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# ASSESSMENT OF GENETIC VARIABILITY, TRAIT ASSOCIATION AND GENETIC DIVERSITY IN OAT (*AVENA SATIVA* L.) FOR FODDER YIELD AND QUALITY

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## ABSTRACT

Fifty-five oats genotypes were evaluated in randomized block design with three replications to examine the nature and magnitude of variability, heritability, genetic advance and genetic divergence. Analysis of variance revealed that differences among the genotypes were significant for all the characters studied. The highest genotypic and phenotypic coefficient of variation, heritability and genetic advance as % of mean correspond to plant height, culm diameter, no. of tillers $m^{-1}$ and green fodder yield and direct selection for these traits would be useful for yield improvement in oats. Correlation analysis studies revealed that, many yield contributing traits viz., plant height, no. of tillers $m^{-1}$, flag leaf length (cm), leaf area index and culm diameter (mm) had significant and positive correlation with green fodder yield. The $D^2$ analysis on morphological traits grouped into 12 clusters. Cluster I comprised of maximum genotypes (35). The inter cluster distance $D^2$ value was highest between cluster V and cluster XII (356.36) followed by cluster III and cluster XII (303.40) So, crossing between lines belonging to these clusters may result into high heterosis. Contribution (%) towards the total divergence was maximum through no. of tillers $m^{-1}$ followed by green fodder yield, leaf stem ratio and plant height.

***Keywords*:** Oats, genetic variability, genetic divergence, correlation, fodder quality

## Introduction

Oats (*Avena sativa* L.) is one of the most important *Rabi* fodder crops of India and the world. It is an annual forage crop which belongs to family Gramineae. This cultivated oat species (*Avena sativa L.*) evolved as a natural allopolyploid (2n=6x=42, AACCDD) through several cycles of interspecific hybridization and polyploidization. In India, oats is a significant winter crop, primarily cultivated in the Northern, Central and Western regions. On a global scale, oats hold the sixth position in cereal production, following wheat, maize, rice, barley, and sorghum (FAO STAT, 2019). Annually, approximately 10 million hectares are dedicated to oats cultivation globally, producing around 23 million metric tonnes of grain (USDA, 2020-21).

India's livestock sector is growing much faster (4.6% rate) than its crop sector in terms of gross value output. However, achieving optimal livestock productivity hinges on having enough high-quality fodder. A key reason for low dairy animal productivity in India is the shortage of such quality feed (Kumari *et al*., 2022). Both the availability and nutritional quality (including protein, fat, minerals and fiber) of fodder significantly impact animal growth, milk yield and overall condition (Singh *et al*., 2012). Currently, India faces considerable strain on its feed resources, with a net deficit of 30.7% in dry fodder. This deficit is projected to decrease but remain substantial at 24.6% by 2030 and 18.4% by 2050 (Anonymous, 2020a).

Oats (*Avena sativa* L.) serves as forage (green fodder, hay, silage) and its grain is a livestock/poultry concentrate. Green fodder (DM basis) contains approx. 10-11% CP, 55-63% NDF, and 30-32% ADF (Das *et al.*, 2015). Oats is a fast-growing crop, yielding substantial, nutritious fresh fodder in 60-70 days. This fodder is a valuable source of protein, fiber, and minerals (Bilal *et al.*, 2017). Widely cultivated for green fodder, oats is favored for its vigorous growth, high palatability (preferred over wheat and barley), rich nutrition, and soluble carbohydrates (Hameed *et al.*, 2014). It is also well-suited for marginal environments like cool, wet climates and low-fertility soils, performing better than other cereals (Welch, 2012). Oats hold a prominent place among India's rabi fodders, providing high tonnage. It is well adapted across India, particularly in the North and Northwest due to good growth, quick regrowth, and nutritional quality. Fodder oats cover about 0.25 million hectares in India, with major cultivation in Uttar Pradesh (34%), Punjab (20%), Bihar (16%), Haryana (9%), and Madhya Pradesh (6%) (Chand *et al.*, 2025).

