Association of morpho-physiological traits with forage yield and quality in single cut oat

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in partial fulfilment of the requirements for the degree of
Master of Science in Agriculture
(Plant Physiology)

By

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CERTIFICATE - I

This is to certify that the thesis entitled **"Association of morpho–physiological traits with forage yield and quality in single cut oat"** submitted in partial fulfilment of the requirements for the award of the degree of **MASTER OF SCIENCE IN AGRICULTURE (PLANT PHYSIOLOGY)** to the Odisha University of Agriculture and Technology is a faithful record of *bona fide* and original research work carried out by **Swagatika Behera, Adm. No. 211222301** under my guidance and supervision. No part of this thesis has been submitted for the award of any other degree or diploma.

It is further certified that the assistance and help received by her from various sources during the course of investigation has been duly acknowledged.

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CERTIFICATE –II

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ABSTRACT

The present investigation was undertaken to study **"Association of morpho-physiological traits with forage yield and quality in single cut oat".** The material of present study consisted of twenty-two genotypes forage oat and the genotypes were evaluated at field of AICRP on Forage crop and Utilization, OUAT, Bhubaneswar during Rabi 2022-23 in a Randomized Block Design with three replications. Observations were recorded on different physiological parameters like CGR, RGR, dry matter content, chlorophyll content and morphological traits like plant height, days to 50 % flowering, leaf to stem ratio, leaf length & breadth, number of leaves per plant, green forage yield per plant, panicle length, 100 seed weight, seed yield per plant and nutritional traits like crude protein content, phosphorus content, potash content and ash content. The analysis of variance revealed significant difference among the genotypes for all the characteristics being examined, with the exception of RGR. The maximum error mean sum of square was observed in case of green forage yield (69.734) followed by plant height (62.182) and seed yield (60.633). Characters viz., number tillers per plant, leaf area, leaf area index, leaves per plant, flag leaf area and seed yield showed high estimates of GCV and PCV indicating enough variability for these characters. High heritability recorded for plant height (84.01), days to 50% flowering (95.95), number of tillers (81.82), leaf area (90.39), leaf area index (89.66) and seed yield (92.28). The traits Plant height (23.68), Days to 50% flowering (30.09), leaf area (48.12), flag leaf area (53.22), green forage yield (24.05), seed yield per plant (94.32) showed high genetic advance as percent of mean. These traits indicate the selection will be rewarding due to additive gene action. The trait viz., plant height (0.697**), number of leaves per plant (0.296*), number of tillers per plant (0.276*), leaf length (0.125), leaf breadth (0.486**), leaf area (0.425**), CGR (0.4202), RGR (0.2774), leaf to stem ratio (0.09) showed positive relation with GFY indicating their importance for selection of green forage improvement programme. The genotype OL-2000 and UPO-22-1 had the highest nutritional index (4.0) followed by HFO-1013(3.0), OL-1980 (3.0), HFO-1211 (3.0) and UPO 22-2 (3.0) and these genotypes were considered as the good genotypes for nutritional quality.

The genotype OS-403 having GFY of 141.033g/plant surpassed the best national check OL-1821(130.80 g). The genotypes with high GFY, better nutritional quality and high seed yield were UPO 22-2, OL-1964 and OL-1976-1.

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ABBREVIATIONS

AICRP	:	All India Coordinated Research Project
b.s.	:	Broad sense
C.D.	:	Critical difference
CGR	:	Crop growth rate
C.V.	:	Coefficient of variation
Cov.	:	Covariance
DAS	:	Days after sowing
d.f.	:	Degrees of freedom
et al.	:	And others (etalia)
Fig	:	Figure
g	:	Gramme(s)
GA	:	Genetic advance
GCV	:	Genotypic coefficients of variation
ha	:	Hectare
h^2	:	Heritability
LAI	:	Leaf area Index
L/S ratio	:	Leaf to stem ratio
MSS	:	Mean sum of squares
PCV	:	Phenotypic coefficient of variation
RBD	:	Randomized Block Design
RGR	:	Relative growth rate
r	:	Correlation coefficient
S.Em	:	Standard Error mean
Σ	:	Summation
%	:	Per cent

INTRODUCTION

Oats (scientifically known as *Avena sativa* L.) are a cereal crop native to the western Mediterranean region and have a relatively short history in agriculture. They belong to the Poaceae family, which includes the *Avena* genus comprising approximately 70 species, but only *A. sativa*, *A. nuda*, and *A. byzantina* are cultivated extensively for commercial purposes. According to FAOSTAT (2015), oats (*Avena sativa* L.) rank as the world's sixth most produced cereal crop, following wheat, rice, maize, barley, sorghum, and millets. Oats are a versatile crop used for grain, pasture, and forage, and they are especially important as a winter forage crop in various regions globally. Oats are unique among cereal grains like wheat and barley because they are rich in dietary fiber, including a soluble fiber known as β-glucan, and contain antioxidants such as α-tocotrienol, α-tocopherol, and avenanthramides. In recent times, oats have gained significant interest among breeders, especially in the context of our growing dairy industry, owing to their high-quality, nutritious forage for livestock and grains utilized as animal feed (Ruwali *et al.*, 2013).

In India, oats have gained significant importance as a livestock feed, particularly for young animals like calves, horses, poultry, and sheep. Oats are known for their high protein content and can be successfully cultivated in both the plains and hilly regions of the country, thanks to their preference for colder growing seasons. Oat fodder plays a vital role on dairy farms, where it can be fed when green and any surplus can be converted into silage or hay for use during periods of scarcity. Oats exhibit an impressive growth pattern, rapid post-harvest regeneration, and offer high- quality forage. Their feed is not only palatable but also rich in nutrients. On average, a hectare of oat crops yields between 45 to 55 tonnes of green feed. Oats can be grown on various soil types, and they thrive on relatively rich, well-drained soils when temperature and moisture conditions are favorable. However, to achieve maximum oat yields, it's often necessary to add lime to the soil to raise its pH to the range of 5.3-5.7. It has been observed that oats can even grow on acidic soils with a pH of 4.5.

In India, oats are cultivated as a fodder crop during the Rabi season in the northwestern, central, and increasingly in eastern regions. The total oat cultivation area in the country is approximately 500,000 hectares, with Uttar Pradesh being the most prominent state, accounting for 34% of the cultivation. The crop is most extensively grown in Punjab (20%), Bihar (16%), Haryana (9%), and Madhya Pradesh (6%). Other states such as Gujarat, Maharashtra, Orissa, Uttaranchal, and others share the remaining oat cultivation area (Anonymous, 2012).

Livestock plays a crucial role in Indian agriculture and the economy, contributing to over 32% of the country's agricultural output and approximately 4.11% of the GDP. India provides assistance to 20% of the world's livestock population over a 2.3% geographic region. The economic coordination of crop production and livestock raising is Indian agriculture. Nearly 70% of total holdings are owned by small and marginal farmers, while 64% of people work in agriculture either as cultivators or farm labourers. India's overall livestock population is 535.82 million, up 4.6% from the last Census in 2012, according to the 20th Livestock Census-2019. According to the 2019 DAHD& F report, this includes 36.04% cattle, 20.4% buffalo, 13.8% sheep, 1.69% pigs, and 27.7% goats. According to the IGFRI Vision 2050, all animal husbandry and dairy farming units depend heavily on sufficient supplies of high-quality green and dry fodder, both of which are in low supply (35.6 and 11.0 percent, respectively).

Establishing effective methods is always necessary to close the demand-supply gap. Consequently, cultivars with the potential to reduce yield losses and increase yields should be the focus of breeding efforts. Oats are becoming more widely used as a multipurpose crop for grain, pasture, and forage as well as a crop for rotation and for conserving forage (Suttie and Reynolds, 2004). India is the world's top producer of milk, despite the fact that animal output is low (1538 kg/year) compared to the global average (2238 kg/year), which can be connected to malnutrition because of the severe shortage of animal feed (Vijay et al., 2018).

According to the IGFRI Vision 2050, the country is currently facing a net deficit of 35.6% in green fodder, 10.95% in dry fodder, and 44% in concentrate feed ingredients. The projected demand for dry feed will reach 1012 million

tonnes, and the demand for green feed will be 631 million tonnes by the year 2050. However, at the current rate of expansion in forage supply, it is anticipated that there will still be an 18.4% deficit in green fodder and a 13.2% deficit in dry fodder by 2050. To bridge this gap, there is a need for an annual increase in green forage production at a rate of 1.69%. It's worth noting that the area dedicated to fodder cultivation currently accounts for just 4% of the nation's total cultivated land, which is approximately 8.4 million hectares, and this area has seen minimal growth in recent years (Halli et al., 2018; Meena et al., 2018; Dagar, 2017).

Energy and protein deficiencies in animals range from 40% to 60%. However, the forage production of our native cultivars is so small that it is not enough to meet the needs of animals. As a result, fodder crop quality and quantity still need to be raised to the necessary level. High yields of dry matter, high levels of crude protein that are digestible, and low levels of crude fibre should all be present in an ideal forage. Oats are a good source of total digestible nutrients (TDN), fat, vitamin B1, and digestible crude protein. The straw is soft and superior to that of wheat and barley, making it an excellent feed for animals.

To operate a productive cattle sector, which is becoming more and more dependent on an expanding population, more nutrient-rich and high-yielding fodder types are required. As a result, fodder cultivars must yield significant quantities of highly digestible green feed for animals and exhibit strong regeneration after cuts (Stevens et al. 2004) Collecting germplasm from diverse regions is crucial as it represents a valuable natural resource for introducing the necessary variability in traits required for the development of new oat cultivars. To fully leverage the genetic diversity and genomic information present in various oat species and cultivars, it's important to have a comprehensive understanding of their genetic relationships. This knowledge will be helpful in creating superior cultivars that incorporate the advantageous characteristics inherent in this wide-ranging germplasm. In general, when you have a diverse set of individuals, they are more likely to exhibit heterotic effects during breeding programs. This can result in the production of desirable offspring with a combination of favorable traits.

Keeping this in view, the present investigation entitled **"Association of morpho-physiological traits with forage yield and quality in single cut oat"** was undertaken with following objectives.

- Evaluating oat genotypes for physiological and nutritional quality parameters associated with green forage yield
- Variability analysis for
  a) Physiological
  b) Morphological
  c) Nutritional parameters
- Identifying oat genotypes having high green forage yield and better nutritional quality parameter

REVIEW OF LITERATURE

A thorough review of the literature is an essential component of any scientific study. It serves the purpose of comparing the current findings with previous research conducted by scholars, making it an indispensable step in the research process.

The literature relating to the current study named "Association of morpho-physiological traits with forage yield and quality in single cut oat " was studied under the following distinct aspects.

2.1 Yield and yield attributing traits

2.2 Genetic variability

2.3 Correlation

2.1 Yield and yield attributing traits

Bakhsh *et al*. (2007) evaluated the performance of ten fodder oats cultivars and revealing significant variations in all the traits examined. Notably, the exotic oats cultivars "Scott" and "Cascade" exhibited taller plant growth, a higher number of tillers per plant, a larger leaf area, and more leaves per tiller compared to the standard oat varieties. These exotic oats, "Scott" and "Cascade," also produced the highest yields of green fodder and dry matter at 68.77, 60.19, and 18.82, 16.47 tonnes per hectare, respectively

Lodhi *et al*. (2009) conducted a series of fodder production trials at the Large Ruminant Research Institute in Sibi, where nine oat cultivars of *Avena sativa* were evaluated for various yield components. The study measured parameters such as plant height, leaf area, and fodder yield per unit area.

Malakar *et al*. (2009) conducted an experiment on forage oat. Plant height, dry matter accumulation, LAI, CGR, GFY, DFY, and CPY observations were made.

Amanullah *et al.* (2013) analysed Shoot: root ratio, dry matter partitioning, growth analysis, and water use efficiency of oat (Avena sativa) and observed the character like leaf, stem, root and total dry weight per plant.

Ahmad *et al.* (2014) studied on Oat (Avena sativa) and investigated general combining ability, specific combining ability for fodder yield, and other important characteristics such as plant height, number of tillers, days to 50% flowering, leaf stem ratio, and green forage yield.

Siloriya *et al.* (2014) studied on six different oat varieties (Kent, UPO 2005-1, NDO-1, JO 2003-78, OS-6, and JHO-822). The results of their research indicated that the variety NDO-1 exhibited the highest number of tillers per square meter, panicle weight, and 1000 grain weight, resulting in a higher seed yield of 3.64 tonnes per hectare, surpassing all other varieties. Kent followed closely with a yield of 3.52 tonnes per hectare, while OS-6 recorded the lowest seed yield at 2.86 tonnes per hectare. The differences between OS-6 and JO 2003-78 (2.95 t/ha), UPO 2005-1 (3.10 t/ha), and JHO-822 (3.18 t/ha) were not statistically significant. OS-6, however, produced more straw at 10.62 tonnes per hectare. Variety NDO-1 also exhibited a higher crop growth rate, relative growth rate, and leaf area index.

Hameed *et al*. (2014) conducted an experiment to assess the forage yield and quality response of three oat cultivars. The research focused on parameters such as growth, yield, quality, and the number of leaves per tiller.

Khan *et al*. (2014) compared forage yield and quality of oat genotypes (F-413, SGD-46, F-408, F-301, SGD-2011, SGD-3, SGD-37, SGD-40, SGD-5, and S-2000). The results demonstrated significant variations in yield, growth, and quality measures among the oat varieties (with a significance level of $P < 0.05$). SGD-40 stood out by producing notably higher green forage yield at 80.00 tonnes per hectare and dry matter yield at 10.95 tonnes per hectare. This superior performance was attributed to the taller plant height (145.73 cm), a larger number of tillers per square meter (7.78 m^2), and more extensive leaf area per plant (95.08 cm^2). Additionally, SGD-40 exhibited an impressive crude protein content of 13.84%.

Beyene *et al.* (2015) evaluated various oat varieties for fodder yield and yield-related traits in Ethiopia's central highlands. The research involved the assessment of seven forage oat varieties, and data on plant height, leaf number per tiller, tiller number per plant, tillers per square meter, and green fodder yield were collected. The study found that the different oat varieties showed variations in their yield and yield-related parameters.

Jat *et al.* (2015) conducted a study on fodder oat and character like crop growth rate, dry fodder production was observed.

Liu *et al.* (2015) examined the nutrient composition and protein extractability of two oat forage varieties harvested at different maturity. The results indicated that oat forages harvested at an early stage can have nutrient compositions that are comparable to or even superior to oat grains. However, their potential use as an alternative protein source for non-ruminant animals is limited due to low protein extractability.

Muhammad *et al*. (2015) conducted a field experiment on oat forage, noting yields of green forage at 85.2 tonnes per hectare, dry matter at 14.1 tonnes per hectare, and crude protein content at 11.5%.

Mut *et al.* (2015) studied hay yield and quality of oat genotypes from around the world. Their research revealed that oat plant height ranged from 76.2 to 141.2 cm, hay yield ranged from 6.03 to 11.83 tonnes per hectare, crude protein content ranged from 58.8 to 136.4 g per kg of dry matter, acid detergent fiber ranged from 333.2 to 424.8 g per kg of dry matter, and neutral detergent fiber ranged from 522.5 to 652.4 g per kg of dry matter. Total digestible nutrients (TDN) levels varied from 465.1 to 583.3 g per kg, with a relative feed value ranging from 80.9 to 11.2%.

Surje *et al.* (2015) conducted an experiment to estimate the mean performance of yield and other morpho-physiological characteristics, as well as their effects (both direct and indirect) on yield (fodder and grain yield).

Irfan *et al.* (2016) carried out an experiment with four oat cultivars (PD2-LV65, S-2000, NZ0034, and NARC-11), and observed that var. PD2-LV65 outperformed the other varieties in terms of plant height, number of leaves, biomass attributes, green forage production, dry matter yield, and dry matter content.

Mukesh Choudhary and G. Prabhu (2016) assessed two fodder oat varieties (JHO 99-1 and JHO 99-2) and found that there were no significant differences between the oat cultivars in terms of growth, yield, or water-use efficiency. However, JHO 99-2 accumulated more crude protein than JHO 99-1.

Verma *et al.* (2016) investigated the effect of cereal crops (Wheat, Oat, and Barley) and harvesting schedule on forage and grain yield. The study discovered that at

95 DAS, barley and wheat had the highest chlorophyll accumulation and at 30 DAS in wheat and barley during the reproductive stage. It has been demonstrated that cutting at 50 DAS improves chlorophyll accumulation. At 90 DAS, wheat had the highest photosynthetic rate, with no effect on photosynthesis rate, stomatal conductance, or transpiration rate. Barley produced the highest fodder yield (fresh/day). Cutting at 50 DAS resulted in optimum forage output without affecting cereal crop grain yield. The average maximum LAI and LAD in crops were barely detected during cutting at 50 DAS among cutting management systems found maximum LAI and LAD.

