed significant differences among the genotypes for all traits, indicating substantial genetic variability. Phenotypic variance exceeded genotypic variance for most of the traits, reflecting environmental influence, whereas traits such as days to 50% flowering, number of tillers per plant and fiber fractions were largely genetically controlled. Genetic divergence assessed using Mahalanobis D^2 statistics grouped the genotypes into six clusters, with Cluster V comprising the largest number of genotypes and Cluster VI representing a highly diverse single genotype. Inter-cluster distances exceeded intra-cluster distances, highlighting greater divergence between clusters and identifying potential parents for hybridization. Cluster mean analysis showed marked differences for growth, yield and quality traits, with green fodder yield contributing maximum (86.27%) to overall divergence. These findings indicate that genetic variability is predominantly governed by yield-related traits, providing valuable insights for the selection of genetically diverse and superior parents to develop high-performing fodder oat cultivars and it could be utilized in the further hybridization programme to enhance the biomass yield in fodder oat.

Key words: *Avena sativa* L., Genetic Diversity, Fodder Yield, Quality traits, Mahalanobis D^2, Cluster analysis

Introduction

Oat (*Avena sativa* L.), a member of the family Poaceae, is an important cool-season cereal crop cultivated predominantly for green fodder, hay and silage and is extensively grown during the rabi season in India as a dependable source of quality winter fodder (IGFRI, 2011). The genus *Avena* comprises diploid, tetraploid and hexaploid species, among which cultivated oat (*A. sativa* L.) is an allohexaploid (2n = 6x = 42) and largely self-pollinated. The crop is characterized by rapid growth, multi-cut potential and good regenerative capacity, making it well suited for intensive fodder production systems. Oat fodder is highly palatable and nutritionally rich, containing 9.0–11.5% crude protein with favourable digestibility and balanced fibre fractions (Sterna *et al.*, 2016), and oat ranks sixth among cereal crops globally in terms of production (FAO, 2012). Livestock constitutes a vital component of Indian agriculture; however, the country faces an acute green fodder deficit of about 35.6% against a requirement of 850.9 million tones, which

Table 1: Analysis of variance (mean sum of square) for thirteen yield attributing characters.

Sr.	Source of variation	d.f	DTF	PH	NTP	LL	LW	DM	LF	CP	ADF (%)	NDF (%)	IVMD (%)	GFY (q/ha)	DMY (q/ha)
1.	Replication	2	1.53	5.68	0.03	17.51	0.06	1.87	0.155	1.56	0.39	0.03	1.16	7870.04	31.53
2.	Genotypes	33	11.27 **	58.97 **	2.21 **	27.64 **	0.16 **	20.02 **	0.02 **	9.19 **	18.53 **	19.76 **	11.81 **	2734.35 **	447.78 **
3.	Error	6	1.23	7.23	0.09	10.38	0.04	3.43	0.0074	0.01	0.32	0.24	0.21	1334.94	54.62
4.	SEm (±)		0.64	1.55	0.17	1.86	0.11	1.07	0.05	0.06	0.32	0.28	0.27	21.09	4.27
5.	C.D at 5%		1.81	4.39	0.48	5.25	0.32	3.02	0.14	0.17	0.92	0.80	0.75	59.56	12.05

*,** significant at 5% and 1% ; DTF: Days to 50% flowering; PH: Plant height (cm); NTP: No. of tillers/plant; LL: Leaf length (cm); LW: Leaf width (cm); DM: Dry matter (%); LR: Leaf /stem ratio; CP: Crude protein (%)

Table 2: Mean performance of genotypes for yield and yield attributing characters.

