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Research article

Morpho-metric characterization of oat genotypes (*Avena sativa* L.) for agricultural sustainability under changing climatic conditions

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Abstract

In the present investigation, DUS (distinctness, uniformity, stability) characterization of 112 oat genotypes performed using 29 qualitative and quantitative descriptors showed a wide range of genetic diversity, with stable expression under both seasons, but main culm pithiness had no variation and all the genotypes were without pith. High variability was reported for lowest leaves, hairiness of sheaths, leaf color, flag leaf blade width and plant height. Correlation analysis revealed that 1000 seed weight was highly significant and positively associated, while plant height positively correlated with early plant growth habits, flag leaf blade length, and main culm peduncle length. The dendrogram was constructed for 112 oat genotypes and grouped these genotypes into eight clusters. The maximum genotypes were grouped into cluster 2 with 55 genotypes, and minimum numbers were found in clusters 1 and 8 with two genotypes in each cluster. The study will be helpful for breeders in deciding efficient methods and strategies for future oat improvement and selecting primary material for the hybridization program.

Keywords: Characterization, Crop improvement, Distinctness, Germplasm, Oat

Introduction

Oat (*Avena sativa* L.) is a cereal crop popularly grown for animal feed but nowadays exploited for human consumption because of its superior nutritional quality and added health benefits (Poonia *et al.*, 2022; Kaur *et al.*, 2024). The increasing commercial importance of this crop for the seed industry and as an ingredient of functional foods creates challenges for researchers to develop cultivars to improve seed components. This crop is grown during the *Rabi* season on marginal lands where wheat, barley, and other economically important crops yield low. The demand for green fodder for livestock has been rising, while the availability of land for cultivating green fodder crops has remained stagnant at around 5% of the total cropped area (Roy *et al.*, 2019). Despite this, there has been a noticeable shift in focus towards developing dual-purpose varieties that can serve as feed and multi-cut types intended for fodder utilization (Poonia *et al.*, 2020; Bharti *et al.*, 2024). Additionally, oats can be grown as an intercrop with berseem during *Rabi* season to meet green fodder demand (Khan *et al.*, 2022).

Oat germplasm has great potential for crop improvement, but it has not yet been fully exploited. Genetic variability indicates the differences in individuals due to differences in their genetic constitution and environmental influences (Allard, 1988). The wide range of available variability in field crops is analyzed using descriptors in crop breeding programs. These descriptors are qualitative or quantitative observed at different phenological stages. Quantitative, descriptors are measured or counted numerically, whereas qualitative descriptors have characteristics assessed visually (Bioversity International, 2007). Different types of descriptors play a crucial role in crop improvement and variety development programs, from germplasm characterization and evaluation stage to cultivar protection stage. Descriptor choice for a given plant species is governed by the most striking morphological, physiological and molecular characteristics that may be transmitted to each generation as that cultivar is propagated. Therefore, morphological characterization provides a data set on the genetic variability among the germplasm (Guimarães *et al.*, 2007), which is effective in crop breeding programs for determining high heterosis combinations. DUS characterization and evaluation of different accessions describes the qualitative and quantitative characteristics of different genotypes of a particular species to differentiate them. This process defines the importance, genetic variability, genetic diversity and association between these traits. Characterizing these accessions also helps to determine the highly heritable traits unaffected by environmental conditions and gives stable expression. At the same time, preliminary evaluation is also based on the agronomic characteristics of the crop (IBPGR, 1985). Genetic diversity in any crop improvement program is a pre-requisite and of utmost importance, as it is beneficial in selecting parents and developing superior recombinants (Poonia *et al.*, 2020). The characterization of oat genotypes was conducted, and the utilization of these traits was recommended to investigate plant architecture and their interaction within a specified environment, with the ultimate goal of crop improvement (Kumari *et al*., 2018). In addition, the morphometric characterization of oats can be used as stable descriptors for efficiently characterizing oat genotypes in breeding programs (Diederichsen 2008; Chakraborty *et al.* 2014; Sumathi and Balamurugan, 2014).