Premkumar *et al.* (2017) observed high genetic variation among genotypes for most of the traits like tillers per plant, grain weight per panicle, fodder yield per plant, plant height, 50% flowering, panicle length, single plant grain weight.

Mir *et al*. (2018) assessed a variety of oat varieties over two consecutive Rabi (winter) seasons, focusing on growth parameters such as plant height, number of tillers per meter row length, leaf-stem ratio, and leaf area index (LAI). They also examined yield attributes, including seed yield and 1000 seed weight, as well as forage quality parameters.

Poonia *et al.* (2018) analyzed ninety-two oat genotypes for morphological and quality parameters. The study revealed that traits such as plant height (cm), green fodder yield (Kg), dry matter yield (Kg), flag leaf length (cm), inter-node length (cm), axis length (cm), seed index (cm), leaf length (cm), green fodder yield (kg), dry matter yield (Kg), and crude protein (%) exhibited high heritability and a high expected genetic advance as a percentage of the mean.

Singh *et al*. (2018) conducted an experiment involving three oat varieties, Kent, JHO-822, and RO-19, to determine the best oat variety for maximizing fodder seed yield and fodder production. The results indicated that the Kent variety produced the highest number of tillers per square meter and had the greatest plant height. RO-19 excelled in green and dry (without cutting) fodder production (51.20 cm, 265.72 quintals per hectare, and 144 quintals per hectare), panicle weight, and 1000 grain weight, resulting in a higher seed yield of 3.64 tonnes per hectare.

Biswas *et al*. (2019) investigated on periodic dry matter accumulation (DMA) and crop growth rate (CGR) of oat and lathyrus in various intercropping systems and maximum DMA (287.58 g/m2, 175.96 g/m2, and 288.88 g/m2 of oat, and 182.8 g/m2,277.26 g/m2, and 334.39 g/m2 of lathyrus) was observed at 60, 90, and 120 DAS.

Ahmed *et al.* (2020) evaluated performance of oat variety Bundel Jai-15-1 for fodder and seed yield. Observation like green fodder, dry matter, crude protein yield (q/h) and content (%) and the number of tillers present in per meter row length were recorded.

Bibi *et al.* (2021) tested exotic oat varieties for forage and grain yield. The Australian variety exhibited higher emergence (49 plants per square meter) and various growth parameters, including days to emergence (15 days), days to flowering (122 days), days to maturity (145 days), plant height (142.7 cm), number of leaves (6.03 leaves per plant), and number of tillers (92.2 tillers per square meter).

Hasan *et al.* (2021) conducted a study on the growth and production of three oat types. They recorded parameters such as the number of tillers (457,422 per square meter), panicles (376, 355 per square meter), grain in panicle (28.54 and 25.97 per square meter), 1000 grain weight (26.77, 26.48 grams), grain yield (3.96, 3.71 tons per hectare), biological yield (17.53, 16.43 tons per hectare), average plant growth (12.30, 11.55 grams per square meter), and harvest index (22.52, 23.08%) for both seasons.

Kumar *et al.* (2021) conducted an experiment with oats (*Avena sativa*). They observed various growth-related parameters such as plant height, number of leaves, leaf length, leaf width, stem girth, number of tillers, cumulative growth rate (CGR), and relative growth rate (RGR) during both cuts.

Sumanth *et al.* (2021) studied the green fodder yield and quality of fodder oats (*Avena sativa*). They recorded data for dry matter accumulation (97.73 plants per 0.5 meters row length), green fodder yield (28.88 tonnes per hectare), dry fodder yield (5.79 tonnes per hectare), crude protein content (6.39%), crude protein yield (3.70 quintals per hectare), total ash (9.47%), and ether extract (2.97%).

Pant *et al.* (2022) investigated the fodder and seed yield of eleven different oat varieties. They recorded various growth and yielding characteristics, including plant

height, leaf area, number of tillers per plant, number of leaves per tiller, fodder dry matter yield, seed yield, and straw yield. Dry matter yields ranged from 2.35 to 3.58 tons per hectare and did not show statistically significant differences between the varieties. However, seed and straw yields differed significantly among the oat varieties. Higher seed yields were achieved by Netra (2.90 tons per hectare) and Kona (2.88 tons per hectare), while the cultivar Longford provided the highest straw production (8.73 tons per hectare).

2.2 Genetic variability

Bedis and Patil (1996) found high heritability and genetic advance for the number of tillers per meter and dry forage yield per plant, indicating the potential for effective selection in 45 different strains of forage oat.

Singh (1999) investigated oat variability, heritability, and genetic advancement. High heritability values for traits such as plant height, number of leaves per plant, number of tillers per plant, green forage yield (GFY), dry forage yield (DFY), and leaf-stem ratio suggested that selection for these characters could be effective. The high heritability and genetic advance for the number of tillers per plant and GFY indicated a predominance of additive gene effects.

Chaubey *et al.* (2001) reported a high heritability of 66.6% for plant height and 64.2% for days to 50% blooming. The study also observed a wide range of variation in blooming time, plant height, tiller number, internode length, green fodder output, and dry fodder yield in forage oat.

Shankar *et al.* (2002) found high estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) for traits like grain yield, leaf-stem ratio (L:S), grain weight, green forage yield, and dry matter yield. These traits also exhibited high heritability and PCV, indicating significant genetic progress. The high GCV and heritability estimates for grain yield, grain weight, green forage yield, and dry matter yield suggested substantial genetic potential.

Prasad *et al*. (2003) observed that plant height and the number of days to flowering were highly heritable, indicating that these traits are primarily controlled by genetic factors.

Pundir *et al*. (2003) reported high heritability estimates for green and dry fodder yield, leaf length, leaf width, leaf weight, and dry leaf weight. These traits were associated with significant genetic progress. Green fodder yield per plant had the highest genotypic and phenotypic coefficients of variation, while leaf width had the lowest. All the studied traits exhibited high estimates of genetic advancement and heritability, highlighting their potential for selection and improvement.

Kumar *et al.* (2004) conducted a study on genetic diversity in fodder oat. They found a significant difference between all germplasm lines for various traits. High coefficients of variation were observed for the number of tillers, flag leaf length, green fodder yield, number of leaves, dry matter yield, and longest internode length, indicating substantial trait variation within the germplasm.

Mall *et al*. (2005) examined 48 oat genotypes and reported high genotypic and phenotypic coefficients of variation for traits such as dry matter yield per plant, green fodder yield per plant, and harvest index. Additionally, several traits, including grain number per panicle, tiller number per plant, biological yield per plant, and grain yield per plant, displayed strong broad-sense heritability and genetic progress.

Gautam *et al.* (2006) investigated genetic variation in morpho-physiological traits in oats. They observed that the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all traits. Dry matter yield and green fodder yield exhibited wide ranges. Green fodder yield, leaf: stem ratio, grain yield, tillers per plant, and flag leaf length demonstrated significant heritability and genetic progress, emphasizing the role of additive genetic effects in these traits.

Shekhawat *et al*. (2006) studied green fodder yield and 11 associated traits in 69 oat genotypes. They found the highest heritability (66%) for days to 50% panicle emergence and the greatest genetic progress as a percentage of the mean for dry fodder production (29.18). All the traits displayed extensive variability.

Naeem *et al*. (2007) assessed the fodder yield potential of seventeen oat cultivars, noting significant differences in plant height, number of tillers per meter, leaf area, and green fodder output among the cultivars.

Bahadur and Chaubey (2008) discovered significant diversity in all of the traits. In almost all traits, the magnitude of the genotypic coefficient of variation was relatively close to the estimates of the phenotypic coefficient of variance. Almost all of the features, including quality variables, had strong heritability, but genetic progress was moderate for green and dry fodder yield/plant.

Feyissa *et al.* (2008) evaluated 20 oat varieties and discovered that various variations had significant variances in the proportion of morphological components at different growth stages. Using the physiological maturity for forage harvest of the soft dough stage as a guide, the oats varieties PI - 5800, CI - 8251, and Grayalgeris were found to have a higher proportion of leaf in their dry matter (DM) than the other varieties, while the oats varieties PI - 244480, SRCP X 80 Ab 2291, and SRCP X 80 Ab 2806 had a comparatively higher proportion of stem. The results revealed significant varietal differences in the proportion of morphological fractions, indicating the possibility of enhancing oat forage production through proper exploitation of the varietal differences.

Singh and Singh (2010) observed PCV estimations outperformed GCV estimates for every attribute. This proved that the characters' expressiveness was influenced by their environment. The GCV estimates for plant height, tillers per plant, dry matter output, and green fodder production were all high. However, the dry matter percentage only reached moderate values. Days to blooming, crop length, and L/S ratio had low GCV projections. Significant GCV, heritability, and genetic progress were observed for dry matter yield, green fodder productivity, green fodder yield, tillers per plant, and plant height, indicating that additive gene effects dominated in determining these attributes. These characters could be effectively used in selection as a result of such selection.

Kapoor *et al.* (2011) observed strong variability for various parameters, including internode length (cm), number of tillers per plant, flag leaf length (cm), plant height (cm), axis length (cm), number of axis branches, number of seeds per panicle, and seed yield (g/plant). High GCV and PCV estimates were found for internode length, number of tillers per plant, axis branch number, number of seeds per plant, and seed yield per plant, indicating substantial genetic variation in these traits.

Bibi *et al*. (2012) assessed 138 oat genotypes, including five controls and discovered that the number of tillers per meter row had the highest genetic variance, phenotypic variance, GCV, and PCV, while the number of leaves per plant had the lowest.

Sofi *et al.* (2012) discovered that the range of variation was high in parameters such as seed yield per hectare, seed width, tillers per m2, seed length, and green fodder production, as indicated by higher C.V. percent values. Except for days to maturity, all features had higher PCV and GCV values. Heritability (b.s.) estimations were usually high for all variables, ranging from 79.236 percent for seed length to 97.228 percent for tillers per m2. Genetic gain was high for all variables, particularly seed yield per hectare, tillers per m2, seed width, seed length, and green fodder output per hectare.

Chandan *et al.* (2013) examined 32 oat accessions to assess genetic variance, heritability, and genetic progress. GCV was highest for traits like flag leaf length and leaf length at the 50% heading stage, followed by grain yield, harvest index, straw yield, growth rate, and panicle length at maturity. Traits like panicle length, leaf length, straw yield, number of leaves, leaf width, and number of tillers were also highly heritable.

Krishna *et al.* (2013) investigated the genotypic and phenotypic coefficients of variation for various oat traits. Dry matter yield and spikelets per panicle exhibited a large magnitude of genotypic and phenotypic coefficients of variation, indicating substantial genetic and phenotypic variability for these traits. The number of tillers per plant, stem girth, leaf area, and green fodder output had a moderate level of genotypic and phenotypic coefficient of variation. Some traits like the number of leaves, leaf length, leaf breadth, spike length, and 1000 seed weight also showed heritability, indicating a genetic component in their expression.

Kumari *et al.* (2013) investigated trait correlation and path analysis for grain yield in oat in the western zone of Tamil Nadu. The estimates of genotypic coefficient variation (GCV) and phenotypic coefficient variation (PCV) were high for the number of basal tillers per plant, productive tillers per plant, and grains per panicle. The broad sense heritability estimates for various variables ranged from 71% to 96%. The traits with the highest heritability and genetic progress were found to be number of productive

tillers per plant (86.00 and 85.06%), number of grains per panicle (92.00 and 64.87%), and panicle length (96.00 and 37.23%).

Ahmad *et al.* (2013) conducted experiment with ten oat genotypes and and their 45 F1 crosses observed the variability present for different parameters like chlorophyll content, LAI, green fodder yield, crude protein, crude fibre, ash content and seed yield.

Dubey *et al.* (2014) examined 34 genotypes and discovered a significant amount of variation in leaf area, axis length, and crude protein yield, followed by leaf area, total dry matter content, and total green fodder yield.

Bind *et al*. (2016) discovered that the level of PCV for all characters was greater than that of GCV, demonstrating the importance of environment in character expression. Seeds per panicle, dry matter yield per plant, green fodder yield per plant, and harvest index all had high GCV and heritability, as well as high genetic advance as a percentage of mean, indicating that these four traits may be under the control of additive gene effects and thus more accurate for efficient selection.

Jaipal and Shekhawat (2016) investigated oat genetic diversity for green fodder and grain output. Tillers per metre row length, leaf:stem ratio, seed index, straw yield (q/ha), and green fodder yield (q/ha) all had strong heritability and genetic progress.

Premkumar *et al* (2017) observed that GCV, PCV were high for grain weight per panicle, single plant grain weight, harvest index and single plant kernel weight.

Kumar *et al.* (2018) investigated the fodder and grain yield performance of six oat genotypes in Leh's cold, arid climate. There were significant differences in plant height, number of tillers per plant, and fodder yield among all oat varieties, according to the data.

Sabreena *et al.* (2018) discovered substantial differences in genotypes for all of the traits investigated. GCV and PCV estimates were high for grain yield quintal per hectare, culm diameter (mm), green fodder yield quintal per hectare, inflorescence length (cm), seeds per panicle (g), and seed yield per plant. Almost all of the characters have high heritability and genetic progress.

Wagh *et al.* (2018) discovered that the leaf/stem ratio and green forage production had high GCV and PCV values, but the dry matter content and number of leaves per tiller had low values. In forage oat plant height, number of tillers per metre row length, leaf length, leaf width, leaf/stem ratio, stem thickness, and green forage production, they also demonstrated strong heritability and genetic advancement.

Zeki *et al.* (2018) examined local oat cultivars of 25 oat genotypes' grain production and quality features and observed that Genotype, environment and genotype× environment interaction had highly significant effects on grain yield and quality traits.

Chauhan and Singh (2019) discovered highly significant differences between genotypes for all characteristics, the study found highly significant differences between genotypes for all characteristics. Traits such as the number of leaves per plant, number of tillers per plant, leaf stem ratio, and green fodder yield per plant exhibited the highest genotypic and phenotypic coefficients of variation, with values exceeding 25%. Traits, including the number of leaves per plant, leaf area, plant height, number of tillers per plant, stem girth, number of green pods per spike, spike length, and green fodder yield per plant, displayed high heritability and genetic advance as a percentage of the mean.

Sahu and Tiwari (2020) examined the genetic and phenotypic coefficients of variation (GCV and PCV) for the days up to 50% flowering, green forage yield, and dry matter yield. And found that green forage yield exhibited the highest genetic advance, while dry matter yield also showed a significant genetic advance as a percentage of the mean.

Vanjare *et al.* (2021) examined forty-four forage oat genotypes and discovered a wide range of variability in plant height, days to 50% flowering, leaf length, leaf width, and dry matter. The traits leaf:stem ratio, leaf width, green forage yield, stem girth, plant height, leaf length, number of leaves/tiller, and number of internodes/tiller had high heritability estimates and a high genetic advance percent of mean, indicating that additive gene action is at work and that direct selection for such traits is beneficial in crop improvement.

2.3 Correlation

Knowledge of one or more yield-related characteristics is useful in selecting the individual in crop improvement. Correlation coefficients quantitatively elaborate this link between plant characteristics.

Estimates of correlation coefficient are measurements of association between characters and give essential information in identifying characteristics that have little or no value in the selection programme.

Chaubey *et al*. (2001) analysed that green fodder yield was significantly related to tiller number (0.61), plant height (0.43 cm), leaf width (0.43 cm), and dry fodder yield (0.80 g).

Shankar *et al.* (2002) discovered that GFY was positively and strongly linked with Days to floweing, and Grain weight. Positive and substantial associations of GFY with L:S and DMY were also identified, as was a negative but significant correlation of GY with GFY and L:S.

Kumar *et al*. (2004) found that plant height, number of leaves and number of tillers per plant, flag leaf length and width, longest leaf length and width, stem thickness, longest internode length, and dry matter yield per plant were all highly and positively correlated.

Mall *et al.* (2005) discovered that tiller number, grain number, dry matter yield, and harvest index were all highly and positively linked with grain production. Green fodder yield, dry matter yield, harvest index, and green yield were all highly and positively linked with tiller number. Grain number/panicle and dry matter were also found to be associated with green fodder yield and dry matter yield per plant.

Gautam *et al.* (2006) observed that GFY had a strong positive correlation with tillers per plant and grain yield per plant. Grain yield was positively related to tillers per plant, flag leaf length, green fodder production, and dry matter yield.

Bahadur *et al.* (2008) studied plant height, stem diameter, number of leaves per plant, leaf length, and leaf width have been positively and significantly correlated with green and dry fodder yield.