Sr.	Genotypes variation	DTF	PH	NTP	LL	LW	DM	LF	CP	ADF (%)	NDF (%)	IVMD (%)	GFY (q/ha)	DMY (q/ha)
1.	BAUO-101	108.00	113.27	9.33	42.63	1.60	23.83	0.56	7.53	36.50	56.13	60.10	392.64	93.58
2.	BAUO-104	106.00	110.93	10.47	41.53	1.54	22.50	0.55	7.10	38.63	57.87	58.44	390.61	87.89
3.	BAUO-105	105.00	109.20	9.27	39.47	1.63	23.00	0.52	8.90	41.20	61.13	56.39	352.51	81.08
4.	BAUO-103	107.33	103.53	9.80	35.87	1.59	19.67	0.61	8.43	40.10	59.63	57.26	345.76	68.00
5.	BAUO-108	108.67	112.67	10.80	41.00	2.08	18.33	0.59	7.33	35.30	56.13	61.05	418.92	76.80
6.	BAUO-109	106.67	116.27	10.20	42.80	1.52	16.00	0.68	8.23	40.27	58.87	57.10	393.70	62.99
7.	HFO-607	104.67	111.40	10.73	43.80	2.02	18.67	0.75	10.27	38.60	56.03	58.44	404.69	75.54
8.	HFO-609	107.00	114.33	10.47	43.80	2.36	18.50	0.75	11.43	39.80	56.17	57.50	401.94	74.36
9.	HFO-610	107.67	112.87	9.47	40.80	1.98	17.67	0.71	11.20	37.30	53.10	59.47	383.72	67.79
10.	HFO-611	104.00	109.47	11.60	40.00	1.33	20.00	0.54	7.07	39.80	59.03	57.50	382.79	76.56
11.	HFO-904	105.67	112.27	11.87	44.53	1.68	16.83	0.65	9.60	36.10	57.97	60.42	371.99	62.62
12.	HFO-113	106.00	115.33	10.07	45.33	1.54	19.50	0.60	9.13	36.80	56.43	59.86	426.04	83.08
13.	JHO-13-14	103.33	112.47	10.20	43.13	1.68	18.00	0.54	10.97	36.80	53.03	59.86	362.77	65.30
14.	NDO-10	105.33	117.13	11.20	43.53	1.55	16.83	0.57	7.10	40.07	59.33	57.26	376.61	63.39
15.	NDO-1501	104.00	116.60	10.07	39.80	1.93	16.17	0.63	7.77	39.90	56.37	57.42	409.99	66.28
16.	NDO-1	104.67	108.80	11.00	39.33	1.51	25.00	0.55	8.93	38.40	58.63	58.60	362.26	90.56
17.	NDO-2	101.67	107.47	9.73	37.47	1.47	22.50	0.51	6.40	40.20	60.07	57.18	392.41	88.29
18.	SKO-40	104.00	119.33	10.93	48.80	1.76	21.50	0.53	6.17	40.30	60.60	57.10	449.77	96.70
19.	OL-11	104.00	110.47	10.47	42.60	1.57	17.33	0.64	10.27	35.30	55.23	61.05	408.09	70.74
20.	SKO-241	106.33	117.87	9.47	42.00	1.44	21.00	0.54	9.83	42.50	61.20	55.37	406.40	85.34
21.	OL-14	106.00	117.53	9.47	41.60	1.47	20.17	0.53	9.13	37.03	56.73	59.71	407.63	82.21
22.	OL-1869-1	105.00	113.53	9.07	42.87	1.53	21.00	0.53	10.97	37.53	54.80	59.31	411.86	86.49
23.	OL-1871	106.00	106.47	8.93	42.00	1.91	18.00	0.66	11.20	41.27	61.20	56.31	455.72	82.03
24.	OL-1861	106.67	110.20	10.20	40.73	1.55	21.17	0.57	11.63	32.67	52.00	63.10	430.15	91.05
25.	OL-1906	105.33	109.20	9.27	38.60	1.51	19.00	0.53	12.33	33.90	54.67	62.15	369.29	70.17
26.	OL-1919	106.33	117.13	11.33	49.53	1.50	19.17	0.56	7.10	36.90	57.30	59.79	470.59	90.20
27.	OS-403	108.67	103.33	10.60	37.87	1.36	22.33	0.51	10.73	38.37	54.13	58.60	431.86	96.45
28.	OS-6	106.33	116.53	10.00	38.73	1.76	25.00	0.51	9.57	35.10	53.43	61.21	414.30	103.58
29.	BAUO-102	109.00	103.33	11.73	42.27	1.51	19.50	0.51	9.83	36.47	55.20	61.10	360.05	70.21
30.	JHO-2000-4	108.33	114.33	12.00	48.07	1.33	23.83	0.53	10.50	37.37	56.90	59.39	454.80	108.39
31.	JHO-2009-1	107.00	109.53	10.27	40.87	1.45	23.17	0.53	9.37	35.47	56.70	60.89	391.14	90.61
32.	UPO-212 (NC)	110.00	119.40	9.27	40.17	1.77	22.83	0.54	11.20	33.27	53.50	62.63	401.75	91.73
33.	Kent (NC)	108.33	110.67	10.20	40.00	1.39	23.67	0.52	10.97	40.17	59.30	57.18	392.46	92.88
34.	RO-19 (NC)	110.00	108.13	9.07	43.33	1.55	21.00	0.83	12.10	34.33	55.10	61.84	411.71	86.46
Mean		**106.26**	**112.09**	**10.25**	**41.91**	**1.63**	**20.37**	**0.59**	**9.42**	**37.76**	**56.88**	**59.14**	**401.09**	**81.75**
SEm(±)		**0.64**	**1.55**	**0.18**	**1.86**	**0.11**	**1.07**	**0.05**	**0.06**	**0.32**	**0.28**	**0.27**	**21.09**	**4.27**
CD at 5%		**1.81**	**4.39**	**0.48**	**5.25**	**0.32**	**3.02**	**0.14**	**0.17**	**0.92**	**0.80**	**0.75**	**59.56**	**12.05**
C.V (%)		**1.04**	**2.40**	**2.85**	**7.69**	**12.09**	**9.10**	**14.83**	**1.09**	**1.49**	**0.87**	**0.78**	**9.11**	**9.04**