In response to changing climatic conditions, the phenotypic expression of yield and its associated characteristics undergoes modifications, which may not accurately reflect the full potential of a genotype. Therefore, it is imperative to identify stable morphological traits that are not susceptible to environmental influences. These traits can prove invaluable to breeders for future crop breeding programs. Consequently, this investigation aims to assess and characterize the available germplasm and leverage it to enhance oat crops, as DUS traits often exhibit climate resilience and stability in the face of changing environmental conditions. Therefore, this study was conducted to harness the available germplasm through adherence to DUS guidelines, and the characterized genotypes were identified based on various morphometric traits, with the objective of their utilization in crop improvement programs.

Materials and Methods

Seed material: The experimental material comprised 112 oat genotypes selected from available germplasm maintained in the Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The germplasm material was collected from five leading oat breeding institutes of different states (including Haryana, Punjab, Uttarakhand, Uttar Pradesh, and Jammu and Kashmir) in India and two other countries (Algeria and Australia). These genotypes were evaluated in augmented design during *Rabi* 2018-19 and 2019-20 at Forage Research Area, CCS Haryana Agricultural University, Hisar, India.

Experimental site and meteorological data: Geographically, Hisar is situated in semi-arid sub-tropics at 29°10' N latitude and 75°46' E longitude with an altitude of 215.2 m above the mean sea level. Each germplasm was sown in two rows 3 m long with a row-to-row distance of 25 cm and plant-to-plant spacing of 10 cm. The recommended cultural and agronomic practices were followed to raise crops. During experimentation, weekly mean of minimum and maximum temperature exhibited a wide range (1.85–40.7ºC) and relative humidity (28–91%).

***Recording of experimental data*:** The augmented design was used to conduct an experiment and data were recorded for dual purpose oat. DUS characterization was done according to the DUS guidelines given by PPVFRA (2001) for morpho-metric traits at specified crop growth stages. Quantitative traits were recorded on five randomly selected competitive plants of each genotype when the character under study had full expression (ICAR-IGFRI, 2019).

***Statistical analysis*:** The MS-EXCEL software was used to categorize different genotypes based on code given to different groups of specific traits. The cluster analysis was performed using the SAS JMP Pro 14 software to draw a multicolor dendrogram, while correlation analysis was performed using R-studio software based on their codes.

Results and Discussion

A total of 29 DUS descriptors were assessed in 112 oat genotypes during *Rabi* 2018-19 and 2019-20 at Forage Section, CCS Haryana Agricultural University, Hisar, India. DUS characterization conducted in this study with different oat descriptors has great importance in exploiting and utilizing the available oat gene pool for crop improvement. The changing environmental conditions worldwide require a stable and more methods for screening and characterization of the germplasm resources. The characteristics such as early plant growth habit, hairiness on the uppermost node of the main culm, hairiness on the lemma surface, days to maturity and color of lemma are associated with a grouping of bread oat varieties (DUS guidelines oat, PPVFRA (2001). The germplasm material showed a wide range of genetic diversity, with stable expression under both seasons. Still, the main culm pithiness had no variation, and all the genotypes were without pith.

***Observations recorded for quantitative traits*:** Among 29 DUS descriptors, nine were qualitative traits, while mean and range were observed for the remaining 20 quantitative traits in 112 oat genotypes (Table 1). Understanding the nature and extent of genetic variability in genotypes is essential for a successful breeding program. Higher genetic variability enables the selection of promising genotypes (Kebede *et al.*, 2023). Hence, metric traits presented with results that showed a wide range of variability, indicating great scope for improvement of oat.