Bukhari *et al.* (2009) discovered that parameters such as days to 50% blooming, plant height (cm), number of tillers (sq^{-1}), green fodder yield (q ha^{-1}), dry fodder yield (q ha^{-1}), LAI, L:S ratio, and crude protein all have an important influence on the production potential of fodder oats.

Kapoor *et al.* (2011) analyzed that trait such as leaf number, length of internode (cm), flag leaf width (cm), axis length (cm), axis branch number, and number of seeds per panicle showed positive and significant correlations with seed yield at both the genotypic and phenotypic levels.

Bibi *et al*. (2012) found significant associations between various traits and green fodder yield. Inter nodal length, leaf area, tiller count, and dry matter yield exhibited positive correlations with green fodder production. On the other hand, days to 50% flowering, days to 50% maturity, and plant height showed negative and non-significant correlations with green fodder yield

Sofi *et al.* (2012) stated that green fodder per hectare was significantly related to plant height and tillers per m^2, whereas seed output per hectare was significantly related to seed width, 1000-seed weight, plant height, and seed length.

Amanullah *et al* (2013) analysed Shoot:root ratio, dry matter partitioning, growth analysis, and water use efficiency of oat (Avena sativa). The increase in total dry matter accumulation per plant showed positive relationship with absolute growth rate (AGR), crop growth rate (CGR), and net assimilation rate (NAR).

Amanullah *et al* (2013) studied on forage oat and observed that The NAR had negative relationship with increase in LAI and positive relationship with increase in CGR.

Krishna *et al.* (2014) stated that green fodder output was positively linked with the majority of the parameters tested with the exception of the number of leaves and stem girth. Plant height and leaf length had the most positive correlations with the most attributes evaluated.

Dubey *et al*. (2015) discovered that total green fodder yield was highly significantly and positively correlated with chlorophyll content, followed by dry matter

yield per day, number of tillers plant per plant, number of leaves per plant, number of spikelets per panicle, and panicle weight at both genotypic and phenotypic levels, indicating that these attributes primarily influenced green fodder yield.

Premkumar *et al* (2017) observed that single plant kernel weight showed significant positive corelation with no of tillers per plant, no of grains per panicle, kernel weight per panicle, single plant grain weight and green fodder yield.

Atman *et al.* (2018) investigated the amount of correlation between yield and quality characteristics, as well as their consequences, in 92 genotypes of multi-cut Oat. Plant height, number of tillers per plant, germination percentage, seed vigour index-I, and green fodder yield had positive and significant genotypic and phenotypic correlations of dry matter yield per metre row length in the first cut of multi-cut, while in the second cut, plant height, number of tillers per plant, germination percentage, seed vigour index-I, and green fodder yield had positive and highly significant genotypic and phenotypic correlations.

Wagh *et al*. (2018) stated green forage yield was substantially and positively linked with the number of tillers per metre row length, crude protein content, stem thickness, leaf breadth, plant height, and number of leaves per tiller.

Sahu and Tiwari (2020) studied fourteen genotypes of fodder oat (*Avena sativa* L.) to assess the genetic variability and association analysis and discovered that green fodder output was positively connected with the majority of the variables evaluated, with the exception of days to 50% blooming and plant height (cm).

MATERIALS AND METHODS

The present investigation entitled “Association of morpho-physiological traits with forage yield and quality in single cut oat” was carried out at experimental site of All India Coordinated Research Project on Forage Crop & Utilization, Odisha University of Agriculture and Technology, Bhubaneswar during November 2022 to March 2023.

3.1 Experimental site

Location

The experimental site is situated inside the farm of AICRP on Forage crop & Utilization, Odisha University of Agriculture and Technology, Bhubaneswar which is located at $20^0$15’ N latitude and $85^0$52’ E longitude with an altitude of 25.9 meter above mean sea level. The experimental site is situated at a distance of 8 km from the university headquarters on the site of Bermunda.

Climate and weather condition

The experimental site is located in a subtropical climate. It is approximately 64 kilometers east of the Bay of Bengal. It has a warm and humid climate with humid summers and mild winters. Bhubaneswar's climate generally falls into the moist and hot category.

Experimental design

The experiment was designed with a Randomized Block Design (RBD) and three replications. The experiment included 22 genotypes.

Experimental materials

In the present study twenty-two single cut genotypes were used. The list of different genotypes is furnished below.

Table 3.1 List of genotypes

SL NO	GENOTYPE	SOURCE
1	HFO-1013	CCS, HAU, HISAR
2	JO-7-28	JNKVV, JABALPUR
3	OL-1977	PAU, LUDHIANA
4	OS-403	PAU, LUDHIANA
5	SKO244	SKVAST-K, SRINAGAR
6	OL-1980	PAU, LUDHIANA
7	HFO-1009	CCS, HAU, HISAR
8	KENT(NC)	CCS, HAU, HISAR
9	JO-08-37	JNKVV, JABALPUR
10	HFO-1003	CCS, HAU, HISAR
11	HFO-1221	CCS, HAU, HISAR
12	JO-09-14	JNKVV, JABALPUR
13	SKO-246	SKUAST, SRINAGAR
14	HFO-1211	CCS, HAU, HISAR
15	UPO 22-2	GBPUAT, PANTNAGAR
16	0S-6(NC)	RAHURI
17	OL-2000	PAU, LUDHIANA
18	HFO-718-1	CCS, HAU, HISAR
19	OL-1964	PAU, LUDHIANA
20	OL-1821(NC)	PAU, LUDHIANA
21	OL-1976-1	PAU, LUDHIANA
22	UPO 22-1	GBPUAT, PANTNAGAR

Experimental details

Year of planting : Rabi-(2022-23)

Date of planting : 24/11/2022

Crop : Oat

Design : RBD

No. of genotypes : 22

No. of replications : 3

Total no of plots : 66

Plot size : 3m × 3m accommodating 3m long 10 rows at 30 cm

N

R1			R2			R3	N
HFO 1221	JO-09-14		OS-6 (NC)	KENT(NC)		UPO22-1	HFO 1013
HFO 1003	SKO 246		SKO 244	OL 1977		OL19761	JO-7-28
JO 08-37	HFO 1211		HFO 1003	OL 1980		OL1821(NC)	OL 1977
KENT(NC)	UPO 22-1		OS 403	HFO 1013		OL 1964	OS 403
HFO-1009	OS-6 (NC)		JO 08-37	HFO 1009		HFO718-1	SKO 244
OL1980	OL -2000		JO 09-14	HFO718-1		OL -2000	OL1980
SKO 244	HFO718-1		OL 1964	OL 1976-1		OS-6 (NC)	HFO-1009
OS 403	OL-1964		UPO 22-1	SKO 246		UPO 22-1	KENT(NC)
OL 1977	OL 1821(NC)		OL1821(NC)	JO-7-28		HFO 1211	JO 08-37
JO-7-28	OL 1976-1		HFO 1211	HFO1211		SKO 246	HFO 1003
HFO 1013	UPO 22-1		SKO 244	OL 2000		JO-09-14	HFO 1221

Fig. 3.1 Experimental plan layout

Fig. 3.2 View of experimental field

Details of field operations

Field preparation

To prepare the soil for sowing, one cross cultivation with a tractor-drawn cultivator was performed, followed by two harrowings before seeding. The trial field was laid out according to the layout plan. Following the layout of the plan, prepare the 25 cm high hills to maintain a row to distance of 30cm and a plant to plant distance of 5cm.

Sowing:

Sowing of the seeds was done on 24th November, 2022 in line sowing method. After sowing, the seeds were covered properly with soil, so that the seed may come in contact with the soil.

Irrigation

First irrigation was given immediately after sowing for uniform germination. Subsequently A subsequently at 10-15 days intervals depending on depending on soil moisture content and important phonological stages of crop.

Harvesting

Harvesting was done when plants were at 50% flowering stage. 50% plants were harvested for green fodder and rest 50% were left for seed yield.

Observation recorded

The observations were recorded on following parameters which are described below.

Growth parameters

Plant height (cm)

At 50% flowering, plant height was measured in centimeters. Using a meter scale, measure from the base of the plant to the tip of the plant.

Number of tillers

The number of tillers that sprouted from the main stem of each tagged plant was counted, and the average of five plants was calculated.

Fig. 3.3 Measuring plant height

Fig. 3.4 Weighing green forage

Days to 50 per cent flowering

The number of days between the date of sowing and the day on which 50% of the plants bloomed.

Number of leaves per plant

The number of leaves on each tagged plant was counted across all genotypes, and the mean of five plants from each genotype was calculated.

Internodes length (cm)

The tiller internode lengths of the five observational plants were measured and recorded in each replication, and averages were calculated.

Leaf length (cm)

The length of the leaf was measured in centimeters along the midrib of the third leaf from the top of the selected tiller. The length of the flag leaf was also measured.

Leaf width (cm)

Leaf width was measured in centimeters at the leaf's widest point. This observation was made on the same leaf that was used for leaf length. The width of the flag leaf was also measured.

Leaf/stem ratio (g)

A fixed amount of plant sample was taken from each plot to calculate the leaf to stem ratio. The stem and leaves were separated. The ratio was calculated by dividing the weight of the green leaf sample by the weight of the green stem.

The leaf/stem ratio was calculated by using the following formula,

$$\text{L/S ratio} = \frac{\text{Weight of the leaf (g)}}{\text{Weight of the stem (g)}}$$

Leaf area (cm^2)

Leaf area of randomly selected five plants was measured with the help of measuring scale in centimeter by taking the width of leaf blade while leaf length was taken from base to tip of the leaf.

Leaf area = Leaf length × Leaf width × Correction

factor Correction factor = Actual area / Calculated area

Leaf area index (LAI)

The assimilatory surface area (A) was measured in five plants at random from each genotype and replication. LAI is the leaf area (A) or the assimilatory area of the surface over a given ground area (P) as calculated by Watson (1952).

LAI=A/P

where,

A= Leaf area

P= Ground area

Crop growth rate (CGR)

Crop growth rate is defined as the increase in dry weight of plant per unit area of land per unit change in time and expressed as $gm^{-2}day^{-1}$.

$$CGR= \frac{W2-W1}{T2-T1}\times\frac{1}{P}$$

Where, W1= Weight of dry matter (g) at time T1

W2= Weight of dry matter (g) at time T2

T2-T1=Time interval in days

P = Ground area

Relative growth rate (RGR)

Relative growth rate ($g\ g^{-1}day^{-1}$) is the rate of increase in dry weight per unit dry weight per unit time (Radford,1967).

$$RGR= \frac{\ln W2-\ln W1}{T2-T1}$$

Where, W1 = Dry weight of the whole plant at the start of the test period

W2 = Dry weight of the whole plant at the end of the test period

(T2 -T1) = Period in weeks between the initial and final observation

Dry matter % of plant

Plants from each replication were collected and thoroughly washed and shade dried until all the moisture was gone. Then plants were kept in hot air oven at 70^0C for 48 hours and then dry weight is measured.

$$\text{Moisture in sample (\%)} = \frac{\text{Wt of sample} - \text{Wt of dried sample}}{\text{Wt of sample}} \times 100$$

Wt of sample after drying

$$\text{Dry matter \% in sample} = \frac{\text{Wt of dried sample}}{\text{wt of sample}} \times 100$$

Biochemical analysis

Determination of chlorophyll content

The quantification of chlorophyll content in the leaves was done through the use of the acetone extraction method, as originally outlined by Arnon in 1949. The leaf placed immediately below the apex of the plant was chosen for the purpose of sampling. In order to mitigate desiccation, the leaf samples were promptly enclosed in polythene bags to preserve their moisture content. A leaf, weighing 100mg, was selected and minute sections were excised from the central region of the leaf. The leaf fragments were immersed in falcon tubes filled with 10ml acetone solution with a concentration of 80% (V/V). The falcon tubes were effectively sealed with their respective lids in order to prevent any potential light exposure. Subsequently, the falcon tubes, containing the leaf samples immersed in acetone, were placed within a light-restricted setting for a duration of 24 hours. Consequently, the chlorophyll was successfully extracted into the acetone solution. Following a 24-hour incubation period, the chlorophyll extracts underwent filtration using Whatman's No.1 filter paper in order to eliminate any solid particles or plant debris. The filtrate, which contained the extracted chlorophyll, was utilized for spectrophotometric examination. Measurements of absorbance were recorded at three distinct wavelengths: 645nm, 663nm, and 480nm. A solution consisting of 80% acetone was used as a blank reference.

Total Chlorophyll =

$$(20.2 \times \text{O.D at } 645 + 8.02 \times \text{OD at } 663) \times V/1000 \times 1/W \text{ mgg}^{-1} \text{ fresh tissue}$$

Where, V=Volume of 80% acetone (ml)

W=Weight of leaf sample(g)

Estimation of crude protein content

0.3 grams of finely powdered plant sample that had been dried in an oven were placed into the digestion tubes. A digestion mixture consisting of 10 grams of anhydrous potassium sulphate (in a ratio of 10 parts), copper sulphate (in a ratio of 4 parts), and 1 gram of selenium powder was prepared. Additionally, 10 milliliters of concentrated sulfuric acid (H_2SO_4) were added to the mixture. The digestion tubes containing the combination were then placed in the SS insert rack. Following a duration of approximately one hour, the tubes were subjected to a heating process commencing at an initial temperature of 100^0C, subsequently elevated to 350 C till the occurrence of foaming. In order to assess the bubbling two pieces of sodium thiosulphate crystals were introduced into each digestive tube. The digestion procedure, which entailed the application of heat and the addition of sulfuric acid, repeated until the contents of the digestion tubes achieved perfect clarity, resulting in the transformation into a viscous blue liquid devoid of any observable a bubbling effect The tube followed a cooling process, following which the contents were diluted with 50 ml of distilled water. Subsequently, a volume of 10 ml of the diluted sample extract was placed into a Micro-kjeldahl distillation unit. The digesting flask performed two rounds of washing using distilled water, and thereafter, the water was transported to the distillation unit. Subsequently, a solution consisting of 4% boric acid with mixed indicator and 40% NaOH was added into each of the reserve tanks. Subsequently, the samples were distillation for a duration of 6 minutes. Following the conclusion of the distillation process, the resulting distillate was subjected to titration using a standard solution of H2SO4 (0.1N) until the appearance of a wine red colour.

Calculation:

$$\text{Percent N content in sample} = \frac{\text{TV} \times \text{ N of H2SO4} \times 0.014}{\text{sample weight}\left(\text{gm}\right)} \times 100$$

Where, N=Normality of H_2SO_4

TV = Titrate value

Crude protein content (%)

Protein content of plant sample was determined by estimating the nitrogen content as per the modified Kjeldhal's method (Jackson, 1967) and multiplying the

nitrogen content with a factor 6.25 (Dubetz and Welis, 1968) and expressed on per cent basis for each genotype.

Determination of Phosphorus content in plant sample by Vanadomolybdo-phosphoric acid yellow colour method.

A quantity of 1 gram of finely powdered plant sample that had been dried in an oven was placed into a conical flask with a volume of 150 milliliters. A volume of 10 milliliters of a ternary acid combination consisting of concentrated nitric acid, concentrated sulfuric acid, and concentrated perchloric acid in a ratio of 5:1:2 was introduced into the sample. The mixture was subjected to a gradual pre-digestion process for a duration of 15 minutes on a hotplate. Subsequently, the temperature of the hot plate was incrementally increased until the solution within the conical flask achieved clarity, accompanied by the formation of a white fume ring encircling the flask. The specimen was subjected to a cooling process prior to its transfer into a 50ml volumetric flask containing 30ml of distilled water. The digested sample was subjected to filtration using Whatman No. 42 filter paper, and the resulting filtrate was retained for the purpose of estimating the concentration of potassium (K). The filtrate was subjected to spectrophotometric analysis in order to determine the absorbance at a wavelength of 640nm.