Driven by the expanding dairy industry, there is growing interest in improving oats for its nutritious fodder and high-energy grains used in animal feed (Ruwali *et al.*, 2013). Developing new, specific oat varieties requires effectively utilizing available genetic resources. Analyzing the genetic makeup and managing variability are crucial steps for identifying promising parent genotypes with long-term potential. Standard genetic parameters like variance (GCV & PCV), heritability, and genetic advance are used to assess variation magnitude. High heritability and genetic advance for yield components are key indicators for selecting high-yielding lines. Understanding correlations between yield and its related traits helps streamline the selection process by identifying the most relevant characteristics. Genetic diversity provides a broad base for incorporating genes related to yield and other beneficial traits. Consequently, this research aimed to estimate the genetic parameters of variability, correlation, and diversity in oats.

## Materials and Methods

The present investigation was carried out at Dryland Agriculture Research Station (DARS), Rangreth, Sher-e-Kashmir University of Agricultural Sciences & Technology of Kashmir (SKUAST-K), Shalimar. In this study, fifty-five oats genotypes were evaluated using a randomized block design with three replications. Recommended package of practices were followed to raise a good crop. The observations were recorded on the following eight quantitative traits viz., days to 50 per cent flowering, leaf area index (LAI), number of tillers meter$^{-1}$ row, culm diameter (mm), plant height (cm), leaf stem ratio, green fodder yield meter$^{-1}$ row (kg), flag leaf length (cm) and four quality parameters viz., Crude Protein (CP%), Neutral Detergent Fibre (NDF) (%), Acid Detergent Fibre (ADF) (%) and Total Ash (TA %). The data was recorded by randomly selecting five plants from each genotype.

Estimation of quality parameters like crude protein was done by oven drying a sample of dry fodder (500g) at 100$^{o}$ C for 24 hours and then dried sample was crushed, replication wise, to a fine powder in order to estimate the per cent crude protein content by Kjeldahl method. Crude protein (CP) and total ash (TA) yields were calculated by multiplying their content (AOAC, 2005) with dry fodder yield. The fibre fraction such as neutral detergent fibre (NDF) and acid detergent fibre (ADF) were estimated using Soest *et al.* (1991) method.

The data was statistically analyzed for each trait using Analysis of Variance (ANOVA) as per the procedure suggested by Verma *et al.* (1987), with broad-sense heritability and genetic advance (as a percentage of means) calculated using Johnson *et al.* (1955a). Genotypic and phenotypic variances and covariances were substituted into formulae suggested by Johnson *et al.* (1955b) to derive correlation coefficients for all character pairs. Genetic divergence was assessed through method proposed by Rao (1952) and Singh and Chaudhary (1985), while Wilk's criterion tested the significance of pooled differences in mean values across characters. Plot means for genotypes were transformed into uncorrelated variables via pivotal condensation method, and genotype clustering was performed using Tocher's method.

## Results and Discussion

### ANOVA

Analysis of variance revealed highly significant differences among the genotypes for all the traits under study (Table 1). This signifies a wide range of genetic variability within the experimental material which provides a basis for selecting superior genotypes. This was in conformation with those reported by other researchers like Ahmad *et al.* (2013) and Jaipal and Shekhawat (2016).

The estimates of phenotypic coefficient of variation (PCV) were found to be higher than genotypic coefficients of variation (GCV) for all the characters studied (Table 2), suggesting a considerable influence from the environment. Higher estimates of PCV and GCV were recorded for culm diameter, no. of tillers $m^{-1}$, green fodder yield and plant height. Whereas, moderate estimates were observed in leaf area index and leaf stem ratio. Lower estimates of PCV and GCV were recorded for days to 50% flowering. Earlier oat researchers (Singh, 1989; Sahu and Tiwari, 2020) also reported similar results. To accurately assess inheritable variation in a genotype, relying solely on genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is insufficient. A complete and accurate picture requires considering heritability and genetic advance together, as both are critical for effective trait improvement via selection.