Flag leaf length was measured lowest at 22 cm (HFO-103) to 54.10 cm (HFO-922) with an average of 35.96 cm, whereas flag leaf blade width measured minimum for HFO-103 (1.44 cm) and maximum for HFO-922 (3.68 cm) with a mean of 2.54 cm. The leaf length of the main culm was the longest in HFO-402 (60 cm), and HFO-18 had the shortest length (28 cm), with a mean of 43.85 cm for all the genotypes. Regarding the leaf width of the main culm, it ranged from 0.93 cm in OL-1802 to 2.63 cm in HFO-878, with a mean value across all genotypes of 1.67 cm. The diameter of the main culm ranged from 2.19 mm (HFO-862) to 7.89 mm (HFO-568) with a mean value of 5.11 mm, while the numbers of nodes were found lowest (4.30) in OL-12, HFO-236, HFO-500, HFO-555 and HFO-640 and highest for genotypes HFO-607 and OS-403 (7.10). Main culm Internode length ranged from 15.58 cm (HFO-164) to 30.8 cm (HFO-460), whereas the total number of tillers per plant was found to be minimum in JO-1 (7.32) and maximum in HFO-106 (12.03) with a mean of 9.56. The peduncle length of the main culm ranged from 16 cm in HFO-114 to 57 cm in HFO-460, with a mean length of 34.63 cm. Further, the most extended panicle length was reported in JO-1 at 39 cm and the smallest in genotype HFO-52 at 21 cm, resulting in an average length of 29.88 cm.

Primary grain lemma length varied from 1.23 to 2.06 cm, averaging 1.67 cm. The minimum glume length was 2.04 cm, and the maximum was 3.59 cm. The shortest plant height at 65 days was 48 cm, while the tallest averaged 82.29 cm. At 50% flowering, plant height ranged from 73 to 161 cm, averaging 122.28 cm. The days to 50% flowering ranged between 89 days (HFO-62) to 109 days (JHO-2006-2), and the mean was found to be 100.79 days, whereas the days to maturity were recorded as a minimum for HFO-164 (104 days) and maximum for HFO-446 (131 days). The average number of days counted for days to maturity was 116.66. The 1000 seed weight recorded

Table 1. Mean and range obtained in 112 oat genotypes for quantitative traits

Trait name	Range		Mean
	Minimum	Maximum	
Days to 50% flowering	89	109	100.79
FLBW- Flag leaf blade length (cm)	22.2	54.1	35.96
FLBL - Flag leaf blade length (cm)	1.44	3.68	2.54
Leaf length main culm (cm)	28	60	43.85
Leaf width main culm (cm)	0.93	2.63	1.67
MCDI - Main culm diameter of internode (cm)	2.19	7.89	5.11
Main culm number of nodes	4.3	7.1	5.59
MCIL - Main culm internode length (cm)	15.58	30.85	21.63
Number of panicle bearing tillers (cm)	7.32	12.03	9.56
Main culm peduncle length (cm)	16	57	34.63
Main culm panicle length (cm)	21	39	29.88
PGLL - Primary grain length of lemma (cm)	1.23	2.06	1.67
Outer glume length (cm)	2.04	3.59	2.73
Plant height at 65 days (cm)	48	105	82.29
Plant height at 50% flowering (cm)	73	161	122.28
DM - Number of days to maturity	104	131	116.66
1000 SW - 1000-Seed weight (g)	18.88	40.86	28.25
Green fodder yield (g)	350	1215	869.59
Dry matter yield (g)	67	234	129.26
Seed yield (g)	14.62	139.8	49.05

minimum for HFO-333 (18.88 g) and the maximum in HFO-460 (40.86 g) found an average weight of 28.25 g for the studied genotypes.

