Range Management and Agroforestry 46 (1) : 157-164, 2025
ISSN 0971-2070 (Print); 2249-5231 (Online)
https://doi.org/10.59515/rma.2025.v46.i1.22

Short communication

Genetic variability and multivariate analysis on oats (*Avena sativa* L.) genotypes grown for fodder

Parameshwaran Mathavaraj[*]**, Prasanta Kumar Goswami, Seuji Bora Neog and Kishore Kumar Sharma**

Assam Agricultural University, Jorhat-785013, India
[*]Corresponding author email: madhavparamesh07@gmail.com

Received: 31st January, 2024 Accepted: 16th January, 2025

Abstract

Oats (*Avena sativa* L.), widely cultivated for grain, also provide quality green herbage for livestock. In Rabi 2021–22, 31 genotypes were evaluated for genetic diversity using univariate and multivariate analyses. Significant differences were found across all 12 recorded traits, including fodder yield. High genotypic and phenotypic coefficients of variation (GCV and PCV), heritability (h^{2b}), and genetic advance as a percentage of mean (GAM %) were noted for number of tillers per plant (NOTP), dry matter yield (DMY), and green fodder yield (GFY). GFY ranged from 0.77 kg/m² (NDO-1101) to 2.09 kg/m² (NDO-711), and DMY ranged from 0.14 kg/m² (NDO-1101) to 0.33 kg/m² (OL-1861). Hierarchical clustering grouped the genotypes into three clusters, with Cluster I showing the highest mean values for most traits, including fodder yield. Maximum intra-cluster distance (3.87) was within Cluster I, while the highest inter-cluster distance (5.71) was between Clusters I and II. Principal Component Analysis (PCA) highlighted fodder yield, NDVI, and crude protein as key contributors to genetic variation, with the first four principal components explaining 83.88% of the total variation. Genotypes NDO-711, OS-1861, and JHO-851 demonstrated high yield and crude protein potential. These genotypes merit further evaluation for desirable traits to develop elite, high-yielding varieties suitable for the Brahmaputra Valley of Assam.

Keywords: Fodder yield, Genetic diversity, Hierarchical clustering, Oats, PCA Variability

Oats (*Avena sativa* L.), a highly adaptable cereal crop from the western Mediterranean, ranks sixth globally among cultivated cereals. Unlike wheat and barley, oats were domesticated later due to their initial misidentification as weeds. Despite this, their resilience in cooler climates and low-fertility soils has contributed to their widespread cultivation. Oats, belonging to the Poaceae family and the genus *Avena*, include over 30 species, with *A. sativa*, *A. nuda*, and *A. byzantina* being the most commonly grown. Cultivated oats are primarily allohexaploid (2n = 6x = 42), with genomes represented as AACCDD, resulting in considerable genome size variation (4.10-12.80 Gb)(Yan *et al.*, 2016). Their grains and herbage are nutritionally valuable, offering high levels of crude protein, digestible nutrients, and fibers, making oats a critical crop for both human consumption and animal feed (Kaur *et al.*, 2023). Animal husbandry forms the backbone of Indian agriculture, yet fodder shortages significantly hinder livestock productivity. Feed constitutes 60-70% of livestock maintenance costs, and India faces deficits of 11.24% and 23.40% in green and dry fodder, respectively, with Assam experiencing even higher deficits (Roy *et al.*, 2019). In this context, oats serve as a vital fodder resource, especially during winter when other options are scarce. Though widely cultivated as a dual-purpose crop in central and north-western India, oats have only recently been introduced to the Brahmaputra plains of Assam. However, the region still relies on obsolete varieties developed for other agroclimatic zones. This underscores the need to develop region-specific, high-yielding oat varieties suitable for Assam's unique conditions.

Understanding and utilizing genetic variability is fundamental to crop improvement. Evaluating agro-morphological traits enables breeders to identify superior genotypes and harness heterosis (Kebede *et al.*, 2023; Mathavaraj *et al.*, 2024). Multivariate analysis techniques such as principal component analysis (PCA) and hierarchical cluster analysis (HCA) are effective for dissecting complex datasets to reveal genetic diversity (Zahid *et al.*, 2023). PCA uses eigenvalues and eigenvectors to identify key traits contributing to variation, while hierarchical clustering- particularly agglomerative methods- organizes data into dendrograms to visualize relationships between genotypes (Greenacre *et al.*, 2022). Given the lack of research on oat genetic variability under Assam's agroclimatic conditions, this study aimed to assess genetic diversity among oat germplasm collected across India using PCA and HCA, providing a foundation for targeted breeding efforts in the region.