DTF: Days to 50% flowering; PH: Plant height (cm); NTP: No. of tillers/plant; LL: Leaf length (cm); LW: Leaf width (cm); DM: Dry matter (%); LR: Leaf /stem ratio; CP: Crude protein (%)

Table 3: Mean, range and variance for different characters in oats.

Characters	Mean	Range	σ^2 e	σ^2p	σ^2 g	C. V. (%)
Days to 50% flowering	106.27	101.67 – 110.00	1.23	12.09	10.86	1.04
Plant height (cm)	112.09	103.33 - 119.40	7.23	63.79	56.56	2.40
No. of tillers/plant	10.25	8.93 - 12.00	0.096	2.27	2.18	2.85
Leaf length (cm)	41.99	35.87 - 49.53	10.37	34.56	24.18	7.69
Leaf width (cm)	1.63	1.32 - 2.36	0.04	0.19	0.15	12.09
Dry Matter (%)	20.37	16.00 - 25.00	3.43	22.30	18.87	9.10
Leaf /stem ratio	0.59	0.51 - 0.83	0.007	0.025	0.017	14.83
Crude Protein (%)	9.42	6.17 - 12.33	0.010	9.20	9.19	1.09
ADF (%)	37.76	32.67 - 42.50	0.31	18.74	18.42	1.49
NDF (%)	56.88	52.00 - 61.20	0.24	19.92	19.68	0.87
IVDMD (%)	59.14	55.37 - 63.10	0.21	11.95	11.74	0.78
GFY (q/ha)	401.09	345.76 - 470.59	1334.93	3624.34	2289.41	9.11
DMY (q/ha)	81.75	62.6 - 108.39	54.61	484.21	429.60	9.041

significantly constrains livestock productivity (20th Livestock Census, 2019). The situation is more severe in Jharkhand, where green fodder availability is deficient by approximately 90.57% against a requirement of 26.1 million tones (Fodder Resource Development Plan, Jharkhand, 2022). In view of these constraints, Oat emerges as a key crop for reducing green fodder scarcity. Genetic diversity constitutes the basis of crop improvement programmes; therefore, assessment of genetic variability among oat genotypes is imperative for the identification of superior lines with enhanced green fodder yield and improved quality traits. Accordingly, the present study was undertaken to evaluate genetic diversity in oat genotypes for green fodder yield and its quality traits.