Oat genotypes for grain production are primarily chosen for high grain yield and its components, while selecting fodder cultivars requires a high biomass yield and superior yield-related traits (Kebede *et al.,* 2023). The fresh green fodder per meter row length at 65 days varied from 350 g (HFO-329) to 1215 g (HFO-79), with an average of 869.59 g. The dry matter yield ranged from 67 g for HFO-329 to 234 g for HFO-79, yielding a mean value of 129.26 g. The seed yield per meter row length reached a maximum of 139.78 g for HFO-460 and a minimum of 14.62 g for HFO-333, resulting in a mean value of 49.05 g for the trait. The earlier work by Poonia *et al.* (2021) and Kumari *et al.* (2018) also categorized the morphometric characteristics based on the mean and range values. It emphasized the use of superior genotypes to exploit heterosis.

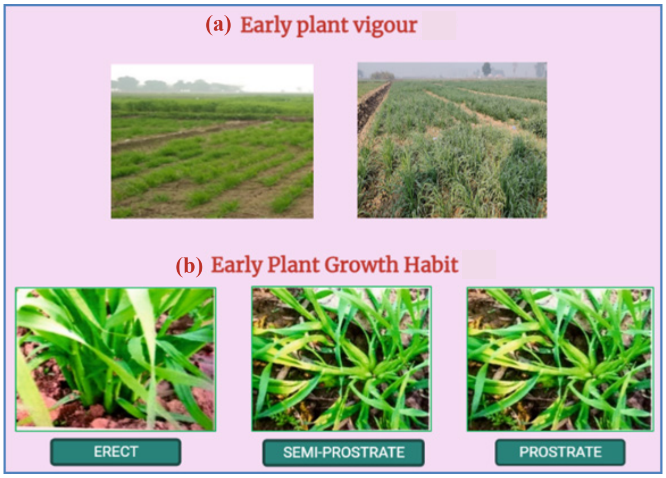

Fig 1. Descriptors variation observed in oat genotypes across two years

Fig 2. Descriptors variation observed in oat genotypes across two years

***Observations recorded at the tillering stage*:** Early plant vigor deals with the early establishment of plants, which were classified into three categories: poor plant growth (8), good plant growth (38), and very good plant growth (66) (Fig 1a). The plant growth habit was classified into two groups *viz*., erect (110) and semi-prostrate (2) (Fig 1b), while on the basis of lowest leaves hairiness of sheath, 49 genotypes were without hairiness, 45 genotypes were with weak and 18 genotypes were with medium hairs (Fig 2a).

***Observations recorded at the booting stage*:** The lowest leaves hairiness of margins (leaf below flag leaf) divided 112 oat genotypes into three categories, *i.e.*, absent or weak lowest leaves hairiness of margins with 20 genotypes, medium lowest leaves hairiness of margins with 86 genotypes, and six genotypes with strong lowest leaves hairiness of margins (Fig 2b). The leaf color is an important character of genotypes, which was classified as dark green, brown green and green leaf color. The 21 genotypes were dark green, 27 were brown-green, and the remaining 64 had green leaf color (Fig 2c). Sumathi and Balamurugan (2014) also characterized different oat varieties for identification through these traits and found them stable. The leaf color, growth habit and stem color were proved to be very useful and stable diagnostic characters to classify the genotypes based on the phenotypic traits (Kumari *et al*., 2018). Earlier, Chakraborty *et al*. (2014) classified different oat genotypes based on growth habit, leaf color, color of panicle, stem girth, panicle length, color of awn, awn nature, lemma color and lemma hairiness and revealed that these traits could be beneficial for characterization under varied environmental conditions.

***Observations recorded at inflorescence stage*:** The genotypes (112) of oat were classified into two groups on the basis of days to 50% flowering. About 35 genotypes were early (< 95 days), 77 genotypes were medium (95–110 days). Whereas, on the basis of main culm hairiness on uppermost node, 112 oat genotypes were classified into two categories as 87 genotypes had absence and 25 genotypes had the presence of main culm hairiness on the uppermost node (Fig 2f). The panicle awnness was observed as the presence or absence of awns. About 26 genotypes had no awns, while 86 genotypes had the presence of awns (Fig 3a). Panicle shape and panicle branch position were proved to be very useful for the characterization of oat accessions (Kumari *et al*., 2018).