In the current investigation, a total of 31 oats genotypes were collected from the Golden Jubilee Forage Garden, AICRP on Forage Crops, Assam Agricultural University, Jorhat (Table1). The field trial was conducted during *Rabi* season of 2021-22 at the Experimental Farm (altitude: 86.6 m MSL, latitude: 26°47′ N, longitude: 94°12′ E), Department of Plant Breeding and Genetics, Assam Agricultural University. A randomized block design (RBD) was used to analyze the variability among the genotypes. The layout consisted of three blocks, each with two rows, each 4 meters in length, for every genotype. A plant spacing of 30 cm × 10 cm was followed. To ensure healthy plant growth, recommended agronomic practices and necessary crop protection measures were implemented in a timely manner.

In each block, five random plants from each genotype were tagged, and observations on the following traits were recorded: plant height (PH) in cm, number of leaves per plant (NOLP), leaf length (LL) in cm, leaf width (LW) in cm (mean of middlemost five leaves), culm diameter (CD) in cm (recorded from the culm of 5 cm above ground level), number of tillers per plant (NOTP), and number of nodes per plant (NON). Data on additional traits, such as green fodder yield (GFY) in kg/m^2, dry matter yield (DMY) in kg/m^2, per day productivity (PDP) in g/m^2/day, normalized difference vegetation index (NDVI) and fodder crude protein (FCP) content in percentage were recorded on a single-row basis. All genotypes were harvested once for fodder as single-cut varieties, 3 months after sowing to maintain uniformity among the genotypes, and data were recorded accordingly.

The NDVI value was measured by placing the handheld GreenSeeker™ (NTech Industries Inc., Ukiah, CA, USA) at an appropriate height above the canopy. The button was held while slowly walking down each row to observe the NDVI. Crude protein analysis was carried out using the micro Kjeldahl method (Concon and Soltess, 1973) with the automatic digestion unit KELPLUS KES 8L E and distillation unit KELPLUS CLASSIC - DX VATS (P). The volume of 0.1N sulphuric acid used was measured, and the nitrogen percentage (N%) was calculated using the following formula:

N% = (Volume of 0.1N sulphuric acid used/Weight of the sample) × 0.0014 × 100

Finally, the crude protein content was calculated by multiplying the percent nitrogen (N%) by a factor of 6.25.

The data recorded from the field were analyzed for variation using ANOVA for a randomized block design (RBD). Genetic parameters, such as the phenotypic and genotypic coefficients of variation (PCV and GCV) (Burton, 1952), broad-sense heritability (h^2_b) (Allard, 1960), genetic advance (GA), and genetic advance as a percentage of the mean (GAM) (Johnson *et al.*, 1955), were estimated. ANOVA and genetic parameters were analyzed in RStudio using the statistical package 'variability' (Popat *et al.*, 2020). The phenotypic coefficient of variation (PCV) and genotypic coefficient

Table 1. List of genotypes evaluated in the present study

S. No.	Genotype	Developed at	S. No.	Genotype	Developed at
1.	OL-10	PAU, Ludhiana	17.	OS-377	CCSHAU, Hisar
2.	OL-1802-1	PAU, Ludhiana	18.	HFO-114	CCSHAU, Hisar
3.	OL-1876-2	PAU, Ludhiana	19.	HJ-16	CCSHAU, Hisar
4.	OL-1861	PAU, Ludhiana	20.	JHO-851	ICAR-IGFRI, Jhansi
5.	OL-14	PAU, Ludhiana	21.	JHO-2000-4	ICAR-IGFRI, Jhansi
6.	OL-1869	PAU, Ludhiana	22.	JHO-212-2	ICAR-IGFRI, Jhansi
7.	OL-1804	PAU, Ludhiana	23.	NDO-711	ANDUAT, Ayodhya
8.	OL-769-1	PAU, Ludhiana	24.	NDO-10	ANDUAT, Ayodhya
9.	OL-1802	PAU, Ludhiana	25.	NDO-2	ANDUAT, Ayodhya
10.	OL-1896	PAU, Ludhiana	26.	NDO-1101	ANDUAT, Ayodhya
11.	OL-1760	PAU, Ludhiana	27.	UPO-06-1	GBPUAT, Pantnagar
12.	OS-346	CCSHAU, Hisar	28.	UPO-94	GBPUAT, Pantnagar
13.	OS-405	CCSHAU, Hisar	29.	UPO-212	GBPUAT, Pantnagar
14.	OS-424	CCSHAU, Hisar	30.	RO-11-1	MPKV, Rahuri
15.	OS-6	CCSHAU, Hisar	31.	PLP-1	HPKV, Palampur
16.	OS-7	CCSHAU, Hisar			

of variation (GCV) values were categorized according to Sivasubramanian and Menon (1973) as follows: 0 to 10% as low, 11 to 20% as moderate, and more than 20% as high. Similarly, according to Johnson *et al.,* (1955), broad-sense heritability was classified as follows: 0 to 30% as low, 31 to 60% as moderate, and more than 60% as high.