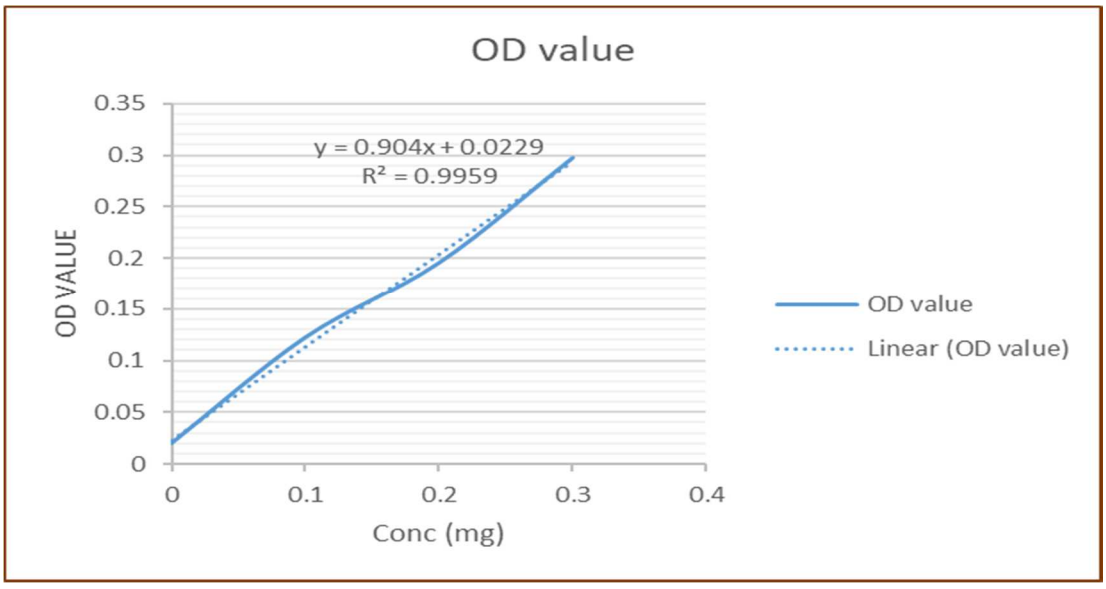

Fig. 3.5 Standard curve for phosphorus

Estimation of potassium content in plant sample by flame photometry method (by digesting through tri-acid or di-acid mixture)

A 1ml of the digested sample extract was transferred into a 25ml volumetric flask, and the final volume was adjusted to 25ml using distilled water. The utilization of a flame photometer is employed to get measurements for both standard solutions and test samples. The K content of the plant sample was subsequently determined by employing standard curve data.

Determination of Ash content

Crucibles were dried in hot air oven and weight of crucible (without sample) were taken. 2-5g of dried sample were weighed and kept these in crucibles. Crucibles are placed in the muffle furnace at temperature 550^0c for 6 hours. After all the materials are brunt leaving white ash cooled it in a desiccator and weighed.

$$\% \text{ Total ash} = \frac{(\text{Wt of empty crucible} + \text{ash}) - \text{Wt of empty crucible}}{(\text{Wt of empty crucible} + \text{sample}) - \text{Wt of empty crucible}} \times 100$$

Green forage yield and seed yield:

Green forage yield (kg)

Plants are harvested at the 50% flowering stage and the weight was recorded. Total green forage yield (kg) per plot was measured in kg

Panicle length (cm)

At the peak flowering stage, the length of five randomly selected panicles was measured in centimetres

100 Seed weight (g)

The seeds of all five randomly selected plants were mixed, and 100 seeds were randomly selected and weighed from this set.

Seed yield per plant (g)

Seeds of individual plants were collected and measured the weight in gram.

Statistical analysis

Assessment of variability

a. Analysis of variance

The data obtained on each character were subjected to the analysis of variance method, which is commonly used in the randomized block design. (Panse and Sukhatme, 1985).

$$Yij = \mu + Gi + Rj + Eij$$

Where,

i= 1, 2, 3.....G

j= 1, 2, 3.....R

Yij = Observation on i^{th} genotype in j^{th} replication

μ= General mean

Gi =Effect of i^{th} genotype

Rj =Effect of j^{th} replication

Eij = Random error associated with Yij observation

ANOVA TABLE

Source	**d.f.**	**m.s.**	**Expected m.s.**
Replication	r-1	RMS	$б^2e + gб^2r$
Treatment	g-1	GMS	$б^2e + rб^2g$
Error	(r-1)(g-1)	EMS	$б^2e$

Where,

r = Number of replications

g = Number of genotypes

$б^2g$ = Variance due to genotypes and

$б^2e$ = Variance due to error

The genotype mean square (GMS) was tested against error mean square (EMS) by 'F' test for n1 = (g-1) and n2 = (r-1) (g-1) degrees of freedom,

where,

g = number of genotypes and

r = number of replications. The characters showing significant differences were subjected to further analysis.

b. Estimation of S.E. and C. D.

S.E. of mean (S.Em) = $\sqrt{\sigma^2}_{e/r}$

C.D. = t at error d.f. × S.E.m × $\sqrt{2}$

c. Estimation of mean and range

The mean values for each of the characters were calculated by dividing the total by the number of observations:

$$X = \frac{1}{n}(\sum_1^n Xi)$$

Where, X = Mean of character

$\sum X_i$ = Total of all the observations for character

N = Number of observations

Estimation of components of variation

The phenotypic and genotypic variances were calculated as follows.

Environmental variance ($\sigma^2 e$) = EMS

Genotypic variance ($\sigma^2 g$) = $\frac{GMS - EMS}{r}$

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications

Estimation of coefficient of variation

Burton (1952) employed this method to calculate the genotypic and phenotypic coefficients of variation.

i. Genotypic coefficient of variation (GCV)

GCV (%) = $\frac{\sigma 2g}{X} \times 100$

Where,

$\sigma^2 g$ = Genotypic variance and,

X = Mean of character

ii. Phenotypic coefficient of variation (PCV)

$$PCV\ (\%) = \frac{\sigma 2p}{X} \times 100$$

Where,

σ^2p = Phenotypic variance and,

X = Mean of character

The high, medium and low GCV and PCV estimates were classified as:

Low: 10 per cent

Medium: 10 to 20 per cent

High: > 20 per cent

Estimation of heritability (b.s.)

Hanson et al. (1956) suggested estimating heritability in a broad sense.

$$h^2\ (b.s.) = \frac{\sigma 2g}{\sigma 2p} \times 100$$

Where,

h^2 = Heritability

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

The high, medium and low heritability estimates were classified on the basis of values given by Johnson et al., (1955).

Low heritability = < 10 %

Moderate heritability = 10-30 %

High heritability = > 30 %

Genetic advance (G.A.)

The genetic advance (at 5% selection intensity) was calculated using Allard's (1960) formula.

i. Genetic advance (G.A.)

$$G.A. = k \times \frac{\sigma 2g}{\sigma 2p} \times \sqrt{\sigma^2 p}$$

Where,

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

k = Selection differential (at 5 % selection = 2.06)

$\sqrt{\sigma^2}p$= Phenotypic standard deviation

ii. **G.A. as percentage of means** (GAM)

$$GAM = \frac{GA}{X} \times 100$$

Where,

G. A.= Genetic advance

X = Character mean

GA (As percentage of mean) was classified as

Low: 10 per cent

Medium: 10 to 20 per cent

High: > 20 per cent

Correlation

Analysis of covariance was performed out by taking two characters at a time. The genotypic covariance was calculated according to Johnson et al., (1955), as shown below:

Source	d.f.	m.s.	Expected m.s.	Expectation of mean sum of product
Replication	r-1	RMS	$б^2e + gб^2r$	$COV_{e1.2} + {}_gCOV_{r1.2}$
Treatment	g-1	GMS	$б^2e + rб^2g$	$COV_{e1.2} + {}_rCOV_{g1.2}$
Error	(r-1)(g-1)	EMS	$б^2e$	$COV_{e1.2}$

Environmental covariance (COV. $_{e1.2}$) = EMP

Genotypic covariance (COV. $_{g1.2}$) = $\frac{GMP - EMP}{r}$

Phenotypic covariance (COV. $_{p1.2}$) = (COV. $_{g1.2}$) + (COV. $_{e1.2}$)

Where,

GMP = Genotypic mean sum of product

EMP = Error mean sum of product

r = Replication

For calculating phenotypic and genotypic correlation coefficients, appropriate variances and covariances were used (Johnson et al., 1955).

The phenotypic correlation coefficient (rp) was calculated as

$$r_{p1.2} = \frac{COV.p1.2}{\sqrt{(\sigma 2p1).(\sigma 2p2)}}$$

Where,

$r_{p1.2}$ = Phenotypic correlation coefficient between character 1 and 2

$COV._{p1.2}$= Phenotypic covariance between character 1 and 2.

σ^2_{p1}, σ^2_{p2}= Phenotypic variance of character 1 and 2 respectively.

The significance of the phenotypic correlation coefficient was assessed using the Fisher and Yates (1943) formula.

The genotypic correlation coefficient (rg) was calculated as:

$$r_{g1.2} = \frac{COV.g1.2}{\sqrt{(\sigma 2g1).(\sigma 2g2)}}$$

Where,

$r_{g1.2}$= Genotypic correlation coefficient between character 1 and 2

$COV._{g1.2}$=Genotypic covariance between character 1 and 2

σ^2_{g1}, σ^2_{g2} = Genotypic variance of character 1 and 2 respectively.

The significance of correlation coefficients was tested from the statistical table of correlation coefficient at 1 and 5 per cent level of significance (Snedcor and Cochran, 1967).

RESULTS

The present research involved the evaluation of twenty-two different fodder oat genotypes in the coastal plain zone of Odisha. Enhancement of forage productivity only by phenotypic selection is unattainable due to the polygenic nature and limited inheritance of this trait. Therefore, it would be most suitable to choose a method of selection that involves a correlated response and takes into account different contributing aspects. Given the complex nature of yield as a feature and its dependence on other traits, it becomes crucial to identify the morphological and physiological characteristics that are correlated with yield. This knowledge is essential for the purpose of selecting genotypes that exhibit high yield potential. The present investigation was carried out at AICRP on Forage Crops & Utilization, OUAT, Bhubaneswar. Different physiological parameters like CGR, RGR, leaf area index, dry matter content, chlorophyll content was correlated with green forage yield along with some morphological traits. The data were analysed and the results were presented under following sections.

4.1 Analysis of variance for morphological and physiological traits

4.2 Performance of oat genotypes for morpho-physiological and nutritional quality parameters

4.3 Estimates of genetic parameters for morphological and physiological traits

4.4 Association of morphological and physiological traits with green forage yield

4.5 Identification of oat genotype having high green forage yield and better nutritional quality

4.1 Analysis of variance for morphological and physiological traits

The variance analysis for morphological and physiological characteristics is presented in Table 4.1. The degrees of freedom for the genotype and error were 21 and 42, respectively. Significant variations were noted within the genotypes with regards to all the investigated characteristics, except the RGR. The green forage yield had the highest mean sum of square error (69.734), followed by plant height (62.182)

and seed yield (60.633). Significant findings were observed for leaf length, flag leaf area, and crude protein percentage, with significant results observed at both the 5% and 1% probability levels.

Table 4.1 Analysis of variance for different traits of oat genotypes

Character	Degrees of freedom		Mean sum of square	
	Genotype	Error	Genotype	Error
Plant height (cm)	21	42	1042.183*	62.182
Days to 50% flowering	21	42	445.991*	16.727
Internode length (cm)	21	42	16.294*	1.081
Number of tillers per plant	21	42	2.15*	0.148
Leaf length (cm)	21	42	160.137**	11.473
Leaf breadth (cm)	21	42	0.316*	0.02
Leaf Area	21	42	1281.8*	47.849
Leaf Area Index	21	42	0.165*	0.02
Number of leaves per plant	21	42	16.285*	0.747
Leaf to Stem Ratio(L:S)	21	42	0.014*	0.002
CGR	21	42	64.406*	1.547
RGR	21	42	0.005	0.005
GFY per plant (g)	21	42	1061.547*	69.734
Flag leaf length (cm)	21	42	96.148*	4.119
Flag leaf area (cm2)	21	42	689.263**	17.972
Panicle length (cm)	21	42	40.445*	8.371
100 seed weight (g)	21	42	0.616*	0.046
Seed yield per plant (g)	21	42	5316.147*	60.633
Crude protein (%)	21	42	7.127**	0.268
Dry matter (%)	21	42	33.387*	5.409
P- content(%)	21	42	0.02*	0.003
K- content(%)	21	42	0.15*	0.02
Ash content(%)	21	42	8.65*	0.31
Total chlorophyll content	21	42	1.541*	0.123

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

4.2 Performance of oat genotypes for morpho-physiological traits and nutritional quality parameters

4.2.1 Morpho-physiological traits

Mean performance of single cut oat genotypes in respect of different morpho-physiological traits is presented in Table 4.2.

Plant height (cm)

Plant height of the genotypes varied from 93.35cm to 174.63 cm with a mean of 144.13 cm. The tallest height was recorded in OS-403 (174.63cm). It was at par with genotype OL-1821(169.46 cm), OL-1976-1 (165.24 cm), OS-6 (171.20 cm)

Days to 50% flowering

Days to 50% flowering ranged from 65 days in HFO-1013 genotype to 112 days in SKO-244 genotype with an overall mean value of 81.09 days. In this study HFO (65 days) and OS-6 (NC) (67 days) had earlier flowering. 50% flowering was late in variety SKO -244 (112 days).

Internode length (cm)

The overall mean of internode length was 14.18 cm with a range of 9.72 cm to 17.40 cm. The lowest internode length was measured in genotype OL-2000 whereas the highest in genotype OS-6 (NC). Seven genotypes were at par with the tallest variety.

Tillers per plant

Number of tillers per plant varied among the genotypes from 2.42 to 5.28 with a mean value of 3.82. The highest number of tillers per plant was observed in UPO-22-1 followed by KENT (5.17) and SKO-244(4.98) respectively.

Leaf Length (cm)

Leaf length of the genotypes varied from 37.07 cm to 60.33 cm with a mean value of 48.76 cm. The highest leaf length was observed for SKO -244 (60.33 cm) followed by JO-09-14 (57.40 cm), OS-6 (57.33cm) and HFO -718-1 (56.53cm) and lowest was measured in genotype JO-07-28 (37.07cm).

Leaf breadth (cm)

Leaf breadth varied from 1.37 cm to 2.85 cm. The highest leaf breadth was observed for OS-403 (2.85) followed by OL-1821 (NC) (2.31cm), OL-1976-1 (2.15cm), HFO-1013 (2.12cm).

Leaf Area (cm^2)

Leaf area ranged from 58.81 cm2 to 147.10 cm2 with an overall mean value of 82.68 cm^2. The highest leaf area was measured in OS-403 followed by in genotype OL-1821 (NC) (108.67 cm^2).