***Observations recorded at the anthesis stage*:** The flag leaf blade length of 112 oat genotypes grouped into short (< 30 cm) for 15 genotypes, medium (30–40 cm) in 66 genotypes and 31 genotypes had long flag leaf blade lengths (> 40 cm), while based on flag leaf width, 112 oat genotypes were classified into three categories *viz*.,

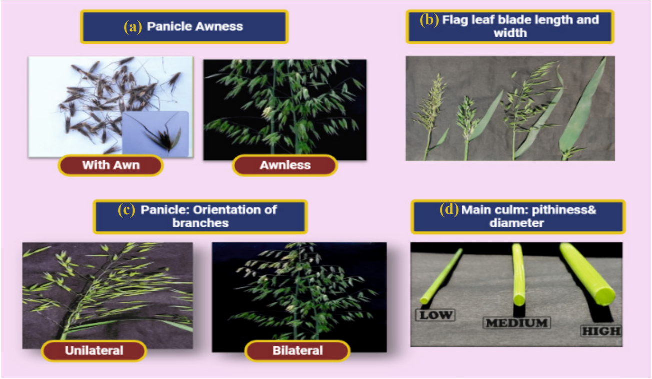

Fig 3. Descriptors variation observed in oat genotypes across two years

narrow (11 genotypes), medium (40 genotypes) and broad (61 genotypes) (Fig 3b). The trait main culm pithiness showed no variability and all oat genotypes were without pith. The main culm diameter trait also had low variability as 108 genotypes were low (< 7.00 mm), and four genotypes were medium (7.50–8.50 mm) in diameter (Fig 3d). Santos *et al.* (2017) reported lemma color and flag leaf length as the most stable oat descriptors. On the basis of the main culm number of nodes, oat genotypes were classified into three categories: low in six genotypes, medium in 104 and high in two oat genotypes. The main culm internode length was classified into two groups *viz*., medium (15–20 cm) for 37 genotypes and long (> 20 cm) for 75 genotypes. Based on number of panicle-bearing tillers, genotypes were categorized into three groups: one genotype in low, 68 genotypes in medium, and 43 genotypes observed with a high number of panicle-bearing tillers.

***Observations recorded at grain filling stage*:** Main culm peduncle length was grouped into two categories *viz*., medium (5–10 cm) with two and long (> 10 cm) with 110 oat genotypes, whereas the main culm panicle length had 67 genotypes with short (< 30 cm) and 45 genotypes recorded medium (30–40 cm) main culm panicle length. Based on the panicle orientation of branches, 38 genotypes were unilateral; four genotypes were sub-unilateral, and 70 genotypes were equilateral (Fig 3c), while based on the panicle attitude of branches, 59 genotypes were semi-erect, nine were horizontal, and 44 genotypes were medium drooping type.

***Observations recorded at ripening stage*:** Primary grain hairiness of the lemma (Fig 4a) was absent in 88 genotypes and present in 24 genotypes, while primary grain length of the lemma (Fig 4b) was short in 38 genotypes, medium in 40 and long in two genotypes. The 112 oat genotypes were classified into four categories for grain color of lemma *viz*., yellow-white (102 oat genotypes), grey yellow (8 oat genotypes), grey-brown (one oat genotype) and brown (two oat genotypes) (Fig 4c). Based on outer glume length, 112 oat genotypes were classified into three categories: 22 short, 79 medium and 11 genotypes with long glume length. Based on hairiness at the base, 90 genotypes had an absence of base hairs, and 22 had medium hairs at the base. The primary grain length of basal hairs was short in 83 genotypes and medium in 29 genotypes. Based on the primary grain length of rachilla, 13 genotypes had short, 57 had medium, and 42 had long primary grain length of rachilla. In a previous study by Kumari *et al.* (2018), oats genotypes were characterized based on morphological traits such as leaf color, growth habit, stem color, awnness, awn color, panicle shape, and panicle branch position. The study suggested using these stable traits to study plant architecture and their interaction within a specified environment, aiming for further improvement.