Materials and Method

The present study was undertaken to assess genetic diversity in Oat (*Avena sativa* L.) for green fodder yield and quality traits during the Rabi season of 2024–25 at RVC, Forage Research field of Birsa Agricultural University, Ranchi, Jharkhand. Geographically, the Ranchi district is situated in the plateau region with latitude 23°17'N and 85°10'E longitude at an altitude of about 625 meters above mean sea level. The area receives an average annual rainfall of about 368 mm. The climate of the site is sub-tropical humid. The experimental materials in the present study comprises of thirty-four genotypes, including three checks, were evaluated in a Randomized Block Design with three replications. Each genotype was grown in plots consisting of four rows, maintaining a row spacing of 25 cm with a plot size of 4 m × 1 m and observations were recorded at both plot and plant levels. Plot-level data included days to 50% flowering, dry matter percentage, green fodder yield (q/ha) and dry matter yield (q/ha), while plant-level measurements were recorded

Table 4: Estimation of genetic parameters for thirteen characters in fodder oat.

Characters	GC	PC	HB	G.A.	GAM
Days to 50% flowering	1.72	2.01	73.19	3.22	3.03
Plant height (cm)	3.71	4.41	70.45	7.18	6.41
No. of tillers/plant	8.21	8.69	89.28	1.64	15.98
Leaf length (cm)	5.73	9.58	35.68	2.95	7.04
Leaf width (cm)	12.47	17.37	51.56	0.30	18.45
Dry matter (%)	11.54	14.69	61.69	3.80	18.67
Leaf /stem ratio	10.82	18.36	34.74	0.07	13.14
Crude Protein (%)	18.57	18.60	99.66	3.60	38.19
ADF (%)	6.53	6.69	95.04	4.95	13.10
NDF (%)	4.49	4.57	96.41	5.16	9.07
IVDMD (%)	3.33	3.42	94.80	3.94	6.67
GFY (q/ha)	5.39	10.58	25.90	22.64	5.65
DMY (q/ha)	14.00	16.67	70.56	19.81	24.24

GC: Genetic coefficient of variation;
PC: Phenotypic coefficient of variation;
HB: Heritability (%); GAM: G. A. as % of mean

Table 5: Cluster-wise distribution of thirty-four genotypes based on yield-related traits.

Sr.	Cluster	GT	List of Genotypes
1.	Cluster I	7	NDO-1, NDO-2, BAUO-103, BAUO-105, BAUO-101, BAUO-104, JHO-2009-1
2.	Cluster II	6	SKO-40, JHO-2000-4, OS-6, UPO-212 (NC), BAUO-108, HFO-904
3.	Cluster III	6	SKO-41, Kent (NC), NDO-1501, HFO-611, BAUO-109, NDO-10
4.	Cluster IV	4	RO-19 (NC), HFO-610, HFO-607, HFO-609
5.	Cluster V	10	OL-1919, JHO-13-14, OL-1869-1, HFO-113, OL-14, OL-1906, OL-11, OL-1861, OL-1871, OS-403
6.	Cluster VI	1	BAUO-102

GT: No. of Genotypes

Table 6: Average inter and intra-cluster distances for yield and yield-related traits.

Cluster	C-I	C-II	C-III	C-IV	C-IV	C-V
Cluster I	**9.37**	27.70	22.34	26.07	24.68	45.07
Cluster II		**13.68**	26.38	29.56	28.45	48.77
Cluster III			**7.62**	25.01	22.72	43.85
Cluster IV				**9.67**	26.86	46.96
Cluster V					**10.70**	45.23
Cluster VI						**0.00**
C = Cluster						

on five randomly selected competitive plants per plot for plant height, leaf length, leaf width, number of tillers per plant and leaf/stem ratio. Fodder quality traits, including crude protein content, neutral detergent fiber (NDF %), acid detergent fiber (ADF %) and *in vitro* dry matter digestibility (IVDMD %), were analyzed using standard laboratory techniques.