Table 4.2 Mean performance of single cut oat genotypes

Genotype	Plant height	Days to 50% flowering (days)	Internode length (cm)	Tillers per plant	Leaf length (cm)	Leaf breadth (cm)	Leaf area (cm^2)	LAI	No of leaf per plant	L:S	CGR	RGR	GFY (g)	Flag leaf length (cm)	Fag leaf area (cm^2)	Panicle length (cm)	100 seed wt. (g)	Seed yield (g)
HFO-1013	146.11	65	17.23	3.11	41.20	2.12	78.92	1.79	8.61	0.46	35.60	0.04	128.90	32.08	69.94	34.00	3.00	82.92
JO-7-28	136.66	67	16.60	3.50	37.06	1.93	65.06	1.72	8.31	31.77	37.20	0.05	94.64	31.77	71.40	27.87	2.43	60.64
OL-1977	144.08	84	16.24	3.93	45.13	2.05	83.66	1.69	9.11	0.49	23.60	0.04	112.50	32.05	78.51	34.63	2.30	132.21
OS-403	174.63	75	17.14	4.38	57.33	2.85	147.10	1.85	10.81	0.60	40.00	0.04	141.03	30.38	86.11	34.00	2.35	140.15
SKO244	122.54	112	14.38	4.98	60.33	1.80	103.88	1.49	9.93	0.44	20.80	0.03	93.90	30.70	54.8	34.95	1.67	39.71
OL-1980	153.16	73	15.88	2.53	55.26	1.65	82.29	1.65	9.92	0.37	27.60	0.05	98.48	24.54	45.17	33.63	2.55	136.31
HFO-1009	143.74	81	14.50	4.78	54.40	1.82	88.61	1.51	9.95	0.37	30.00	0.04	97.37	31.46	57.10	32.23	3.00	63.50
KENT(NC)	142.87	82	13.84	5.16	55.73	1.37	69.31	1.44	10.43	0.37	44.80	0.07	97.03	34.23	55.49	31.65	3.18	170.69
JO-08-37	133.90	77	12.98	2.41	57.40	1.80	90.09	1.35	10.38	0.48	34.40	0.05	94.67	30.10	61.78	33.27	1.80	94.07
HFO-1003	122.45	103	11.78	3.63	46.26	1.56	64.82	1.22	10.50	0.41	39.60	0.05	111.73	24.02	37.59	36.31	2.65	76.21
HFO-1221	131.94	83	12.96	3.81	43.13	1.59	61.60	1.35	10.37	0.42	34.00	0.04	82.90	29.91	47.36	32.47	2.77	70.20
JO-09-14	138.70	95	11.62	2.65	40.53	1.60	58.80	1.21	12.12	0.44	22.40	0.03	117.07	19.90	33.03	36.75	2.77	57.74
SKO-246	93.35	102	11.46	3.25	44.26	2.06	81.19	8.46	8.25	0.49	20.40	0.03	70.37	15.82	32.71	29.51	1.38	12.68
HFO-1211	151.31	76	16.08	4.8	41.33	1.76	65.86	1.67	9.49	0.46	19.60	0.03	88.73	20.43	39.14	35.34	1.71	59.58
UPO 22-2	160.53	74	14.22	3.81	41.33	1.66	64.77	1.48	11.46	0.43	19.20	0.03	110.60	18.70	35.18	35.50	2.60	170.78
OS-6(NC)	171.20	68	17.4	3.63	53.73	1.65	79.21	1.81	10.05	0.40	20.00	0.02	114.70	35.28	58.07	37.12	2.18	78.81
OL-2000	154.83	70	9.72	3.53	53.93	1.64	80.78	1.01	16.90	0.58	22.30	0.03	85.40	19.88	35.75	39.08	2.50	101.87
HFO-718-1	134.56	81	16.40	3.36	56.53	2.10	106.71	1.70	8.49	0.39	17.20	0.02	83.60	20.11	42.02	46.01	2.34	21.12
OL-1964	144.16	75	11.57	4.65	53.33	2.10	94.53	1.20	12.52	0.42	22.00	0.03	102.83	29.42	61.03	33.93	2.32	93.80
OL-1821(NC)	169.46	78	10.45	3.11	52.33	2.31	108.67	1.08	17.09	0.50	40.40	0.06	130.80	27.78	63.73	39.36	2.36	90.36
OL-1976-1	165.24	77	14.81	3.56	43.20	2.15	80.99	1.54	11.20	0.55	28.00	0.03	114.86	25.63	54.83	35.93	2.54	87.21
UPO-22-1	135.33	86	14.58	5.28	38.93	1.72	61.99	1.51	9.64	0.58	25. 60	0.03	68.33	24.30	44.55	36.17	2.70	75.84
Mean	144.13	81.09	14.18	3.82	48.76	1.88	82.62	1.41	10.71	0.46	27.16	0.04	101.84	26.75	52.97	34.99	2.41	87.11
CD (0.05)	12.99	4.09	2.85	0.63	7.43	0.33	10.92	0.83	2.74	0.06	4.66	0.003	25.98	3.27	9.83	4.77	0.35	19.79
CV	5.47	3.06	12.19	10.09	9.24	10.55	8.01	9.44	15.51	7.75	10.53	10.24	15.48	7.42	11.27	8.27	8.88	13.79

Leaf area index

Leaf area index of the genotypes ranged from 1.01 to 1.85 with an overall mean of 1.41. The lowest LAI is recorded in genotype OL-2000 whereas the highest in genotype OS-403.

Number of leaves per plant

The observed range of leaf numbers per plant ranged from 8.24 to 17.10, with an average value of 10.71. The genotype SKO-246 exhibited the lowest recorded number of leaves per plant, while the genotype OL-1821(NC) had the highest recorded number of leaves per plant.

Leaf- stem ratio (L:S)

Leaf-stem ratio of the genotypes ranged from 0.37 to 0.60 with a mean of 0.46. The highest L:S value was observed in genotype OS-403 (0.60) and it was at par with OL-1976-1(0.55), UPO 22-1(0.58), OL-2000 (0.58).

Crop growth rate (CGR) (g $m^{-2}day^{-1}$)

The CGR value of the genotypes ranged from 9.32 to 24.81 g/m^2/day with a mean of 17.53g/m^2/day at 30-45 DAS. At 30-45 DAS the highest value was observed in OL-1964 (24.81g/m^2/day) and it was at par with HFO-718-1(22.80g/m^2/day).

A comparison was made between the CGR value of the genotypes at 30-45 DAS and 45-60 DAS (Table 4.3). It was observed that the CGR of the genotype recorded at 30-45 DAS was not the same at 45-60 DAS. The genotypes were ranked for their CGR value to find a difference at 30-45 DAS and 45-60 DAS. The top five genotypes at 30-45 DAS were OL-1964(1^{st}), UPO-22-1(2^{nd}), HFO-718-1(3^{rd}), JO-09-14 (4^{th}) and OS-6(5^{th}) and at 45-60 DAS their rank was 16^{th}, 12^{th}, 22^{nd}, 14^{th} and 19^{th} respectively. At 45-60 DAS the top five rankers were KENT(1^{st}; 44.8g/m^2/day) the national check,OS-403(2^{nd}; 44.0g/m^2/day), OL-1821(3^{rd};40.4g/m^2/day) the national check, HFO-1003 (4^{th}; 39.6g/m^2/day) and JO-7-28(5^{th};37.2 g/m^2/day) and their rank at 30-45 DAS was 20^{th}, 7^{th}, 18^{th}, 17^{th} and 13^{th}respectively.The rank of HFO-1221 at 30-45 DAS and 45-60 DAS was 6^{th} and 8^{th} and it was more consistent in its rank followed by OS-403 having the rank 7^{th} (30-45 DAS) and 2^{nd}(45-60 DAS). At 30-45 DAS CGR was negatively correlated with green forage yield whereas at 45-60 DAS it was positively correlated.

Table 4.3 Crop growth rate ($gm^{-2}day^{-1}$) of different genotype at 30-45 and 45-60 DAS

Genotypes	30-45 days	45-60 days	% increase
HFO-1013	16.1(15)	35.6 (6)	121.4
JO-7-28	16.6 (13)	37.2 (5)	123.6
OL-1977	9.6 (21)	23.6 (13)	145.8
OS-403	20.2(7)	44.0 (2)	120.0
SKO244	18.4(10)	20.8 (17)	13.04
OL-1980	9.3 (22)	27.6 (11)	196.8
HFO-1009	14.0 (16)	30.0 (9)	114.3
KENT(NC)	11.0 (20)	44.8 (1)	308.7
JO-08-37	12.5 (19)	34.4 (7)	168.8
HFO-1003	12.8 (17)	39.6 (4)	209.4
HFO-1221	20.4(6)	34.0 (8)	66.7
JO-09-14	21.6 (4)	22.4(14)	1.85
SKO-246	16.8 (12)	20.4 (18)	21.5
HFO-1211	18.0 (11)	19.6 (20)	8.88
UPO 22-2	16.4 (14)	19.2 (21)	14.3
OS-6(NC)	21.2(5)	20.0 (19)	-5.66
OL-2000	18.8 (9)	22.3 (15)	17.0
HFO-718-1	22.5 (3)	17.2 (22)	-24.6
OL-1964	24.8 (1)	22.0 (16)	-11.3
OL-1821(NC)	12.7 (18)	40.4 (3)	215.6
OL-1976-1	20.0 (8)	28.0 (10)	40.0
UPO-22-1	22.8(2)	25.6 (12)	12.3
Mean	17.15	27.16	
CV	8.99	10.53	
CD(0.05)	2.52	4.66	
SE(m)	0.89	1.65	

RGR (Relative growth rate)

At 30-45 days after sowing the RGR value of the genotypes ranged from0.03 to 0.070g/g/day with a mean of 0.06. The highest value was observed in JO-09-14 (0.07) as well as in OL-1964 (0.07) and they had recorded significantly higher value than other genotypes.

A comparison of RGR value at 30-45 DAS and 45-60 DAS is presented in Table 4.4. The relative growth rate of the genotypes was found to be different at 30-45 DAS and 45-60 DAS. The top five genotypes at 30-45 DAS were JO-09-14 (0.070g/g/day), OL-1964 (0.070g/g/day), OL-2000 (0.065), UPO-22-1(0.060g/g/day) and HFO-1211 (0.057). The top five genotypes at 45-60 DAS were KENT (0.075g/g/day), OL-1821(0.060 g/g/day), HFO-1003(0.057 g/g/day), JO-7-28 (0.055 g/g/day) and OL-1980 (0.051 g/g/day). The mean RGR at 30-45 DAS and 45-60 DAS were 0.050 and 0.040. At 30-45 DAS RGR was negatively correlated with green forage yield whereas as 45-60 DAS it was positively correlated

Table 4.4 Relative growth rate ($gg^{-1}day^{-1}$) of different genotype at 30-45 and 45-60 DAS

Genotypes	30-45 days	45-60 days
HFO-1013	0.043	0.048
JO-7-28	0.057	0.055
OL-1977	0.030	0.043
OS-403	0.042	0.047
SKO244	0.052	0.032
OL-1980	0.033	0.051
HFO-1009	0.045	0.048
KENT(NC)	0.048	0.075
JO-08-37	0.037	0.051
HFO-1003	0.039	0.057
HFO-1221	0.052	0.043
JO-09-14	0.070	0.033
SKO-246	0.047	0.032
HFO-1211	0.057	0.032
UPO 22-2	0.048	0.031
OS-6(NC)	0.053	0.027
OL-2000	0.065	0.036
HFO-718-1	0.057	0.024
OL-1964	0.070	0.030
OL-1821(NC)	0.042	0.060
OL-1976-1	0.055	0.039
UPO-22-1	0.060	0.034
Mean	0.050	0.040
CD (0.05)	0.004	0.003

Green forage yield (g)

The lowest green forage yield was observed in UPO-22-1 (68.33g). The highest green forage yield was observed in OS-403 (141.03) with a mean value of 101.8 g. The genotype OS-403 was at par with OL-1821 (NC), JO-09-14 and HFO-1013.

Flag leaf length (cm)

Flag leaf length varied from 15.82 cm to 35.29 cm in with a mean of 26.75 cm. The lowest flag leaf length was measured in genotype SKO-246 whereas the highest in genotype OS-6 (NC)

Flag leaf area (cm^2)

Flag leaf area varied from 32.71cm^2 to 86.11cm^2 with a mean of 52.97 cm^2. The lowest flag leaf area was measured in genotype SKO-246 whereas the highest in genotype in OS-403.

Panicle length (cm)

Panicle length ranged from 27.87 cm to 46.01cm with an overall mean of 34.99 cm. The highest panicle length was measured in genotype HFO-718-1 and the lowest was recorded in genotype OS-6 (NC).

100 seed weight (g)

The genotype KENT (NC) recorded maximum 100 seed weight 3.18g whereas genotype SKO-246 recorded lowest weight 1.38 with a mean of 2.41.

Seed yield per plant (g)

The maximum seed yield per plant recorded in genotype UPO 22-2 (170.78 g) followed by the national check variety KENT (NC) (170.69) whereas genotype SKO-246 recorded lowest seed yield per plant (12.68).

Total Chlorophyll content (mgg^{-1} FW of leaf)

At 60 DAS, total chlorophyll content of the genotypes varied from 2.838 to 5.693 mg g-1 FW leaf. The minimum is being recorded in HFO-718-1 and the maximum in OS-6(NC) with genotypic mean of 4.17 mg g-1 FW leaf (Table 4.5).

Leaf chlorophyll content of the genotypes was measured following crude acetone method (direct measure) as well as by using SPAD-502 Minolta chlorophyll meter (indirect measure) at 60 and 75 days after sowing (Table 4.5). At 60 DAS, total chlorophyll content of the genotypes varied from 2.838 to 5.693 mg g^{-1} FW leaf. The minimum is being recorded in HFO-718-1 and the maximum in OS-6(NC) with genotypic mean of 4.17 mg g^{-1} FW leaf.

Table 4.5. Chlorophyll content and SPAD Meter reading of Oat genotypes

Genotype	Total chlorophyll (60 days) (mg/g)	SPAD VALUE (60 DAS)	Total chlorophyll (75 DAS)	SPAD VALUE (75 days) (mg/g)
HFO-1013	4.922	23.40	4.252	24.80
JO-7-28	5.693	31.56	4.294	38.74
OL-1977	4.410	28.80	4.189	28.44
OS-403	4.287	19.72	4.323	22.82
SKO244	3.994	32.16	5.029	42.56
OL-1980	3.469	25.84	4.278	16.60
HFO-1009	4.299	18.88	4.282	17.34
KENT(NC)	3.297	24.06	3.656	27.82
JO-08-37	3.978	22.64	4.226	20.04
HFO-1003	3.797	24.84	3.754	23.36
HFO-1221	3.814	26.92	4.639	21.76
JO-09-14	4.626	21.04	3.664	29.44
SKO-246	3.303	32.18	4.103	32.12
HFO-1211	3.109	21.16	3.630	24.96
UPO 22-2	3.521	29.66	4.577	33.66
0S-6(NC)	3.457	26.00	4.242	31.64
OL-2000	3.405	20.84	4.421	23.20
HFO-718-1	2.838	25.58	3.988	21.74
OL-1964	3.288	17.68	4.482	24.90
OL-1821(NC)	2.956	21.46	4.493	23.7
OL-1976-1	2.972	18.46	3.667	29.00
UPO 22-1	3.194	21.10	3.502	26.94
MEAN	4.17	25.35	4.18	26.62
CV	8.34	7.57	9.6	9.03
CD	0.57	3.13	0.65	3.92

At 75 DAS, total chlorophyll content of the genotypes varied from 3.502 to 5.029 mg g^{-1} FW leaf. The minimum is being recorded in UPO 22-1 and the maximum in SKO244 with genotypic mean of 4.18 mg g^{-1} FW leaf.

At 60 DAS, the SPAD meter reading which is indirect measure of chlorophyll content, of the genotypes varied from 17.68 to 32.18. The highest SPAD reading was recorded in SKO-246 and the lowest in OL-1964 with the genotypic mean of 25.25.

At 75 DAS, SPAD value of the genotypes varied from 16.6 to 42.56. The minimum is being observed in OL-1980 and the maximum in SKO-244 with genotypic mean of 26.62. Total chlorophyll content showed a positive correlation with SPAD meter reading at 60 DAS (0.260) and at 75 DAS (0.190).

4.2.2 Nutritional quality parameters

The nutritional quality of single cut oat genotypes is presented in Table 4.6.

Crude protein content (%)

The crude protein content (%) varied between 5.60 (SKO-246) and 10.70 (OL-1964) with overall mean performance of 7.70. Nine genotypes recorded significantly higher protein content over the population mean. However, the highest crude protein content was observed inOL-1964 (10.70) followed by OS -403 (10), UPO-22-1 (10) and HFO-1013 (9.39).

Dry matter content (%)

The lowest dry matter content (%) was observed in OS 403 (23.30) while the highest dry matter content was observed in UPO-22-1 (35 %) with overall mean performance of 27.61. Four genotypes were at par with the highest dry matter content.

Phosphorous content (%)

P content (%) was the highest in genotype OL-2000 (0.413 %) and the lowest in genotype KENT (NC) (0.040). The highest P content in genotype OL-2000 followed by OL-1980 (0.35%), UPO-22-1 (0.33%) and UPO 22-2 (0.31%). Three genotypes are at par with the highest phosphorus content genotype.

Potassium (K) content (%)

K content (%) varied from 1.54 to 2.30 with an overall mean of 1.85. The highest K content was in genotype OS-403 followed by OS-6(NC) (2.23%), JO-09-14 (2.17%) and OL-1976-1 (2.09%).

Ash content

Ash content (%) of the genotype HFO-1013 was the lowest (3.7) and the highest was recorded in national check OL-1821 (10.6). Higher ash content is undesirable for better nutritional quality. Genotype SKO-246 (5.50), OL-1976-1 (5.80) UPO-22-1(5.90) recorded lower Ash content.