To cluster the genotypes, the unweighted pair group method with arithmetic mean (UPGMA) method of hierarchical clustering was used, as it is considered the best and most reliable method (Peeters and Martinelli, 1989). The Euclidean distance measure was used to determine the relative distances within and between the clusters. The distance measure and cluster dendrogram were calculated using the 'stats' package in RStudio. Principal component analysis (PCA) was performed to determine the importance of various traits in explaining the differences among oats genotypes. PCA was conducted in RStudio using the 'prcomp' function from the 'stats' package. The PCA biplot, involving the first two principal component axes, was plotted and visualized using the 'ggplot2' package in RStudio.

The ANOVA, range, mean values, and coefficients of variation for each recorded observation are presented in Table 2. The analysis of variation based on the observed data revealed significant differences among the investigated genotypes, indicating substantial variation in fodder yield and its component traits. Table 3 depicts the mean performance of 31 genotypes for all the fodder component traits. The genotype UPO-06-1 exhibited the highest plant height (103.20 cm), while the lowest height was observed in NDO-1101 (68.78 cm). Additionally, UPO-06-1 also had the longest leaves (64.42 cm), with the shortest leaves recorded in JHO-2000-4 (45.03 cm). The highest number of tillers was observed in OL-1802-1 (10.17), whereas OS-424 (4.74) and OL-10 (4.77) had the lowest tiller numbers. The maximum NDVI values were recorded in OS-405 (0.68) and OS-6 (0.66), with NDO-1101 showing the minimum NDVI value (0.31). Regarding dry matter yield, OL-1861 produced the highest value (0.33 kg/m^2), while NDO-1101 had the lowest (0.14 kg/m^2). The highest per day productivity was observed in OL-1861 (4.91 g/m^2/day), with the lowest recorded in OL-10 (2.67 g/m^2/day). In terms of green fodder yield, NDO-711 emerged as the highest producer (2.09 kg/m^2), while NDO-1101 had the lowest yield (0.77 kg/m^2). Kumar *et al.* (2023) also reported similar results for fodder yield traits while analysing 38 oats genotypes sourced from IGFRI, Jhansi. The highest crude protein content was found in JHO-851 (18.19%), and the lowest was recorded in OL-1760 (10.00%). The extensive variation in protein content among the genotypes was also reported by Ihsan *et al.* (2022). These findings highlight the potential for improving oats germplasm through targeted selection and hybridization.

The estimates of various genetic parameters for fodder yield and its attributing traits are presented in Table 4. For all the traits, PCV was found to be higher than the corresponding GCV, indicating the significant influence of environmental factors on the expression of these traits. This finding is consistent with the observations of Chauhan and Singh (2019). High values of both PCV and GCV were observed for the NOTP and GFY, suggesting that these traits are predominantly controlled by genetic factors, thus making them amenable to improvement through selection. Similar results were reported by Wagh *et al.* (2018) and Kebede *et al.* (2023). In contrast, traits such as NDVI and DMY exhibited moderate GCV, but their higher PCV estimates highlighted the dominant role of environmental factors in their expression. The traits PH and CP showed low GCV values coupled with moderate

Table 2. ANOVA and descriptive statistics for fodder attributing traits

Traits	MSS	Range		Mean ± SEm	CV%
		Min	Max		
Plant height (cm)	278.43**	68.78	103.20	86.88 ± 4.51	8.98
Number of leaves per plant	125.10**	22.22	53.73	39.69 ± 2.65	11.56
Leaf length (cm)	51.87*	45.03	64.42	50.57 ± 3.21	11.00
Leaf width (cm)	0.07**	1.21	1.83	1.59 ± 0.04	4.06
Culm diameter (cm)	0.0085**	0.51	0.72	0.59 ± 0.02	7.17
Number of tillers per plant	8.52**	4.74	10.17	7.98 ± 0.39	8.39
Number of nodes per plant	1.26**	2.69	5.27	4.05 ± 0.16	7.04
NDVI value	0.027**	0.31	0.68	0.47 ± 0.03	9.11
Dry matter yield (kg/m^2)	0.0071**	0.14	0.33	0.24 ± 0.01	9.92
Per day productivity (g/m^2/day)	1.22**	2.67	4.91	3.93 ± 0.24	10.68
Fodder crude protein (%)	13.46**	10.00	18.19	14.30 ± 0.46	5.53
Green fodder yield (kg/m^2)	0.27**	0.77	2.09	1.34 ± 0.08	10.26