In the present investigation very high values of heritability (96.0-97.0 per cent) were exhibited by green fodder yield, leaf stem ratio and number of tillers $m^{-1}$ (Table 2). Whereas, days to 50 per cent flowering exhibited a value of 90.0 per cent, plant height with a value of 95.0 per cent, culm diameter equals to 92.0 percent, leaf area index exhibited a value of 90.0 per cent. The lowest value for heritability was exhibited by flag leaf length (84.0 per cent). The estimates revealed that the expected genetic gain was high (>30.0 per cent) for plant height, number of tillers $m^{-1}$, green fodder yield q $ha^{-1}$, culm diameter, flag leaf length (cm). Whereas, it was moderate (10.0-30.0 per cent) for leaf area index and leaf stem ratio and low (<10.0 per cent) for days to 50 per cent flowering. In the present study, high heritability was coupled with high genetic advance (as per cent of mean) in number tillers $m^{-1}$, green fodder yield (q $ha^{-1}$), leaf stem ratio, plant height (cm), culm diameter (mm), days to 50 per cent flowering, leaf area index. Flag leaf length indicated a low value. Similar results were reported by several workers viz., Khan and Sukumar (2001); Jaipal and Shekhawat (2016).

## Correlation analysis

Estimates of genotypic correlations among the characters have therefore, been found useful in planning and evaluating breeding programmes (Johnson *et al*., 1955b; Al-jibouri *et al*., 1958). Results indicated that many yield contributing traits viz., plant height, no. of tillers $m^{-1}$, flag leaf length (cm), leaf area index and culm diameter (mm) had significant and positive correlation with green fodder yield which illustrated that higher mean values for these traits can increase the yield and days to 50 per cent flowering showed a significant but negative correlation with green fodder yield (q $ha^{-1}$), which is desirable. Leaf area index exhibited significant positive correlation with number of tillers $m^{-1}$, and green fodder yield (q $ha^{-1}$) and a significant negative correlation with culm diameter (mm) and days to 50 per cent flowering. However, culm diameter was negatively and significantly correlated with no. of tillers $m^{-1}$ and plant height. Flag leaf length (cm) was found to exhibit a significant negative correlation with days to 50 per cent flowering. The selection based on these traits will result in improving the green fodder yield in oats. Positive and significant relationship has been reported in oats, for forage yield with plant height (Choubey *et al.,* 1996; Ahmad *et al*., 2014). The results clearly revealed a scope of simultaneous improvement of these traits through selection. Kishore *et al.* (1989) and Srivastava *et al.* (1995) reported similar results in forage oats.

## Genetic diversity

Analysis of variance revealed the significant differences among the germplasm lines (Table 4) indicating the sufficient genetic variation among the lines for all the traits used in the study. The 'V' statistics which is a Wilk's criterion was significant and its value was 5138.59. Similar results have also been reported by Krishan-Pal *et al.* (1993) and Singh and Mishra (1996). The $D^2$ analysis on morphological traits grouped into 12 clusters based on distance ranges for the tree. Cluster I comprised of maximum genotypes (35) followed by cluster VIII (10), Cluster II, III, IV, V, VI, VII, IX, X, XI, XII (1 each) as shown in Table 5 and Fig. 2. Higher number of lines in single cluster depicts that lines had less genetic variation among them and are more closely related. A crossing within these clusters will be of less use in improvement programme. Clustering of genotypes into different groups through $D^2$ statistics has also been reported by Yadav *et al.* (2001).

The mean intra and inter cluster distance ($D^2$) values (Table 6) revealed that cluster VIII had the highest intra cluster distance ($D^2$) value of 69.95 followed by cluster I (53. 48). The inter cluster distance $D^2$ value was highest between cluster V and cluster XII (356.36) followed by cluster III and cluster XII (303.40) and cluster VIII and cluster XII (268.66) suggesting significant diversity among lines of these clusters. So, crossing between lines belonging to these clusters may result into high heterosis, which could be exploited in oat improvement, as the crossing among the pure lines leads to formation of different transgressive segregants which are utilized to study heterotic effects. The minimum inter cluster distance was observed between cluster IV and cluster

VII (19.79) and between cluster III and cluster VI (33.46) indicating the narrow genetic diversity and close relationship for many traits of the lines in these clusters.