Table 4.6 Nutritional quality of single cut oat genotypes

Genotypes	Crude protein %	Dry Matter %	P %	K %	Ash %	Nutritional index
HFO-1013	9.39 (1)	28.00 (0)	0.26(1)	1.77(0)	3.70(1)	**3.0**
JO-7-28	5.60 (0)	32.05 (1)	0.17(0)	1.80(0)	6.20(1)	2.0
OL-1977	5.80(0)	25.20 (0)	0.13(0)	2.03(0)	7.50(0)	0.0
OS-403	10.00 (1)	23.30 (0)	0.25(1)	1.73(0)	9.50(0)	2.0
SKO244	7.20 (0)	25.60 (0)	0.18(0)	2.30(1)	7.00(1)	2.0
OL-1980	8.40(1)	34.00 (1)	0.35(1)	1.92(0)	8.70(0)	**3.0**
HFO-1009	8.43 (1)	23.62 (0)	0.18(0)	1.54(0)	9.30(0)	1.0
KENT(NC)	7.55 (1)	28.20 (1)	0.04(0)	1.60(0)	10.50(0)	2.0
JO-08-37	7.50 (0)	26.40 (0)	0.14(0)	1.84(0)	6.80(1)	1.0
HFO-1003	9.30 (1)	24.50 (0)	0.18(0)	2.02(0)	7.50(0)	1.0
HFO-1221	5.80 (0)	31.31(1)	0.29(1)	1.68(0)	7.50(0)	2.0
JO-09-14	7.20 (0)	26.77 (0)	0.13(0)	2.17(0)	6.50(1)	1.0
SKO-246	5.60 (0)	26.20 (0)	0.23(1)	1.53(0)	5.50(1)	2.0
HFO-1211	8.25(1)	29.68 (1)	0.26(1)	1.64(0)	9.50(0)	**3.0**
UPO 22-2	7.55(1)	26.28 (0)	0.31(1)	1.86(0)	6.80(1)	**3.0**
OS-6(NC)	6.85 (0)	26.09(0)	0.16(0)	2.23 (1)	7.20 (1)	2.0
OL-2000	8.60 (1)	31.51 (1)	0.41(1)	1.56(0)	6.50(1)	**4.0**
HFO-718-1	5.74 (0)	27.50 (0)	0.28(1)	1.75(0)	7.50(0)	1.0
OL-1964	10.70 (1)	24.85 (0)	0.26(1)	1.86(0)	6.50(1)	3.0
OL-1821(NC)	6.45 (0)	27.54(0)	0.22	1.83(0)	10.60(0)	0.0
OL-1976-1	7.55 (1)	23.75 (0)	0.23(1)	2.09(0)	5.80(1)	3.0
UPO-22-1	10.00 (1)	35.00 (1)	0.33(1)	1.95(0)	5.90(1)	**4.0**
Mean	**7.70**	**27.61**	**0.20**	**1.85**	**7.40**	
CD at 5%	**0.85**	**3.83**	**0.13**	**0.12**	**0.36**	
CV	**5.73**	**6.42**	**5.09**	**4.00**	**4.59**	

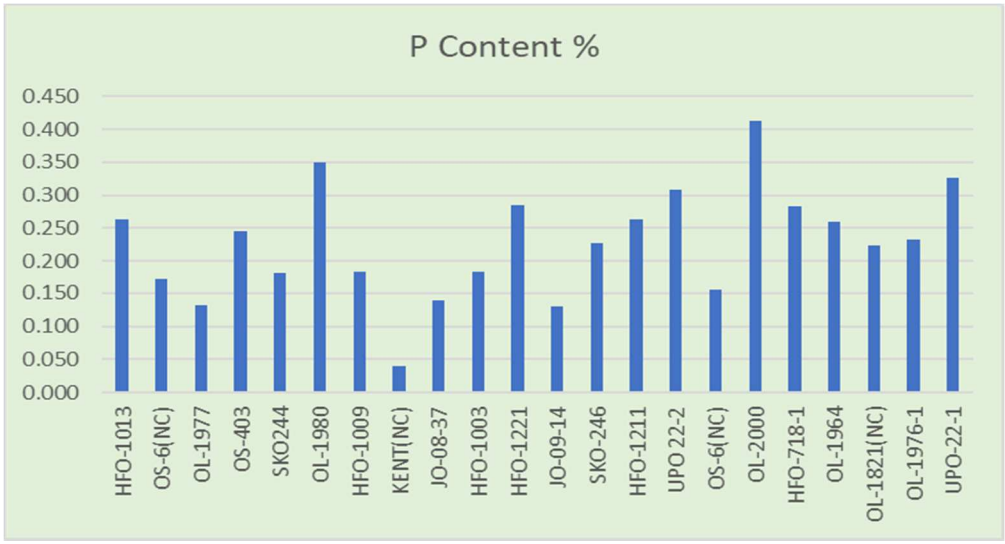

Fig. 4.1 Phosphorus percent in different genotypes

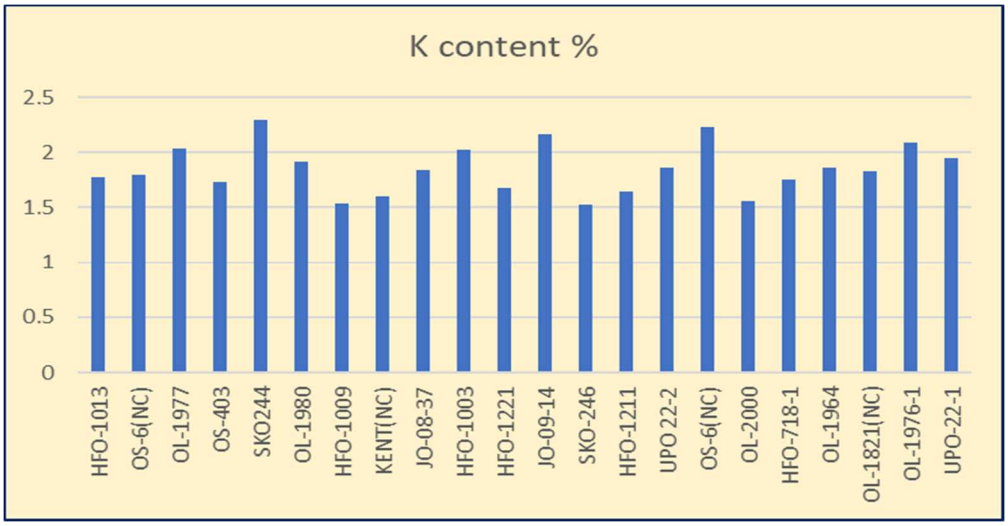

Fig. 4.2 Potassium percent in different genotypes

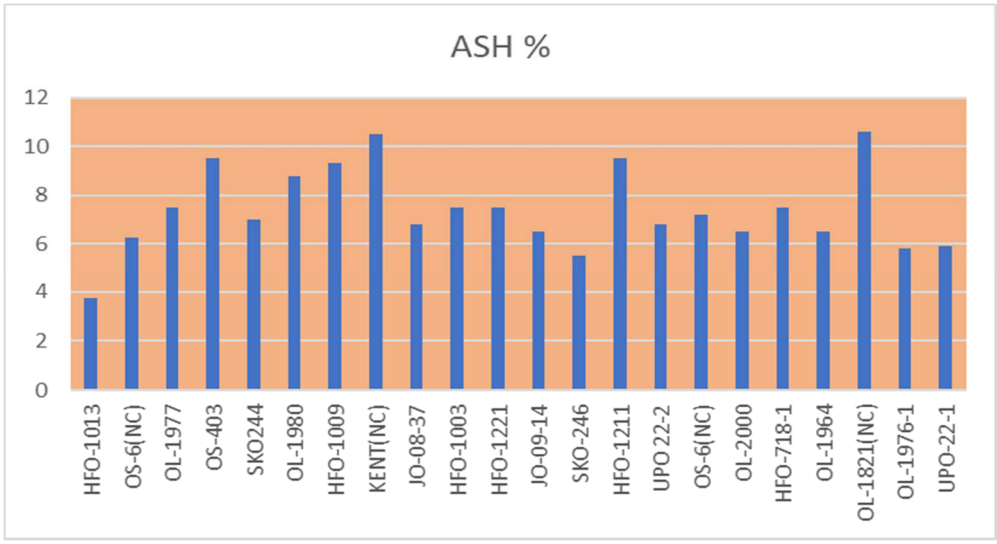

Fig.4.3 Ash content in genotypes

We developed nutritional index to identify genotypes with better nutritional quality. The genotype having higher value than the best check in respect of a trait was scored as “1” and others were scored as “0”. For ash content the genotypes having lower value than the best check was scored as “1” and others were scored as “0”. Finally score value of all the traits were added to get the nutritional index. In the present study the nutritional index of the genotypes ranged from 0.0 to 4.0. The genotype OL-2000 and UPO-22-1 had the highest index (4.0) followed by HFO-1013(3.0), OL-1980 (3.0), HFO-1211 (3.0) and UPO 22-2 (3.0) and these genotypes were considered as the good genotypes for nutritional quality.

4.3 Estimates of genetic parameters for morphological and physiological traits

The genetic parameters for different traits are presented in Table 4.**7**. Significant differences were observed among the genotypes for all the traits. Therefore, it will be effective for selection.

For plant height GCV and PCV, heritability and genetic advance (GA) as per cent of mean were 12.54, 13.68, 84 and 23.68. GCV and PCV were close to each other and it indicates that environment has the least effect on expression of this trait.

For days to 50% flowering GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 14.91, 15.22, 95.95 and 30.09.

For internode length GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 14.85, 19.22, 59.74 and 23.65.

For number of tillers GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 21.40, 23.66, 81.81 and 39.892.

For leaf length GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 14.00, 16.78, 69.65 and 24.07

For leaf breadth GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 16.16, 19.30, 70.11and 27.88

For number of leaves per tiller, GCV, PCV, heritability and genetic advance (GA) as per cent of mean were19.82, 25.17, 62.02 and 32.17.

For LS ratio, GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 14.26, 16.23, 77.21 and 25.82.

For CGR, GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 25.64, 27.95, 84.18 and 48.47.

For RGR, GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 19.85, 109.94, 3.26 and 7.39.

For GFY per plant, GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 16.16, 22.38, 52.16 and 24.05. Environment has the effect on expression of this trait.

For flag leaf length GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 20.72, 22.01, 88.64 and 40.188 respectively.

For flag leaf area GCV, PCV, heritability and genetic advance (GA) as per cent of mean were27.86, 30.05, 85.95 and 53.21. GCV PCV was not close to each other indicating environment had the effect on expression of trait.

For panicle length (cm), GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 9.34, 12.47, 56.08 and 14.41.

For 100 seed weight GCV, PCV, heritability and genetic advance (GA) as per cent of mean were18.05, 20.11, 80.52 and 33.37.

For seed yield per plant (g), GCV, PCV, heritability and genetic advance (GA) as per cent of mean were47.66, 49.62, 92.27 and 94.32

For crude protein (%), GCV, PCV, heritability and genetic advance (GA) as per cent of mean were19.63, 20.75, 89.49 and 38.25.

For dry matter (%), GCV, PCV, heritability and genetic advance (GA) as per cent of mean were11.06, 13.90, 63.29 and 18.129. GCV and PCV were close to each other and it indicates that environment has the least effect on expression of this trait.

Table 4.7 Estimates of genetic parameters (GCV, PCV, Heritability, GA)

Character	Mean	GCV	PCV	Heritability % (Broad Sense)	Genetic Advancement (GA) 5%	GA as % of mean at 5%
Plant height (cm)	144.13	12.54	13.68	84.01	34.126	23.68
Days to 50% flowering	81.09	14.91	15.22	95.95	24.4	30.09
Internode length (cm)	14.18	14.86	19.22	59.74	3.353	23.65
Tillers per plant	3.82	21.41	23.67	81.82	1.522	39.89
Leaf length (cm)	48.76	14.00	16.78	69.65	11.737	24.07
Leaf breadth (cm)	1.88	16.16	19.30	70.11	0.524	27.88
Leaf Area (cm^2)	82.68	24.57	25.84	90.39	39.783	48.12
Leaf Area Index	1.81	81.69	86.28	89.66	2.879	159.34
leaves per plant	10.71	19.83	25.18	62.03	3.445	32.17
LS Ratio	0.46	14.26	16.23	77.21	0.119	25.82
CGR	17.53	25.64	27.95	84.18	8.495	48.47
RGR	0.06	19.85	109.94	3.26	0.005	7.39
GFY per plant(g)	101.84	16.17	22.38	52.16	24.492	24.05
Flag leaf length (cm)	26.75	20.72	22.01	88.64	10.752	40.19
Flag leaf area(cm^2)	52.97	27.87	30.06	85.95	28.192	53.22
Panicle length (cm)	34.99	9.35	12.48	56.09	5.044	14.42
100 seed weight (g)	2.41	18.05	20.12	80.53	0.806	33.37
Seed yield per plant (g)	87.11	47.67	49.62	92.28	82.164	94.32
Crude protein (%)	7.70	19.63	20.75	89.49	2.947	38.26
Dry matter (%)	27.61	11.06	13.90	63.29	5.005	18.13

4.4 Association of morphological and physiological traits with green forage yield

Association of morphological and physiological traits with green forage yield and seed yield is presented in Table 4.8.

Plant height

Plant height showed significant positive association with traits like internode length (0.313*), leaf breadth (0.291*), leaf area (0.324*), number of leaves per plant

(0.470**), green forage yield (0.697**), flag leaf length (0.274*), flag leaf area (0.404**), panicle length (0.368*), 100 seed weight(0.326*), crude protein% (0.293*), seed yield per plant (0.593**) and positive correlation with no. of tillers per plant (0.013), leaf area index (0.176), leaf length (0.154), leaf stem ratio (0.223), and RGR (0.052). It showed negative correlation with days to 50% flowering (-0.731), CGR (-0.151) and dry matter % (-0.088).

Days to 50% flowering

Days to 50% flowering exhibited positive correlation with number of tillers per plant (0.201), leaf length (0.062) and CGR (0.052). It exhibited significant negative correlation with internode length (-0.380*), leaf area index (-0.328*), green forage yield (-0.283*), flag leaf length (-0.270*), flag leaf area (-0.392*), 100 seed weight (-0.327*), seed yield (-0.422*), dry matter % (-0.282*) and negative correlation with leaf breadth (-0.190), leaf area (-0.041), number of leaves (-0.163), L:S ratio (-0.093), panicle length (-0.025) and crude protein (-0.153).

Internode length

Internode length showed positive correlation with no. of tillers (0.156), leaf area (0.158), green forage yield (0.218), 100 seed yield (0.047)), dry matter % (0.001), seed yield per plant (0.105) and significantly positive correlation with leaf breadth (0.253*), leaf area index (0.893*), flag leaf length (0.423**), flag leaf area (0.513**) and other traits like leaf length (-0.072), number of leaves per plant (-0.068), leaf stem ratio (-0.176), CGR (-0.042), RGR (-0.384), panicle length (-0.030) and crude protein (-0.040) showed negative correlation with internode length.

Number of tillers per plant

Number of tillers per plant had positive correlation with leaf length (0.099), leaf area (0.038), leaf area index (0.149), LS ratio (0.019), CGR (0.232), flag leaf area (0.124), 100 seed weight (0.111), seed yield per plant (0.106) and significant positive relation with RGR (0.280*), flag leaf length (0.277*) and crude protein% (0.369*). It showed negative correlation with leaf breadth (-0.062), no of leaves per plant (-0.125), panicle length (-0.132), dry matter% (-0.067) and GFY (-0.276).

Leaf length

Leaf length showed significant positive correlation with leaf area (0.717**), number of leaves (0.243*), flag leaf length (0.309*), panicle length (0.348*) and showed positive correlation with leaf breadth (0.139), RGR (0.208), green forage yield (0.125), flag leaf length (0.089), crude protein (0.109), seed weight per plant (0.146). It had negative correlation with leaf area index (-0.124), LS ratio (-0.198), CGR (-0.180), 100 seed weight (-0.189) and dry matter% (-0.469).

Leaf breadth

Leaf breadth had significant positive correlation with leaf area (0.822**), leaf area index (0.288*), LS ratio (0.557**), CGR (0.245*), GFY (0.486**), flag leaf area (0.636**) and positive correlation with number of leaves (0.048), flag leaf length (0.089), panicle length (0.111), crude protein % (0.106). It had significant negative correlation with RGR (-0.387*), 100 seed weight (-0.257*), dry matter % (-0.469*) and negative correlation seed yield (-0.060).

Leaf area

Leaf area showed positive correlation with leaf area index (0.154), number of leaves (0.176), CGR (0.084), flag leaf length (0.219), crude protein % (0.149), seed yield per plant (0.051) and significant positive relation with L:S ratio (0.304*), green fodder yield (0.425**), flag leaf area (0.560**), panicle length (0.306*). It showed negative correlation with RGR (-0.160), 100 seed weight (-0.280) and dry matter% (-0.051).

Leaf area index

Leaf area index had positive correlation with CGR (0.0375), seed yield per plant (0.012) and significant positive relation with flag leaf length (0.334*), flag leaf area (0.449**). It showed negative correlation with panicle length (-0.155), 100 seed weight (-0.064), crude protein (-0.129), dry matter (-0.033), LS ratio (-0.154) and significant negative correlation with number of tillers (-0.803**) and RGR (-0.421**)

Number of leaves per plant

Number of leaves per plant had significantly positive relation with L:S ratio (0.364*), RGR (0.428*), green fodder yield (0.296*), panicle length (0.387*), seed yield per plant (0.266*) and positive relation with 100 seed weight (0.118), crude

protein% (0.195). It showed negative correlation with CGR (-0.068), flag leaf length (-0.150), flag leaf area (-0.114) and dry matter % (-0.017).