Plant height is an important character and positively correlated with green fodder yield, classified into four classes *viz*., short (< 125 cm), medium (125–150 cm), tall (150–175 cm) and very tall (> 175 cm). A total of 37 genotypes were short, 40 medium, 31 tall, and the remaining four were very tall. The number of days to maturity consists of early category (< 125 days) with 107 genotypes and five genotypes with medium (126–145 days) maturity duration. The 1000-seed weight classified genotypes into three groups: low, medium and high. The six genotypes were in low, 70 in medium, and the remaining 36 were in the high 1000-seed weight group. The earlier findings of Diederichsen (2008), Chakraborty *et al.* (2014), and Sumathi and Balamurugan (2014) on morpho-metric characterization of oats also reported similar results. They advocated using these oat descriptors to characterize oat genotypes in breeding programs efficiently.

***Diversity analysis*:** Genetic variability is depleted quickly due to the developmental activities of man and the continuous use of limited variability in the ongoing crop improvement trials, which increases the importance

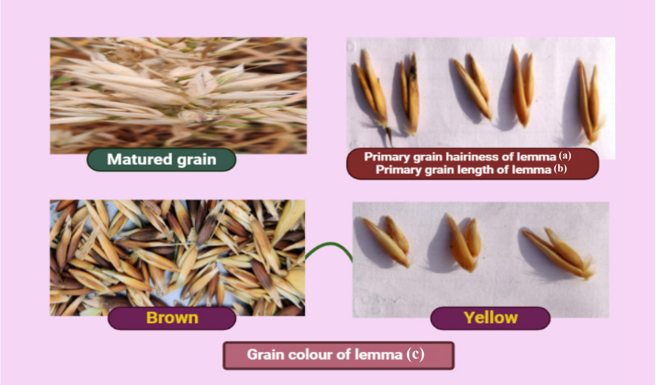

Fig 4. Descriptors variation observed in oat genotypes across two years

of genetic diversity for the sustainability of breeding programs (Poonia *et al.,* 2020). The dendrogram (Fig 5) constructed for 29 DUS descriptors of 112 oat genotypes clustered these genotypes into 8 clusters based on codes given for DUS guidelines (Table 2). The maximum genotypes were grouped into cluster 2 with 55 genotypes, with a minimum number found in clusters 1 and 8 with two genotypes in each cluster. However, substantial genetic variability among the clusters was observed in the present study. In a previous study, Poonia and Phogat (2017) suggested that the cluster with a higher number of lines had low genetic diversity among the lines and were more closely related, indicating lesser variability in cluster 2 of the present study.

The biplot showed a correlation pattern (Fig 6) with the line for different traits, and the trait showing the longest line had the highest variability. A total of 4 groups could be concluded from the biplot, and the first group included MPL, PGLR, DM, FLBW and POB traits, which were positively correlated to both PC 1 and PC 2. The second group was positively correlated with PC 1, while a negative association was observed between these traits (FLBL, PA, OGL, PGLL, LC, and GCL) and PC 2. The third group included, MCPL and PAB, was negatively impacted by both PC 1 and PC 2. The last group included early plant growth habit (EPGH), MCDI and NPBT, which were favorably impacted by PC 2 and negatively correlated with PC1. The utilization of biplot analysis provides a visually informative representation of the categorization of genotypes and their associated key traits. This method comprehensively elucidates the relationships between genotypes and their respective traits (Kebede *et al.,* 2023).