MSS: Mean sum of squares; *(P<005); **(P<0.01); CV%: Coefficient of variation %

Table 3. Mean performance of 31 genotypes for fodder attributing traits

S.No.	Genotypes	PH	NOLP	LL	LW	CD	NOTP	NON	NDVI	*DMY*	*PDP*	*FCP*	*GFY*
1	OL-10	86.08	22.22	46.25	1.81	0.64	4.77	4.57	0.38	0.15	2.67	13.86	0.89
2	PLP-1	91.32	39.01	51.54	1.60	0.58	8.54	3.66	0.48	0.28	4.63	12.59	1.52
3	OS-346	100.48	39.32	55.11	1.74	0.57	9.32	5.27	0.49	0.28	4.64	10.61	1.65
4	JHO-851	94.14	44.70	51.86	1.61	0.55	9.17	4.78	0.53	0.27	4.48	18.19	1.83
5	UPO-06-1	103.20	36.76	64.42	1.70	0.66	6.91	4.13	0.51	0.22	3.68	16.59	1.38
6	OL-1802-1	71.60	48.69	46.05	1.21	0.59	10.17	3.25	0.44	0.17	2.93	14.19	1.04
7	OS-405	92.23	53.73	52.69	1.66	0.55	9.34	4.37	0.68	0.23	3.79	15.86	1.43
8	OL-1876-2	76.54	39.20	47.11	1.40	0.51	9.49	4.58	0.39	0.19	3.22	14.13	1.15
9	NDO-711	94.95	47.80	50.55	1.52	0.55	9.60	4.40	0.55	0.31	5.02	16.01	2.09
10	OS-424	78.70	25.46	51.98	1.60	0.69	4.74	3.30	0.47	0.19	3.24	17.75	1.01
11	OL-1861	102.06	49.40	55.84	1.78	0.61	8.76	5.26	0.50	0.33	5.28	11.56	1.82
12	OS-6	91.44	41.81	51.59	1.68	0.65	9.06	4.67	0.66	0.24	4.02	14.48	1.21
13	UPO-94	87.97	45.65	48.36	1.56	0.56	9.93	4.66	0.58	0.21	3.57	15.54	1.20
14	OL-1802	98.62	39.04	51.65	1.78	0.72	8.24	4.55	0.42	0.25	4.26	16.69	1.56
15	NDO-10	75.19	32.84	46.13	1.53	0.55	6.37	3.90	0.38	0.19	3.23	15.57	1.00
16	OL-1896	77.51	34.27	49.86	1.41	0.59	6.84	3.51	0.40	0.29	4.73	14.88	1.16
17	HFO-114	83.25	38.74	48.22	1.45	0.60	9.34	4.37	0.48	0.20	3.42	14.02	1.27
18	JHO-2000-4	81.01	43.78	45.03	1.62	0.55	8.31	3.42	0.46	0.28	4.53	11.20	1.21
19	OL-14	96.97	24.97	51.54	1.83	0.68	5.12	3.89	0.32	0.18	2.97	11.80	1.05
20	OS-377	83.66	31.49	48.09	1.46	0.54	5.97	3.50	0.34	0.19	3.22	14.88	0.97
21	JHO-212-2	93.26	39.78	51.24	1.65	0.58	9.56	4.47	0.46	0.24	4.10	14.63	1.48
22	NDO-1101	68.78	27.22	47.70	1.21	0.52	6.41	2.69	0.31	0.14	2.51	17.34	0.77
23	OL-1869	82.71	31.49	46.40	1.63	0.58	6.58	3.40	0.43	0.23	3.79	12.95	1.28
24	OL-1804	71.37	30.49	50.29	1.72	0.64	5.20	3.21	0.42	0.21	3.54	15.73	1.25
25	RO-11-1	94.61	44.44	47.62	1.61	0.61	8.89	4.43	0.52	0.29	4.80	11.65	1.60
26	OL-769-1	82.90	42.09	46.79	1.74	0.58	9.09	4.24	0.49	0.26	4.28	15.61	1.62
27	HJ-16	79.63	38.84	49.17	1.69	0.57	7.52	3.86	0.45	0.29	4.79	12.32	1.43
28	NDO-2	94.07	46.44	59.05	1.63	0.62	9.37	3.99	0.56	0.26	4.27	15.28	1.57
29	OL-1760	95.53	46.20	52.73	1.56	0.53	9.86	4.47	0.56	0.24	3.96	10.00	1.34
30	OS-7	86.79	29.90	48.26	1.57	0.58	6.60	3.60	0.37	0.28	4.61	12.92	1.45
31	UPO-212	76.75	41.61	54.40	1.43	0.51	8.37	2.99	0.42	0.22	3.72	14.34	1.29
	Maximum	103.20	53.73	64.42	1.83	0.72	10.17	5.27	0.68	0.33	5.28	18.19	2.09
	Minimum	68.78	22.22	45.03	1.21	0.51	4.74	2.69	0.31	0.14	2.51	10.00	0.77

PH: Plant height in cm; NOLP: Number of leaves per plant; LL: Leaf length in cm; LW: Leaf width in cm; CD: Culm diameter in cm; NOTP: Number of tillers per plant; NON; Number of nodes per plant; NDVI: Normalized difference vegetation index; DMY: Dry matter yield in kg/m²; PDP: Per day productivity in g/m²/day; FCP: Fodder crude protein content in percentage, GFY: Green fodder yield in kg/m²

PCV, indicating a stronger environmental influence on their variation. Other traits exhibited moderate estimates of both PCV and GCV, aligning with the findings of Rawat *et al.* (2022).