Data were statistically analyzed using ANOVA to assess variability among genotypes. Genetic parameters such as genotypic and phenotypic variances, heritability, and expected genetic advance were estimated. Genetic divergence was assessed using Mahalanobis's D^2 statistics and genotypes were grouped using Tocher's method.

Results and Discussions

The analysis of variance revealed highly significant differences for all the traits, indicating substantial genetic variation (Table 1). Considerable variation was observed for growth, yield and quality traits, including days to 50% flowering, plant height (cm), number of tillers per plant, leaf length (cm), leaf width (cm), dry matter percentage, crude protein (%), ADF (%), NDF (%) and IVDMD (%), while green fodder yield and dry matter yield showed wide variability (Table 2). Phenotypic variance generally exceeded genotypic variance, reflecting environmental influence on most of the traits, though days to 50% flowering, number of tillers per plant, crude protein (%), ADF (%), NDF (%) and IVMD (%) were largely under genetic control (Table 3). Moderate heritability and genetic advance were observed for leaf width, dry matter percentage, crude protein (%), green fodder yield and dry matter yield, whereas phenological and fiber traits exhibited low variability, indicating limited direct improvement potential (Table 4). Similar results were reported by Surje and De (2014) and Prasad *et al.*, (2024). The phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits studied, indicating the influence of environmental factors. Similar findings were also reported by Sahu and Tiwari (2020) and Wagh *et al.*, (2018).

Genetic divergence among the genotypes was assessed using Mahalanobis D^2 statistics as suggested by Rao (1952). Based on thirteen yield and quality characters, D^2 analysis grouped into 34 genotypes into six distinct clusters (Table 5), indicating the presence of substantial genetic diversity. Cluster V was the largest, comprising ten genotypes, followed by Cluster I with seven genotypes, suggesting closer genetic affinity among members within these clusters. Clusters II and III each contained six genotypes, while Cluster IV consisted of four genotypes, reflecting moderate levels of divergence. In contrast, Cluster VI was mono-genotypic indicating its unique genetic constitution and wide divergence from the remaining clusters, thereby identifying it as a potential parent for hybridization programmes.

The Intra and Inter-cluster distances (Table 6) revealed that inter-cluster distances were consistently higher than intra-cluster distances, confirming greater genetic divergence between clusters than within clusters. Among the clusters, the highest intra-cluster distance was recorded in Cluster II (13.68), followed by Cluster V (10.70), Cluster IV (9.67), Cluster I (9.37) and Cluster III (7.62), indicating moderate variability within these groups. Cluster VI exhibited zero intra-cluster distance due to the presence of a single genotype. The maximum inter-cluster distance was observed between Cluster II and Cluster VI (48.77), followed by Cluster IV and Cluster VI (46.96), Cluster V and Cluster VI (45.23) and Cluster I and Cluster VI (45.07), suggesting that crosses between

Table 7: Cluster-wise mean performance for thirteen traits in forage oats.

Cluster	No. of Genotypes	DTF	PH	NTP	LL	LW	DM	LF	CP	ADF (%)	NDF (%)	IVMD (%)	GFY (q/ha)	DMY (q/ha)
I	7	105.67	108.96	9.98	39.60	1.54	22.81	0.55	8.08	38.64	58.60	58.41	85.72	375.33
II	6	107.17	115.76	10.81	43.55	1.73	21.39	0.56	9.05	36.24	56.42	60.30	89.97	418.59
III	6	105.78	114.67	10.46	41.36	1.53	18.94	0.58	8.48	40.45	59.02	56.97	74.58	393.66
IV	4	107.33	111.68	9.93	42.93	1.98	18.96	0.76	11.24	37.51	55.10	59.31	76.04	400.51
V	10	105.73	111.57	9.96	42.43	1.56	19.57	0.57	10.33	36.66	55.55	59.97	81.77	417.40
VI	1	109.00	103.33	11.73	42.27	1.51	19.50	0.51	9.81	36.47	55.20	61.10	70.21	360.05

DTF: Days to 50% flowering; PH: Plant height (cm); NTP: No. of tillers/plant;
LL: Leaf length (cm); LW: Leaf width (cm); DM: Dry matter (%); LR: Leaf /stem ratio; CP: Crude protein (%)

Table 8: Partitioning of total divergence among yield-associated traits.