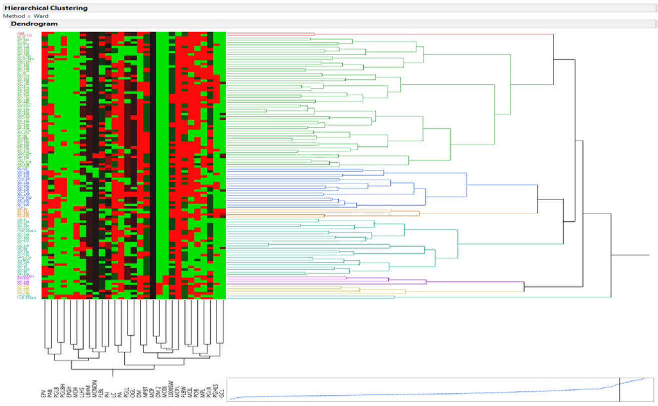

Fig 5. Two-way dendrogram showing clustering pattern of 112 oat genotypes characterized for DUS by WARD's method

***Correlation analysis*:** The correlation analysis sought to identify significant and positive associations between the trait of interest and other traits. Identifying these correlations helps us understand which traits are directly or indirectly linked and how improvement in one trait can lead to improvements in others. This analysis provides valuable insights into how enhancements in associated traits can positively impact the trait of interest (Poonia *et al.,* 2021). The correlation analysis was performed to obtain the association between different morpho-metric traits based on the codes (Fig 7). Qualitative trait correlation studies in oats were not previously conducted. As a result, this study focused on investigating the associations among various qualitative traits in oats. By exploring and analyzing these relationships, we aimed to contribute valuable insights to the field of oat trait analysis. The highest correlation was observed between primary grain length of lemma (PGLL) and outer glume

Table 2. Details of 112 oat genotypes distributed in 8 clusters by Ward's method

Cluster	Count	Genotype name
1	2	Kent, UPO-212
2	55	OL-9, 0L-10, 0L-11, OL-1760, OL-1769-1, OL-1802, OL-1804, HFO-60, HFO-607, OS-377, OS-403, HFO-867, HFO-878, HFO-50, HFO-128, HFO-145, HFO-156, HFO-183, HFO-228, HFO-244, HFO-282, HFO-289, HFO-330, HFO-333, HFO-363, HFO-374, HFO-377, HFO-379, HFO-386, HFO-395, HFO-402, HFO-404, HFO-439, HFO-447, HFO-460, HFO-575, HFO-584, HFO-586, HFO-587, HFO-588, HFO-595, HFO-610, HFO-611, HFO-631, HFO-638, HFO-639, HFO-641, HFO-710, HFO-715, HFO-733, HFO-915, HFO-918, HFO-922, HFO-924, HFO-926
3	17	OL-12, HFO-58, HFO-529, JO-1, HFO-106, HFO-160, HFO-167, HFO-236, HFO-276, HFO-459, HFO-555, HFO-560, HFO-640, HFO-642, HFO-725, HFO-730, HFO-902
4	4	HFO-62, HFO-500, HFO-551, HFO-914
5	24	OS-6, OS-7, HFO-114, OS-346, JHO-2001-1, SUBZAR, HFO-18, HFO-43, HFO-52, HFO-55, HFO-862, HFO-868, HFO-79, HFO-84, HFO-103, HFO-157, HFO-164, HFO-230, HFO-270, HFO-451, HFO-633, HFO-910, HFO-920, HFO-921,
6	4	ALGERIAN, HFO-243, HFO-329, HFO-568
7	4	HFO-201, HFO-380, HFO-446, HFO-498
8	2	JHO-851, JHO-2006-2