High heritability estimates were observed for most fodder attributes, with the exceptions of PH, LL, and CD. Among these, PH and CD exhibited moderate heritability, while LL showed low heritability. These findings were in agreement with the results reported by Pundhir *et al.* (2008), who also observed high heritability estimates for NOLP, DMY, and GFY. High and moderate heritability estimates for various traits were also reported by Wagh *et al.*(2018), Chauhan and Singh (2019), and Kebede *et al.* (2023).Traits such as NOLP, NON, NOTP, NDVI, DMY, PDP, FCP, and GFY exhibited high heritability and high GAM, suggesting that these traits can be effectively improved through selection. Singh and Singh (2011) also reported high heritability and high GAM for NOTP, DMY, and GFY, while Sahu and Tiwari (2020) observed similar findings for GFY and DMY. Additionally, Ihsan *et al.* (2022) reported similar results for FCP.

The hierarchical clustering algorithm grouped the 31 oat genotypes into three distinct clusters: Cluster I (21 genotypes), Cluster III (6 genotypes), and Cluster II (4 genotypes). The dendrogram (Fig 1) illustrates the relationships among genotypes, with rectangular borders indicating cluster boundaries. Genotypes in close proximity are more genetically similar, as per Kumar et al. (2020). Hierarchical Cluster Analysis (HCA) thus effectively reveals underlying genetic similarities and differences. Intra- and inter-cluster distances (Table 5) showed the highest intra-cluster distance in Cluster I (3.87), suggesting greater genetic diversity within it compared to Cluster III (3.58) and Cluster II (3.45). This makes Cluster I a valuable source for breeding due to its higher internal divergence. No clustering pattern based on the place of development was observed. The greatest inter-cluster distance was between Clusters I and II (5.71), followed by Clusters I and III (5.43), and the lowest between Clusters II and III (5.13).Although Cluster I appears to contain multiple subclusters, its intra-cluster distance (3.87) was substantially lower than its inter-cluster distances with the other two clusters (Table 5). Therefore, it may be redundant to consider these subpopulations as separate clusters. It is well known that greater distances between clusters indicate greater genetic diversity among the genotypes within them. Consequently, such divergent genotypes are more likely to produce segregating generations with a wide range of genetic variation and may result in the development of desirable transgressive segregants upon hybridization.

Considerable variations in the mean performances of the three different clusters for all the traits measured were observed (Table 6). Cluster I, comprising 21 diverse genotypes, recorded the highest mean values for most traits, including PH, NOLP, LL, NOTP, NON, NDVI,

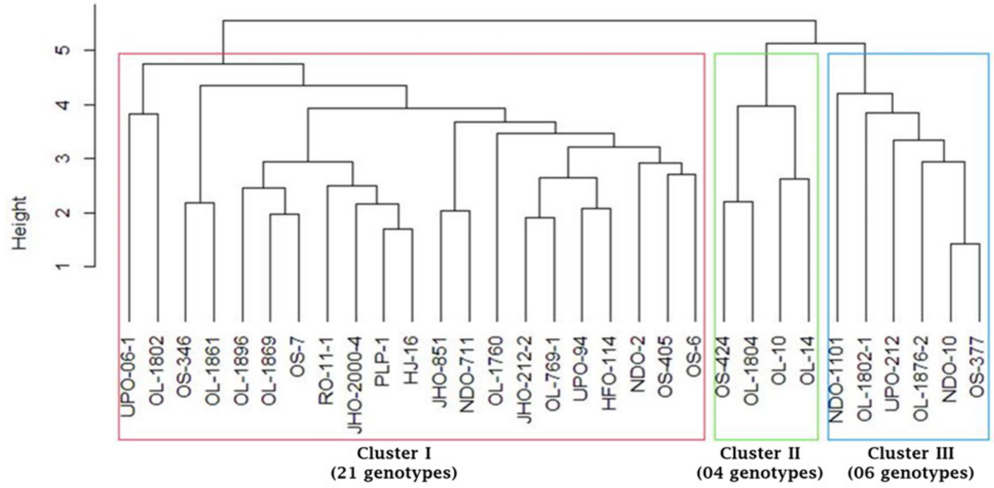

Fig 1. Dendrogram depicting the results of hierarchical cluster analysis using 31 oats genotypes