Leaf: Stem ratio

L:S ratio showed positive correlation with RGR (0.080), green forage yield (0.09), panicle length (0.088), crude protein % (0.223), dry matter % (0.076), seed yield per plant (0.045) and significant positive correlation with CGR (0.295*), flag leaf area (0.261*). It had negative correlation with flag leaf length (-0.216) and 100 seed weight (-0.212).

CGR

CGR showed positive relation with RGR (0.015), panicle length (0.180), crude protein (0.076), green forage yield (0.4202), seed yield per plant (0.3489) and significant negative correlation with GFY (-0.339), flag leaf length (-0.376), flag leaf area (-0.279),100 seed weight (-0.357), dry matter (%) (-0.029), seed yield (-0.501).

RGR

RGR had significant positive correlation with 100 seed weight (0.280), dry matter% (0.260), seed yield (0.4474) and positive correlation with panicle length (0.054), crude protein% (0.078), green forage yield (0.2774). It had significant negative correlation with GFY (0.283), flag leaf area (0.247) and negative correlation with flag leaf length (0.057).

Flag leaf length

There was a significant positive correlation observed between the length of the flag leaf and various agronomic traits, including flag leaf area (0.081**), 100 seed weight (0.298*), seed yield (0.272*), and crude protein content (0.057*). The variable exhibited significant negative relationship with panicle length (-0.371*) and a negative connection with dry matter percentage (-0.176).

Flag leaf area

The flag leaf area exhibited a significant positive relationship with seed yield per yield (0.292*). Additionally, a positive correlation was observed between flag leaf area and 100 seed weight (0.091) as well as crude protein percentage (0.074). There was a significant negative relation observed with panicle length (-0.298*) and dry matter percentage (-0.316*).

Table 4.8 Association of morphological and physiological traits with green forage yield and seed yield

Characters	Plant height (cm)	Days to 50% flowering	Internode length (cm)	Number of tillers per plant	Leaf length (cm)	Leaf breadth (cm)	Leaf area	Leaf Area Index	Number of leaves per tiller	LS Ratio	CGR	RGR	GFY per plant	Flag leaf length	Flag leaf area	Panicle length (cm)	100 seed weight	Dry matter (%)	Seed yield per plant (g)
Plant height (cm)	1.0	-0.731**	0.311*	0.013	0.154	0.291*	0.324*	0.176	0.470**	0.223	-0.151	0.052	0.697**	0.274*	0.404**	0.368*	0.326*	-0.088	0.593**
Days to 50% flowering		1	-0.380*	0.201	0.062	-0.190	-0.041	-0.328*	-0.163	-0.093	0.052	-0.126	-0.283*	-0.270*	-0.392*	-0.025	-0.327*	-0.282*	-0.422**
Internode length (cm)			1	0.156	-0.072	0.253*	0.158	0.893**	-0.698**	-0.176	-0.042	-0.384*	0.2184	0.423**	0.513**	-0.030	0.047	0.001	0.105
Number of tillers per plant				1	0.099	-0.062	0.038	0.149	-0.125	0.019	0.232	0.280*	-0.276*	0.277*	0.124	-0.132	0.111	-0.067	0.106
Leaf length (cm)					1	0.139	0.717**	-0.124	0.243*	-0.198	-0.180	0.208	0.125	0.309*	0.218	0.348*	-0.189	-0.362*	0.146
Leaf breadth (cm)						1	0.822**	0.288*	0.048	0.557**	0.245*	-0.387*	0.486**	0.0899	0.636**	0.111	-0.257*	-0.469**	-0.060
Leaf Area							1	0.1549	0.176	0.304*	0.0843	-0.1633	0.425**	0.2194	0.560**	0.306*	-0.283*	-0.515**	0.051
Leaf Area Index								1	-0.803**	-0.1542	0.0375	-0.421**	0.105	0.334*	0.449**	-0.1553	-0.064	-0.033	0.012
Number of leaves per plant									1	0.364*	-0.0682	0.428**	0.296*	-0.1502	-0.114	0.387*	0.118	-0.017	0.266*
LS Ratio										1	0.295*	0.0808	0.09	-0.2168	0.261*	0.088	-0.212	0.076	0.045
CGR											1	0.0156	0.4202	-0.376*	-0.279*	0.180	-0.357*	-0.029	0.3489
RGR												1	0.2774	-0.0571	-0.247*	0.054	0.280*	0.260*	0.4474
GFY per plant													1	0.391*	0.575**	0.088	0.296*	-0.600**	0.438**
Flag leaf length														1	0.816**	-0.371*	0.298*	-0.176	0.272*
Flag leaf area															1	-0.298*	0.091	-0.316*	0.299*
Panicle length (cm)																1	0.008	-0.038	-0.164
100 seed weight																	1	0.128	0.446**
Dry matter (%)																		1	-0.004
Seed yield per plant (g)																			1.000

Panicle length

Panicle length showed positive correlation with 100 seed weight (0.008), crude protein% (0.011) and negative correlation with dry matter % (-0.038) and seed yield (-0.164).

Green forage yield

Green forage yield showed significant positive relation with flag leaf length (0.391*), flag leaf area (0.575**), 100 seed weight (0.296*), seed yield per plant (0.438**) and positive relation with panicle length (-0.221), crude protein (-0.221). It had negative correlation with dry matter %.

100 seed weight

100 seed weight showed significant positive correlation with crude protein (0.299*), seed yield per plant (0.446**) and positive relation with dry matter % (0.128).

Dry matter %

The dry matter percentage exhibited a negative relationship with various plant characteristics, including seed yield per plant (-0.004), number of tillers per plant (-0.106), days to 50% blooming (0.422), leaf length (-0.362), leaf breadth (-0.469), leaf area (-0.515), leaf area index (-0.033), number of leaves per tiller (-0.017), and green forage yield (-0.600). There was a positive correlation observed between the relative growth rate (RGR) and the leaf-to-stem ratio (L:S ratio), with correlation coefficients of 0.260 and 0.076, respectively.

4.5 Identification of oat genotype having high green forage yield and better nutritional quality

The green forage yield, nutritional index and seed yield of the genotypes is presented in Table 4.9. From Table 9 it was observed that only one genotype OS-403 having GFY of 141.033g/plant surpassed the best national check OL-1821(130.800 g) in respect of GFY. Considering the genotypic mean as the standard (101.84 g) ten genotypes like HFO-1013 (128.9 g), OL-1977 (112.5 g), OS-403 (141.03 g), HFO-1003 (111.73 g), JO-09-14 (117.07 g), UPO 22-2 (110.60 g), OS-6 (114.70 g), OL-1964 (102.83 g), OL-1821(130.80) and OL-1976-1 (114.87 g) were found to have high GFY. Similarly, ten genotypes were found to have high seed yield and the top most yielder was UPO 22-2 (170.78 g) followed by the national check KENT (170.69 g) and OS-403 (140.15 g).

Table 4.9 GFY, seed yield and nutritional index of oat genotypes

Sl. No.	Genotype	GFY (g)	Nutritional index	Seed yield (g)
V1	HFO-1013	128.90	3.0	82.92
V2	JO-7-28	94.64	2.0	60.64
V3	OL-1977	112.50	0.0	132.21
V4	OS-403	141.03	2.0	140.15
V5	SKO244	93.90	2.0	39.71
V6	OL-1980	98.48	3.0	136.31
V7	HFO-1009	97.37	1.0	63.50
V8	KENT(NC)	97.03	2.0	170.69
V9	JO-08-37	94.67	1.0	94.07
V10	HFO-1003	111.73	1.0	76.21
V11	HFO-1221	82.90	2.0	70.20
V12	JO-09-14	117.07	1.0	57.74
V13	SKO-246	70.37	2.0	12.68
V14	HFO-1211	88.73	3.0	59.58
V15	UPO 22-2	110.60	3.0	170.78
V16	OS-6(NC)	114.70	2.0	78.81
V17	OL-2000	85.40	4.0	101.87
V18	HFO-718-1	83.60	1.0	21.12
V19	OL-1964	102.83	3.0	93.80
V20	OL-1821(NC)	130.80	0.0	90.36
V21	OL-1976-1	114.87	3.0	87.21
V22	UPO-22-1	68.33	4.0	75.84
	Mean	**101.84**	**2.05**	**87.11**

The genotypes having good nutritional quality were HFO-1013 (3.0), OL-1980 (3.0), UPO 22-2 (3.0), OL-2000 (4.0), OL-1964 (3.0), OL-1976-1(3.0) and UPO-22-1(4.0).

The genotypes with high GFY and good nutritional quality were HFO-1013 (128.90 g, 3.0), UPO 22-2 (110.60 g, 3.0) and OL-1976-1 (114.87 g, 3.0).

The genotypes with high GFY and high seed yield wereOL-1977 (112.50 g, 132.21 g), OS-403 (141.03 g, 140.15 g), UPO 22-2 (110.60 g, 170.78 g), OL-1964(102.83 g, 93.80 g), OL-1821(130.80 g, 90.36g) and OL-1976-1(114.87g, 87.21g).

The genotypes with high GFY, better nutritional quality and high seed yield were UPO 22-2, OL-1964 and OL-1976-1. Genotypes having high nutritional quality were marked with a straight line on the glyph (Fig. 4.4).

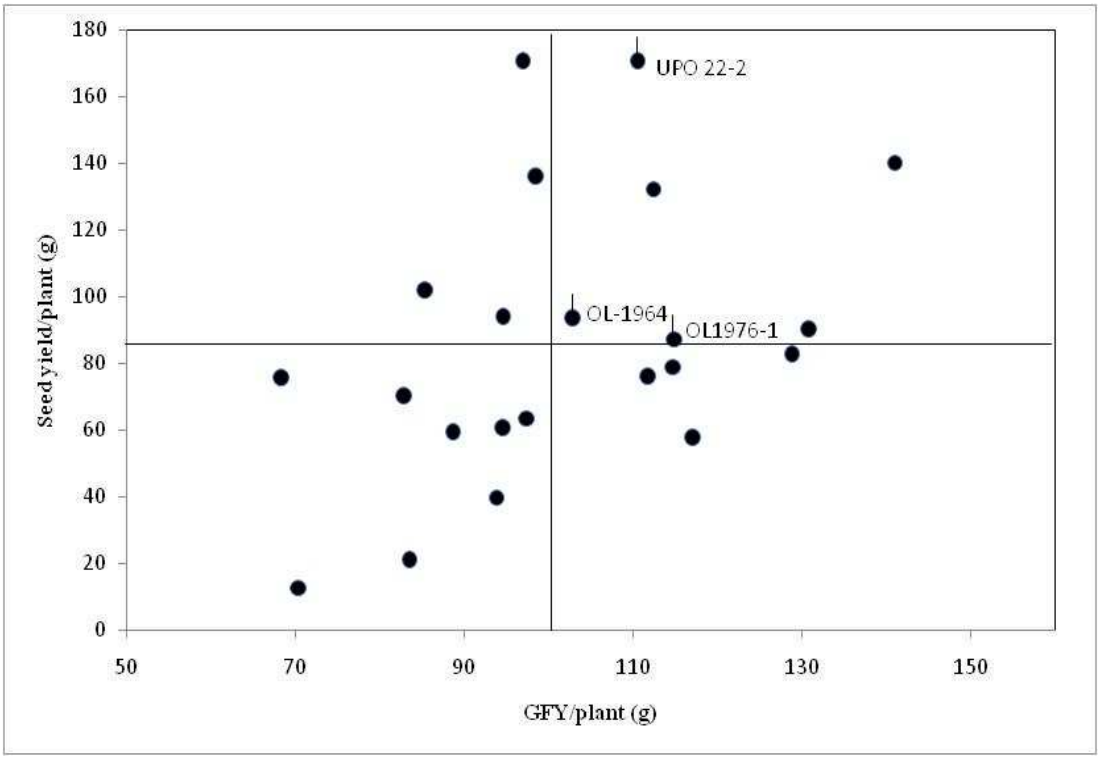

Fig.4.4 GFY vs. seed yield of oat genotypes

FIELD PHOTOGRAPHS

Counting tiller number

Counting number of leaves

Measuring Panicle Length

Flowering in Oat

Tagging of replication

Tagging of plants

Measuring Chlorophyll by SPAD

Chlorophyll by Acetone method

Determination of ash

Determination of Phosphorus

Crude protein estimation

Variation in panicles of genotypes

OL-2000

HFO-718-1

OL-1964

OL-1821 (NC)

OL-1976-1

UPO-22-1

JO-08-37

HFO-1003

HFO-1221

JO-09-14

SKO-246

HFO-1211

UPO-22-2

OS-6(NC)

HFO-1013

OS-6 NC)

OL-1977

OS-403

SKO-244

OL-1980

HFO1009

KENT NC

DISCUSSION

Oats are a versatile crop used for grain, pasture, and forage, and they are especially important as a winter forage crop in various regions globally. Fodder oat plays a vital role on dairy farms, where it can be fed when green and any surplus can be converted into silage or hay for use during periods of scarcity. It exhibits an impressive growth pattern, rapid post-harvest regeneration, and offer high-quality forage. Their feed is not only palatable but also rich in nutrients. In recent years, oats have garnered attention from breeders, particularly in the context of our expanding dairy industry, due to their high-quality, nutritious fodder for livestock and grains used as animal feed (Ruwali *et al*., 2013).

5.1 Mean performance of the cultivars

The current study involved the evaluation of twenty-two single cut oat genotypes using a randomized block design with three replications. Various physiological parameters, including CGR (crop growth rate), RGR (relative growth rate), dry matter content, chlorophyll content, and morphological traits such as plant height, days to 50% flowering, leaf to stem ratio, leaf length and breadth, number of leaves per plant, green forage yield per plant, panicle length, 100 seed weight, seed yield per plant, as well as nutritional traits such as crude protein content, phosphorus content, potash content, and ash content, were recorded and analyzed. There were significant variations discovered among the genotypes with regard to all the traits.

The maximus height was recorded in OS-403 (174.63cm). 50% flowering was late in variety SKO -244 (112 days) and earlier in HFO (65 days). The lowest internode length was measured in genotype OL-2000 (9.72) whereas the highest in genotype OS-6 (NC) (17.40). The highest number of tillers per plant was observed in UPO-22-1(5.28) followed by KENT (5.17) and SKO-244(4.98) respectively. The highest leaf area was measured in OS-403 (147.10). The lowest LAI is recorded in genotype OL-2000 whereas the highest in genotype OS-403(1.85). The minimum number of leaves per plant was recorded in genotype SKO-246 (8.24) and the maximum number of leaves per plant was recorded in OL-1821(NC) (17.10). The highest L:S value was observed in genotype OS-403 (0.60). The lowest green forage yield was observed in UPO-22-1 (68.33g) and the highest green forage yield was observed in OS-403 (141.03).

The lowest flag leaf area was measured in genotype SKO-246 (32.71cm^2) whereas the highest in genotype in OS-403(86.11cm^2). The genotype KENT (NC) recorded maximum 100 seed weight 3.18g. The highest recorded seed results per plant was observed in genotype UPO 22-2 (170.78 g), closely followed by the national check variety KENT (NC) (170.69 g). Bibi et al. (2021) conducted an evaluation of various exotic oat (Avena sativa L.) varieties to assess their forage and grain yield. The study revealed that the Australian oat variety exhibited superior performance on multiple key parameters. Specifically, this variety demonstrated higher days to emergence (49 plants per square meter), longer duration for emergence (15 days), flowering (122 days), and maturity (145 days), taller plant height (142.7 cm), greater number of leaves per plant (6.03 leaves), and higher number of tillers per meter (92.2 tillers). Hasan *et al*. (2021) observed forage oats. Tillers (457,422) per/m^{-2} and number of panicles (376, 355) per/m-2, and number of grain in panicle (28.54 and25.97) per/m^{-2}, weight of 1000 grain (26.77, 26.48) gm, grain yield (3.96, 3.71) ton/h^{-1}, biological yield (17.53, 16.43) ton/h, average of plant growth (12.30, 11.55) gm.m^{-2}, harvest Index (22.52, 23.08) % both of season were recorded. Bakhsh *et al*. (2007), Lodhi *et al*. (2009), Amanullah *et al*. (2013), Ahmad *et al.* (2014), Siloriya *et al*. (2014), Beyene *et al.,* (2015), Premkumar *et al* (2017), Mir *et al*. (2018) and Poonia *et al*. (2018) also studied different yield and yield attributing parameters in forage oat.