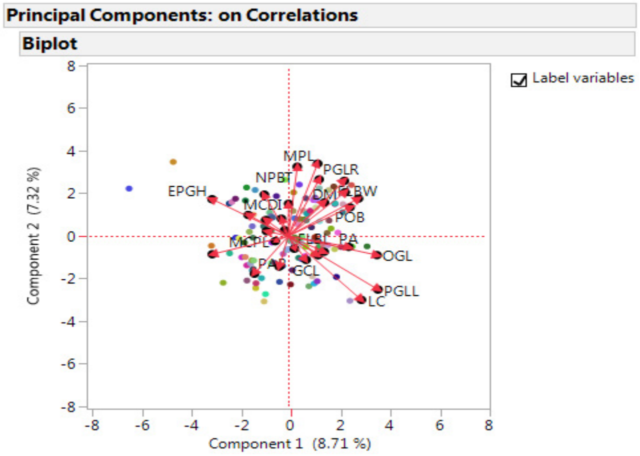

Fig 6. Biplot showing correlation pattern of 112 oat genotypes characterized for DUS

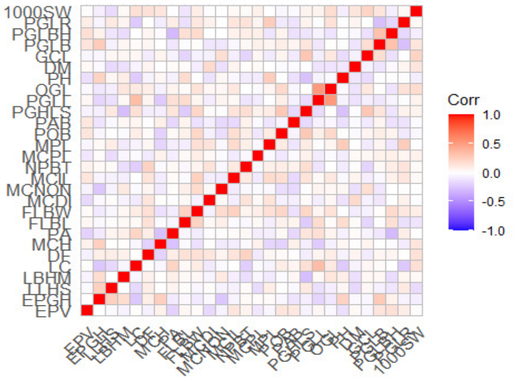

Fig 7. Correlation plot showing correlation among 28 DUS traits for 112 genotypes

length (OGL) traits (0.534). A positive and significant correlation was reported between leaf color (LC) and PGLL (0.345), PGLB and PGLBH (0.323), POB and PGHLS (0.281), grain color of lemma (GCL) and PGHLS (0.287), PGLB and EPHG (0.273), PGLR and MPL (0.261), MPL and PH (0.257), MCH and EPGH (0.252), and main culm internode length (MCIL) and flag leaf blade length (FLBW) (0.243). A highly significant and positive correlation was observed between LLHS and EPGH (0.238), number of panicle bearing tillers (NPBT) and DF (0.235), GCL and 1000SW (0.219), POB and FLBW (0.210), PGHLS and FLBW (0.205), main culm number of nodes (MCNON) and FLBW (0.192), DM and main culm diameter of internode (MCDI) (0.191), and MPL and MCIL (0.188). On the other hand, traits that showed negative and significant correlations were PGLBH and PA (-0.303), PGHLS and LBHM (-0.281), PGLR and PGLB (-0.266), PGHLS and PH (-0.262), LC and EPGH (-0.239), MCNON and EPGH (-0.236). While PGLR and LC (-0.230), PGHLS and FLBL (-0.224), PH and LC (-0.221), PGLL and MCH (-0.218), NPBT and LC (-0.207) and POB and MCH (-0.186) were highly significant and negatively correlated. Poonia *et al.* (2017) revealed that traits like plant height, flag leaf length, internode length, seed yield, leaf length and green fodder yield showed positive and highly significant correlations among each other. Kumari *et al.* (2024) reported that the number of tillers per plant, leaves per plant, area of leaves and dry matter had positive and significant associations with green fodder yield. Additionally, Savova *et al.* (2014) suggested the model for ideal dual-purpose variety with more productive tillers, average height, and panicle with large, well-grained, upright, and resistant to grain shattering and sprouting.

Conclusion

Morphological characterization of oat crops helps in strengthening crop improvement programmes under changing environmental conditions. The assessments of genetic variability suggest significant genetic diversity in oat genotypes. High variability was recorded for the lowest leaf hairiness of sheaths, leaf color, flag leaf blade width and plant height. In contrast, no variability was observed for pithiness, as all the available germplasm had hollow stems. Correlation analysis revealed that 1000 seed weight was highly significant and positively associated. In contrast, plant height positively correlated with early plant growth habits, flag leaf blade length, and main culm peduncle length. The dendrogram constructed revealed considerable diversity among the germplasm materials used in the present study, which could be exploited to improve and develop high-yielding oat cultivars for feed and fodder purposes.

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