Table 4. Estimates of genetic parameters for different traits related to fodder yield

Traits	**PCV (%)**	**GCV (%)**	**h^2_b (%)**	**GA**	**GAM (%)**
Plant height (cm)	13.30	9.80	54.34	12.93	14.88
Number of leaves per plant	18.81	14.83	62.22	9.57	24.11
Leaf length (cm)	12.18	5.22	18.37	2.33	4.61
Leaf width (cm)	10.30	9.46	84.39	0.29	17.90
Culm diameter (cm)	10.74	7.97	55.00	0.07	12.18
Number of tillers per plant	22.19	20.55	85.71	3.13	39.19
Number of nodes per plant	17.05	15.53	83.00	1.18	29.15
NDVI value	20.45	18.31	80.22	0.16	33.78
Dry matter yield (kg/m^2)	22.07	19.93	81.48	0.09	37.04
Per day productivity (g/m^2/day)	18.44	15.04	66.49	0.99	25.26
Fodder crude protein (%)	15.48	14.48	87.27	3.98	27.86
Green fodder yield (kg/m^2)	23.72	21.38	81.21	0.53	39.69

Table 5. Estimates of intra (diagonal) and inter (off-diagonal) cluster distances

Cluster	I	II	III
I	3.87	5.71	5.43
II		3.45	5.13
III			3.58

Table 6. Mean performances of different clusters for various fodder traits

Traits	Cluster I	Cluster II	Cluster III
Plant height (cm)	90.84	83.28	75.42
Number of leaves per plant	41.58	25.79	36.84
Leaf length (cm)	51.33	50.02	48.25
Leaf width (cm)	1.63	1.74	1.37
Culm diameter (cm)	0.59	0.66	0.54
Number of tillers per plant	8.61	4.96	7.80
Number of nodes per plant	4.26	3.74	3.49
NDVI value	0.50	0.40	0.38
Dry matter yield (kg/m^2)	0.26	0.18	0.18
Per day productivity (g/m^2/day)	4.32	3.11	3.14
Fodder crude protein (%)	13.98	14.79	15.08
Green fodder yield (kg/m^2)	1.48	1.05	1.04

Table 7. Eigenvalue, variance proportion and contribution of various component traits (eigenvectors) for the first four principal components

Parameters	Principal components (PCs)			
	PC1	PC2	PC3	PC4
Eigen value	5.31	2.35	1.40	1.00
Variance (%)	44.27	19.61	11.70	8.30
Cumulative variance (%)	44.27	63.88	75.58	83.88
Traits	Factor loadings			
Plant height (cm)	11.407	8.696	0.510	3.544
Number of leaves per plant	10.512	12.172	4.222	0.269
Leaf length (cm)	4.265	6.848	11.866	5.750
Leaf width (cm)	3.771	24.939	1.686	2.522
Culm diameter (cm)	0.020	29.173	2.015	0.524
Number of tillers per plant	8.544	15.633	3.574	4.565
Number of nodes per plant	9.782	1.360	0.952	24.197
NDVI value	9.922	0.754	14.792	0.665
Dry matter yield (kg/m^2)	12.809	0.177	12.115	12.523
Per day productivity(g/m^2/day)	12.708	0.136	12.330	12.732
Fodder crude protein (%)	1.330	0.077	35.441	25.094
Green fodder yield (kg/m^2)	14.930	0.035	0.495	7.613

DMY, PDP, and GFY. Cluster II exhibited the maximum mean values for LW and CD, whereas Cluster III had the highest mean for FCP. Interestingly, Clusters II and III had almost identical mean values for two economically important traits, DMY and GFY.PCA was performed to identify the variation patterns within the germplasm, considering all 12 attributes simultaneously (Table 7).

Principal Component Analysis (PCA) showed that variation in PC1 was mainly contributed by GFY, PDP, DMY, PH and NOLP. PC2 was closely related to LW, CD, NOTP and NOLP, while PC3 was associated with FCP, NDVI, PDP, DMY and LL. PC4 was linked to FCP, NON, PDP and DMY. Since the first four components explained 83.88% of the total variability, it could be concluded that traits like GFY, PDP, DMY, NDVI, and FCP are the major drivers of diversity among the oat genotypes studied. These traits could serve as effective selection indices for identifying genotypes with superior fodder yield. Previous studies (Kumari and Jindal, 2019; Rana *et al*., 2022; Kebede *et al*., 2023; Devi *et al*., 2024) also recognized GFY, PDP and DMY as key selection criteria for high fodder yield. The biplot diagram (Fig 2) illustrates the contribution of vectors and the relationship between genotypes and traits.