The genotype OS- 403 recorded highest leaf area (147.10 cm^2) and lowest leaf area was observed in genotype JO-09-14 (58.81 cm^2) from Table -2. Leaf area is found positive correlated with seed yield leaf act as a source and seed as sink. Leaf area index (LAI) was maximum in genotype OS- 403 (1.85). The highest leaf area index in genotype OS-403 was due to maximum leaf size (leaf length and breadth) and more leaves. LAI, leaf photosynthate rate, and leaf angle all influence crop growth rate, which is an indication of light intercepted. CGR levels were high 45-60 days after sowing. It discovered that dry matter yield was adversely associated to CGR, contradicting the findings of Amanullah *et al* (2013). Similarly, the relative growth rate is an important physiological measure that indicates a plant's ability to produce dry matter per unit of dry matter already present. RGR demonstrated a positive relationship with dry matter yield, which was in accordance with the findings of Amanullah *et al* (2013). Total Chlorophyll content in leaf showed significant difference among genotypes. Chlorophyll content considered as one of the important biochemical parameters for

yield determination as it helps in maintaining leaves active for longer periods which can supply photosynthates to developing seeds. The nutritional quality parameters in the present study included crude protein %, phosphorus %, potassium % Ash % were observed (Table-6). Highest crude protein content was observed in OL-1964 (10.70) followed by OS -403 (10), P content (%) was the highest in genotype OL-2000 (0.413). Highest K content was in genotype OS-403. Ash content (%) of the genotype HFO-1013 was the lowest (3.7) as higher ash content is undesirable for nutritional quality. Khan *et al*. (2014), Muhammad *et al.* (2015), Mut *et al*. (2015), Mir *et al.* (2018), Poonia *et al.* (2018), Ahmed *et al.* (2020), Sumanth *et al*. (2021) also studied quality parameters in forage oat.

5.2 Genetic parameters

The analysis of variance revealed significant variation among the different genotypes for all of the observed attributes. It is not surprising that there is a large level of variability in almost all features, as the material under research has a wide range of genetic variety in terms of plant type, yielding ability, and other traits.

5.2.1 Genotypic and Phenotypic coefficient of variation

The limited difference in the assessments of genotypic and phenotypic variance indicates that the variability observed among genotypes is predominantly attributable to genetic factors, with minimal impact from environmental factors, thus indicating a heritable nature. Earlier researchers, including Prasad *et al.* (2003), Kapoor *et al*. (2011), Bind *et al.* (2016), Jaipal and Shekhawat (2016), and Singh and Singh (2016), reported that the environment influenced the characters' expressiveness.

Tillers per plant, leaf area, leaf area index, leaves per plant, flag leaf area, and seed output exhibited higher (GCV) and (PCV) in the recorded data. The present findings were consistent with Sabreen *et al* (2018) for the yield of seed, Chauhan and Singh (2019) for number of leaves per plant, tillers per plant, kapoor *et al.* (2011) for tillers per plant, seed yield. The study conducted by Dubey *et al.* (2014) focused on the analysis of leaf area. Kumar *et al.* (2004) conducted a study on the number of leaves, whereas Premkumar *et al.* (2017) and Shankar et al. (2002) investigated seed yield. In contrast, Singh (1999), Mall *et al.* (2005), Shankar *et al.* (2002), Singh and Singh (2010), and Gautam *et al*. (2006) showed (GCV) and (PCV) for green forage yield and dry forage yield.

5.2.2 Heritability

A significant degree of heritability has been shown in a variety of traits, including plant height, days to 50% flowering, leaf area, leaf area index, and seed output. The current results exhibited similarities to the observations made by Chaubey *et al.* (2001) and Prasad *et al.* (2003) in terms of plant height and days required for 50% flowering. Furthermore, Pundir *et al.* (2003) reported similar findings for leaf length, leaf width, and number of leaves. The study conducted by Krishna *et al.* (2013) investigated the relationship between plant height and days to flowering. On the other hand, Vanjare *et al.* (2021) examined the variables of plant height, days to 50% blooming, leaf length, and leaf breadth.

5.2.3 Genetic Advance

The concept of genetic advance, as stated by Johnson et al. (1955) which serves as a valuable addition to heritability estimations, particularly in the context of forecasting the efficacy of selection within crop improvement initiatives.

The traits of plant height, days to 50% flowering, leaf area, flag leaf area, green forage production, and seed output per plant exhibited substantial genetic advancement. The findings of several studies have reported comparable outcomes regarding the estimation of various parameters in the context of green forage yield and plant height. Pundir *et al*. (2001) observed similar high estimates for green forage yield, while Kapoor *et al.* (2011) reported analogous results for plant height. Additionally, Chauhan *et al*. (2013) found comparable estimates for plant height, and Jaipal and Shekhawat (2016) reported similar results for green forage yield. Furthermore, Wagh *et al.* (2018) observed analogous estimates for plant height and green forage yield, and Chauhan and Singh (2019) reported similar findings for plant height and green forage yield.

5.3 Correlation among genotypes

In the present investigation correlation coefficient of different trait with green forage yield per plant as well as seed yield and their relationship among themselves are presented in Table 8 and are discussed here under following points.

The variables consisting of plant height, number of leaves, internode length, leaf length, leaf breadth, leaf area, leaf area index, number of leaves, CGR, RGR, and leaf to stem ratio exhibited a significant positive correlation with green forage yield. This observation is supported by the results obtained from the aforementioned studies. The study conducted by Chaubey *et al.* (2001) revealed a substantial correlation between green fodder yield and plant height, as well as leaf breadth. In a study conducted by Kumar *et al.* (2004), it was found that there existed a significant positive correlation between many plant characteristics, including plant height, number of leaves, internode length, longest leaf length, and leaf breadth. In their study, Krishna *et al.* (2014) found that there were positive connections between plant height and leaf length with the majority of the qualities. In their study, Dubey *et al.* (2015) observed a strong positive correlation between green fodder yield and various plant characteristics, including the number of tillers per plant and the number of leaves per plant. According to Wagh *et al.* (2018), there exists a significant and positive correlation between green forage yield and many factors including the number of tillers per metre row length, crude protein content, leaf breadth, plant height, and number of leaves per tiller. In their study, Shankar *et al.* (2002) identified a positive relationship between the L:S ratio and GFY.

The current investigation revealed a significant negative relationship between the number of days to 50% flowering and the yield of green fodder. In their study, Bidi *et al.* (2012) found a statistically significant negative association between the number of days to 50% flowering and green forage production. In contrast, Bukhari *et al*. (2009) identified a substantial positive correlation between the number of days until 50% flowering and green forage yield.

The parameters like plant height, internode length, number of tillers per plant, flag leaf length, flag leaf area, leaf area index, and 100 seed weight have been found to exhibit a positive correlation with seed yield per plant. This correlation has been supported by the research conducted by Mall *et al*. (2005), Gautam *et al*. (2006), Kapoor *et al*. (2011), and Sofi *et al.* (2012).

5.3.1 Association among forage yield component traits.

The present research observed that plant height, leaf length, and number of leaves per plant exhibited substantial to moderate positive direct effects, which were substantially correlated with green forage yield. These findings suggest a strong and significant association between these variables. Therefore, it may be inferred that the selection of these features would provide significant improvements in green forage production. Previous studies conducted by Kumar *et al.* (2004), Bahadur and Lodhi (2009), Bukhari *et al.* (2009), Chaubey *et al.* (2007), and Dubey *et al.* (2015) have also reported a significant beneficial direct impact of these characteristics on the yield of green forage. This further supports the results of the current study.

SUMMARY AND CONCLUSION

Forage oat plays a vital role on dairy farms, where it can be fed when green and any surplus can be converted into silage or hay for use during periods of scarcity. Development of high yielding oat varieties can meet the demand of dairy farms. In the present investigation we studied the association of morpho-physiological traits with green forage yield along with nutritional quality for identification of superior genotypes. In the present study twenty two single cut oat genotypes were evaluated in a randomised block design with three replications and observations were recorded on different physiological parameters like CGR, RGR, dry matter content, chlorophyll content and morphological traits like plant height, days to 50 % flowering, leaf to stem ratio, leaf length & breadth, number of leaves/plant, green forage yield per plant, panicle length, 100 seed weight, seed yield per plant and nutritional traits like crude protein content, phosphorus content, potash content and ash content. Replicated data were subjected to statistical analysis following Windostat software, version 9.3 and the results were summarised below.

6.1 Analysis of variance for morphological and physiological traits

- Significant differences were observed among the genotypes in respect of all the characters under study except RGR
- The maximum error mean sum of square was observed in case of green forage yield (69.734) followed by plant height (62.182) and seed yield (60.633).

6.2 Performance of oat genotypes

6.2.1 Morpho-physiological traits

- Plant height of the genotypes varied from 93.35 cm to 174.63 cm with a mean of 144.13 cm. The tallest height was recorded in OS-403 (174.63cm)
- Days to 50% flowering ranged from 65 days in HFO-1013 genotype to 112 days in SKO-244 genotype with an overall mean value of 81.09 days
- The highest number of tillers per plant was observed in UPO-22-1 (5.28) followed by KENT (5.17) and SKO-244(4.98) respectively

- The highest leaf area was measured in OS-403 (147.10 cm^2) followed by OL-1821 (108.67 cm^2)

- Leaf area index of the genotypes varied from 1.01 in OL-2000 to 1.85 in OS-403 with a mean of 1.41

- The highest L:S value was observed in genotype OS-403 (0.60) and it was at par with OL-1976-1(0.55), UPO 22-1(0.58), OL-2000 (0.58).

- The CGR value of the genotypes ranged from 17.2 to 44.8 $gm^{-2}day^{-1}$ with a mean of 27.16 $gm^{-2}day^{-1}$ at 45-60 days after sowing. The highest value was observed in KENT(NC) (44.8 $g/m^2/day$).

- The RGR value of the genotypes ranged from 0.024 to 0.075 $gg^{-1}day^{-1}$ with a mean of 0.04 at 45-60 days after sowing. The highest value was observed in KENT(NC) (0.075 $gg^{-1}day^{-1}$).

- The highest green forage yield was observed in OS-403 (141.03) and the lowest green forage yield was observed in UPO-22-1 (68.33 g).

- Panicle length varied from 27.87 cm in OS-6 (NC) genotype to 46.01cm in HFO-718-1 with an overall mean of 34.99 cm.

- The genotype KENT (NC) recorded maximum 100 seed weight 3.18 whereas genotype SKO-246 recorded lowest weight 1.38 with a mean of 2.41.

- The national check variety KENT recorded the maximum seed yield per plant (170.78 g) whereas genotype SKO-246 recorded lowest seed yield per plant (12.68).

- At 60 DAS, total chlorophyll content of the genotypes varied from 2.838 to 5.693 mg g^{-1} FW leaf.

- At 60 DAS, the SPAD meter reading which is indirect measure of chlorophyll content, of the genotypes ranged from 17.68 to 32.18. The highest SPAD reading was observed in SKO-246 and the lowest in OL-1964 with the genotypic mean of 25.25.

6.2.2 Nutritional quality parameters

- The crude protein content (%) varied between 5.60 (SKO-246) and 10.70 (OL-1964) with overall mean performance of 7.70.
- The highest crude protein content was observed in OL-1964 (10.70) followed by OS -403 (10), UPO-22-1 (10) and HFO-1013 (9.39).
- The highest dry matter content was observed in UPO-22-1 (35 %) and the lowest dry matter content (%) was observed in OS 403 (23.30).
- P content (%) was the highest in genotype OL-2000 (0.413) and lowest in genotype KENT (NC) (0.040).
- K content (%) varied from 1.54 to 2.30 with an overall mean of 1.85. Highest K content was in genotype OS-403.
- Ash content (%) of the genotype HFO-1013 was the lowest (3.7) and the highest was recorded in national check OL-1821 (10.6). Higher ash content is undesirable for better nutritional quality.
- The genotype OL-2000 and UPO-22-1 had the highest nutritional index (4.0) followed by HFO-1013(3.0), OL-1980 (3.0), HFO-1211 (3.0).

6.3 Estimates of genetic parameters for morphological and physiological traits

- The GCV, PCV, heritability and genetic advance (GA) as per cent of mean in case of plant height were 12.54, 13.68, 84 and 34.12. GCV and PCV were close to each other and it indicates that environment has the least effect on expression of this trait.
- For days to 50% flowering GCV, PCV, heritability and genetic advance (GA) as per cent of mean were14.912, 15.22, 95.95 and 30.09. High heritability with high GA as percent of mean indicates the selection will be rewarding due to additive gene action.
- For internode length GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 14.85, 19.22, 59.74 and 23.65.

- For number of tillers the GCV (21.40) and PCV (23.66) were close to each other.

- For number of leaves per tiller, GCV, PCV, heritability and genetic advance (GA) as per cent of mean were19.82, 25.17, 62.02 and 32.17.

- For GFY per plant, the GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 16.16, 22.38, 52.16 and 24.05. Environment has the effect on expression of this trait.

- For panicle length (cm), GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 9.34, 12.47, 56.08 and 14.41.

- For 100 seed weight GCV, PCV, heritability and genetic advance (GA) as per cent of mean were18.05, 20.11, 80.52 and 33.37.

- For seed yield per plant, GCV, PCV, heritability and genetic advance (GA) as per cent of mean were 47.66, 49.62, 92.27 and 94.32.

- The GCV, PCV, heritability and genetic advance (GA) as per cent of mean in case of crude protein content were19.63, 20.75, 89.49 and 38.25.

- For dry matter content, heritability and genetic advance (GA) as per cent of mean were 63.29 and18.129.

6.4 Association of morphological and physiological traits with green forage yield

- Plant height showed significant positive correlation with traits like internode length (0.313), leaf breadth (0.291), leaf area (0.324), number of leaves per plant (0.470), green fodder yield (0.697), 100 seed weight (0.326) and seed yield per plant (0.593).

- Days to 50% flowering exhibited positive correlation with number of tillers per plant (0.201) and significant negative corelation with internode length (0.380), leaf area index (0.328), green fodder yield (0.283), 100 seed weight (0.327), seed yield (0.422).

- Internode length showed significantly positive correlation with leaf breadth (0.253), leaf area index (0.893), flag leaf length (0.423), flag leaf area (0.513).

- Number of tillers per plant had significant positive relation with RGR (0.280), flag leaf length (0.277) and negative correlation with panicle length (0.132) and GFY (0.276).

- Number of leaves per plant had significant positive association with L:S ratio (0.364), RGR (0.428), green fodder yield (0.296), panicle length (0.387), seed yield per plant (0.266).

- L:S ratio had significant positive relation with CGR (0.295), flag leaf area (0.261). It had negative correlation with flag leaf length (0.216) and 100 seed weight (0.212).

- CGR showed significant negative correlation with flag leaf length (-0.376), flag leaf area (-0.279) and positively correlated with GFY (0.4202), seed yield (0.3489).

- RGR had significant positive correlation with 100 seed weight (0.280), dry matter % (0.260), seed yield (0.270), GFY (0.2774) and significant negative correlation with flag leaf area (-0.247).

- Panicle length showed negative correlation with dry matter% (-0.038) and seed yield -(0.164).

- Green fodder yield showed significant positive relation with flag leaf length (0.391), flag leaf area (0.575), 100 seed weight (0.296), seed yield per plant (0.438) and negative correlation with dry matter %.

- 100 seed weight showed significant positive correlation with seed yield per plant (0.446).

- Crude protein had significant positive correlation with P-content (0.307) and negative correlation with ash content (-0.036), K-content (-0.022) and chlorophyll content (-0.073).

- Dry matter % showed negative correlation with seed yield per plant.

6.5 Identification of oat genotype having high green forage yield and better nutritional quality

- The genotype OS-403 having GFY of 141.033g/plant surpassed the best national check OL-1821(130.80 g).

- The highest seed yielder was UPO 22-2 (170.78 g) followed by the national check KENT (170.69 g) and OS-403 (140.15 g).

- The genotypes having good nutritional quality were HFO-1013 (3.0), OL-1980 (3.0), UPO 22-2 (3.0), OL-2000 (4.0), OL-1964 (3.0), OL-1976-1(3.0) and UPO-22-1(4.0).

- The genotypes with high GFY and good nutritional quality were HFO-1013 (128.90 g, 3.0), UPO 22-2 (110.60 g, 3.0) and OL-1976-1 (114.87 g, 3.0).

- The genotypes with high GFY, better nutritional quality and high seed yield were UPO 22-2, OL-1964 and OL-1976-1.

Conclusion

From the present investigation it may be concluded that green forage yield had significant positive correlation with plant height, leaf breadth, leaf area, number of leaves per tiller, CGR and RGR. The genotypes HFO-1013, UPO 22-2 and OL-1976-1having high GFY and nutritional quality were identified as good genotypes.

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Association of morpho-physiological traits with forage yield and quality in single cut oat

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