Sr.	Trait	Contribution (%)
1	Green fodder yield (q/ha)	86.27
2	Dry matter yield (q/ha)	8.41
3	Plant height (cm)	2.08
4	NDF (%)	0.64
5	ADF (%)	0.59
6	Dry matter percentage	0.58
7	Leaf length (cm)	0.48
8	IVMD (%)	0.39
9	Crude protein (%)	0.31
10	Days to 50% flowering	0.18
11	No. of tillers per plant	0.05
12	Leaf width (cm)	0.01
13	Leaf/stem ratio	0.00

these clusters would be most effective for generating diverse and superior segregants. The minimum inter-cluster distance was recorded between Cluster I and Cluster III (22.34) and between Cluster III and Cluster V (22.72), indicating close genetic relationship and limited scope for effective hybridization among these clusters.

Cluster mean analysis (Table 7) revealed considerable variation among clusters for all the traits studied. Days to 50% flowering ranged from 105.67 days in Cluster I to 109.0 days in Cluster VI. Plant height was highest in Cluster II (115.76 cm) and lowest in Cluster VI (103.33 cm). Cluster VI recorded the maximum number of tillers per plant (11.73), whereas Cluster IV showed the minimum (9.93). Leaf length was highest in Cluster II (43.55 cm) and lowest in Cluster I (39.60 cm), while maximum leaf width was recorded in Cluster IV (1.98 cm). Dry matter percentage ranged from 18.94% in Cluster III to 22.81% in Cluster I. The highest leaf-stem ratio (0.76) and crude protein content (11.24%) were observed in Cluster IV, whereas Cluster I recorded the lowest crude protein content (8.08%). Fibre fractions varied across clusters, with the highest ADF recorded in Cluster III (40.45%) and the lowest in Cluster II (36.24%). Maximum IVDMD was observed in Cluster VI (61.10%), while the minimum was recorded in Cluster III (56.97%). Green fodder yield was highest in Cluster II (418.59 q/ha), followed by Cluster V, whereas Cluster VI recorded the lowest yield (360.05 q/ha), indicating marked differences in productivity among clusters.

The relative contribution of individual traits to total genetic divergence (Table 8) revealed that green fodder yield contributed the maximum (86.27%), followed by dry matter yield (8.41%) and plant height (2.08%). Other traits such as NDF% (0.64%), ADF% (0.59%), dry matter percentage (0.58%), leaf length (0.48%), IVDMD% (0.39%) and crude protein content (0.31%) contributed marginally. Very low contributions were observed for days to 50% flowering (0.18%), number of tillers per plant (0.05%) and leaf width (0.01%), while leaf-stem ratio showed no contribution. These results indicate that genetic divergence among the genotypes was predominantly governed by yield-related traits, with quality and phenological traits contributing comparatively less. This is in agreement with earlier reports by Prasad *et al.*, (2021).

Overall, the study highlights considerable genetic variability for both growth and quality traits, with cluster analysis providing clear guidance for parent selection in hybridization programmes to develop superior fodder oat lines.

Conclusion

Considerable Genetic divergence among the genotypes for yield and quality traits was observed in the present investigation through Mahalanobis D^2 analysis. The formation of six distinct clusters, with wide inter-cluster distances particularly involving the single-genotype Cluster VI demonstrated substantial scope for the effective utilization of Genetic diversity through hybridization. Yield-related traits, notably green fodder yield, contributed the highest proportion to total divergence, indicating their predominant role in genotype differentiation. The pronounced variation in cluster means further suggests that selection of genetically diverse and superior parents from widely separated clusters would be effective for developing improved fodder Oat genotypes.

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