Notably, the genotypes grouped by HCA also showed a similar distribution in the PCA biplot, forming three distinct groups. The four genotypes from Cluster II were located in the upper left quadrant, while the six from Cluster III were in the lower left quadrant. The remaining 21 genotypes, belonging to Cluster I, were spread across the other quadrants. This distribution supported the observation that Cluster I exhibited the highest mean performance for most key productivity traits. The PCA biplot thus serves as a valuable tool for identifying genotypes with desirable trait combinations for use in crop improvement programmes (Singh

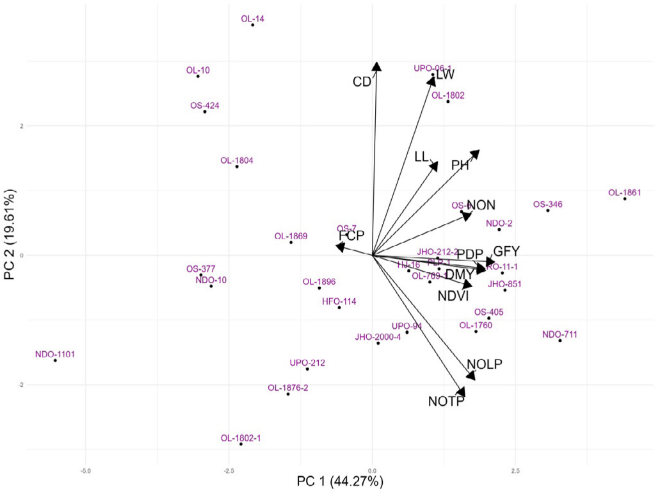

Fig 2. PCA bi-plot of oats genotypes using first two principal components

et al., 2022). Furthermore, if genotypes with similar yield potential differ significantly in other traits, their comparable productivity may stem from distinct gene pools. More specifically, genotypes NDO-711 (GFY: 2.09 kg/m²; DMY: 0.31 kg/m² ; PDP: 5.02 g/m²/day), OS-1861 (GFY: 1.82 kg/m²; DMY: 0.33 kg/m² ; PDP: 5.28 g/m²/day) and JHO-851 (GFY: 1.83 kg/m²; DMY: 0.27 kg/m² ; PDP: 4.48 g/m²/day) could be considered as the suitable genotypes for cultivation in the Brahmaputra plains after further critical evaluation. Among the genotypes enlisted above, NDO-711 (16.01 %) and JHO-851 (18.19 %) are also showing comparatively higher fodder protein content than all other genotypes. In addition, OS-424 also exhibiting as equal FCP as NDO-711. These genotypes could be used to enhance the protein content of the fodder oats.

The study revealed significant variability among oat genotypes for fodder yield and related traits. UPGMA-based hierarchical clustering classified the 31 genotypes into three distinct clusters based on multivariate trait patterns. The PCA biplot highlighted the interaction of key traits with fodder yield, aiding in the identification of superior genotypes with high fodder yield and crude protein content. The genetic diversity observed among the germplasm lines offers valuable resources for breeding. This might be the first report on the variability of oat genotypes bred across India and evaluated in the Brahmaputra Valley of Assam, emphasizing the potential to develop elite winter fodder varieties tailored to the region.

References

Allard, R. W. 1960. *Principles of Plant Breeding*. John Willey and Sons. Inc., New York.

Burton, G.W. 1952. Quantitative inheritance of grasses. In: Proc. *International Grassland Congress* (Aug. 17-23, 1952), Pennsylvania.

Chauhan, C. and S. K. Singh. 2019. Genetic variability, heritability and genetic advance studies in oat (*Avena sativa* L.). *International Journal of Chemical Studies*7: 992-994.

Concon, J. M. and D. Soltess. 1973. Rapid micro Kjeldahl digestion of cereal grains and other biological materials. *Analytical Biochemistry* 53: 35-41.

Devi, R., V. K. Sood, A. R. Anuradha, A. Katoch, S. Kamal and A. Kumar. 2024. Comprehensive assessment of genetic variability and selection strategies in oat germplasm for improved fodder and seed yield in NW Himalayan mid-hill environments. *Indian Journal of Agricultural Research* 1: 9.

Greenacre, M., P. J. Groenen, T. Hastie, A. I. d'Enza, A. Markos and E. Tuzhilina. 2022. Principal component analysis. *Nature Reviews Methods Primers* 2: 100.

Ihsan, M., M. Nisar, N. Nazir, M. Zahoor, A. A. K. Khalil, A. Ghafoor, A. Khan, R. A. Mothana, R. Ullah, and N. Ahmad. 2022. Genetic diversity in nutritional composition of oat (*Avena sativa* L.) germplasm reported from Pakistan. *Saudi Journal of Biological Sciences* 29: 1487-1500.

Johnson, H. W., H. F. Robinson and R. E. Comstock. 1955. Estimate of genetic and environmental variability in soya bean. *Agronomy Journal* 47: 314-318.

Kaur, H., M. Goyal, A. Kaur and R. Kapoor. 2023. Nutritional and yield potential of oat (*Avena sativa* L.) genotypes in dual-purpose crop system. *Cereal Research Communications* 51: 969-980.

Kebede, G., W. Worku, F. Feyissa and H. Jifar. 2023. Agro-morphological traits-based genetic diversity assessment on oat (*Avena sativa* L.) genotypes in the central highlands of Ethiopia. *All Life* 16: 2236313.

Kumar, R., S. Varghese, D. Jayaswal, K. Jayaswall, K. Yadav, G. Mishra, R. P. Vyas, H. C. Singh, H. G. Prakash, A. N. Singh and S. Kumar. 2023. Agro-morphological and genetic variability analysis in oat germplasms with special emphasis on food and feed. *Plos one* 18: e0280450.

Kumar, Y., R. Niwas, S. Nimbal and M. S. Dalal. 2020. Hierarchical cluster analysis in barley genotypes to delineate genetic diversity. *Electronic Journal of Plant Breeding* 11: 742-748.

Kumari, T. and Y. Jindal. 2019. Genetic diversity and variability analysis in oats (*Avena* sp.) genotypes. *Electronic Journal of Plant Breeding* 10: 1-8.

Mathavaraj, P., P. K. Goswami, S. B. Neog and A. R. Baruah. 2024. Assessment of genetic variability in oat (*Avena sativa* L.) germplasm using agro-morphological traits and microsatellite markers. *Electronic Journal of Plant Breeding* 15: 820-831.

Peeters, J. P. and J. A. Martinelli. 1989. Hierarchical cluster analysis as a tool to manage variation in germplasm collections. *Theoretical and Applied Genetics*78: 42-48.

Popat R, R. Patel and D. Parmar. 2020. Variability: genetic variability analysis for plant breeding research. R Package version 0.1.0.

Pundhir, S R., V. P. Singh and D. S. Phogat. 2008. Genetic variability and interrelationship for various grain and seedling characters in oats. *Forage Research* 33: 236-240.

Rana, A., V. K. Sood, S. K. Priyanka and H. K. Chaudhary. 2022. Genetic diversity and combining ability studies in oat (*Avena sativa* L.) for agro-morphological, yield and quality traits. *Range Management and Agroforestry* 43: 212-223.

Rawat, N. S., R. Rana, C. Mohan and S. Kumar. 2022. Estimation of genetic variability, heritability and genetic advance in twenty-one released varieties of oat (*Avena sativa* L.) for grain and fodder yield. *Journal of Eco-Friendly Agriculture* 17: 273-279.

Roy, A. K., R. K. Agrawal, N. R. Bhardwaj, A. K. Mishra, and S. K. Mahanta. 2019. Revisiting national forage demand and availability scenario. In: A. K. Roy, R.

K. Agrawal and N. R. Bhardwaj (eds). *Indian Fodder Scenario: Redefining State Wise Status*. ICAR-AICRP on Forage Crops and Utilization, Jhansi, India. pp. 1-21.

Sahu, M. and A. Tiwari. 2020. Genetic variability and association analysis of oat (*Avena sativa* L.) genotypes for green forage yield and other components. *Current Journal of Applied Science and Technology* 39: 133-141.

Singh, H. P., O. P. Raigar and R. K. Chahota. 2022. Estimation of genetic diversity and its exploitation in plant breeding. *The Botanical Review* 88: 413-435.

Singh, S. B. and A. K. Singh. 2011. Genetic variability and divergence analysis in oat (*Avena sativa*) under rainfed environment of intermediate Himalayan hills. *Indian Journal of Plant Genetic Resources* 24: 56-61.

Sivasubramanian, S. and P. M. Menon. 1973. Genotypic and phenotypic variability in rice. *Madras Agriculture Journal* 60: 1093-1096.

Wagh, V. R., A. H. Sonone and S. V. Damame. 2018. Assessment of genetic variability correlation and path coefficient analysis in forage oat (*Avena sativa* L.). *Forage Research* 44: 172-175.

Yan, H., S. L. Martin, W. A. Bekele, R. G. Latta, A. Diederichsen, Y. Peng and N. A. Tinker. 2016. Genome size variation in the genus *Avena*. *Genome* 59: 209-220.

Zahid, M. I., A. Shakeel, A. Saeed and N. Ahmed. 2023. Multivariate analysis for evaluating diversity in *Avena sativa* germplasm. *SABRAO Journal of Breeding and Genetics* 55: 1205-1221.