The cluster mean values for eight agro-morphological and physiological traits were estimated and summarized in Table 7. A critical analysis into results revealed that all the clusters exhibited varying differences for all the characters under study and variable mean is observed in both the condition. Cluster mean analysis helps in identification of suitable donors for hybridization to obtain superior segregants separately to enhance the seed yield. An overview of cluster means results revealed the highest cluster means for earliness (140.33 days) has been shown by cluster X. Superiority in terms of green fodder yield (444.45 q ha$^{-1}$), number of tillers m$^{-1}$ (184.77) was exhibited by cluster VI accommodating JPO-39. The results clearly indicate that JPO-23 grouped in cluster XII exhibited highest mean performance for plant height (152.67). Whereas, highest cluster means for culm diameter (9.27 mm) was exhibited by Roseffe (cluster V). The highest cluster mean for flag leaf length (26.67 cm) was exhibited by cluster X accommodating JPO-65 and the highest cluster mean for leaf stem ratio was exhibited by cluster IV and cluster VII (0.55 each). Comparative evaluation of cluster means suggested that for improving specific character, the genotypes should be taken from the cluster having high mean value for that character. Sardana *et al.* (1997) was observed that cluster means and coefficient of variation are an interacting picture of diversity.

The characteristics that cause genetic variation in crops vary depending on the specific crop (Murty and Arunachalam, 1967). In the present investigation, it was found that the number of tillers m$^{-1}$ was the primary driver of this divergence (28.55%), followed by green fodder yield (23.29%), leaf-stem ratio (13.0%), and plant height (12.59%). Minor contributors included culm diameter, days to 50% flowering, leaf area index, and flag leaf length (Table 8). This means that breeders should prioritize traits with the greatest contribution to divergence when selecting parents for crossing program (De *et al.*, 1998).

**Table 1 :** Analysis of variance for different morphological, maturity and forage component traits in oats (*Avena sativa* L.)

| Source of variation | d.f | Day to 50% flowering | Plant height (cm) | No. of tillers (m$^{-1}$) | Culm diameter (mm) | Leaf stem ratio | Green fodder yield (qha$^{-1}$) | Flag leaf length (cm) | Leaf Area Index |
|---|---|---|---|---|---|---|---|---|---|
| Replication | 2 | 6.61 | 461.30 | 571.22 | 1.07 | 0.0001 | 0.18 | 16.11 | 0.03 |
| Genotypes | 54 | 195.59** | 2347.91** | 21146.17** | 14.46** | 0.0077** | 156.34** | 52.78** | 0.80** |
| Error | 108 | 6.66 | 35.97 | 206.98 | 0.37 | 0.0001 | 1.64 | 2.94 | 0.02 |

**Table 2.** Estimates of mean, range, phenotypic and genotypic variance, phenotypic and genotypic coefficient of variation for different morphological, maturity and forage component traits in oats (*Avena sativa* L.)

| Parameters | Day to 50% flowering | Plant height (cm) | Culm diameter (mm) | No. of tillers m$^{-1}$ | Flag leaf length (cm) | Leaf area index | Green fodder yield (qha$^{-1}$) | Leaf stem ratio |
|---|---|---|---|---|---|---|---|---|
| **Mean** | 160.34 | 118.59 | 5.26 | 139.77 | 21.48 | 4.21 | 394.15 | 0.43 |
| **Range** | (140.33-174.0) | (78.0-152.66) | (1.10-9.79) | (84.00-190.67) | (13.66-31.66) | (3.33-5.24) | (327.05-444.45) | (0.32-0.55) |
| **Phenotypic variance** | 69.64 | 806.62 | 5.07 | 7186.71 | 19.55 | 0.28 | 53.21 | 0.0026 |
| **Genotypic variance** | 62.97 | 770.64 | 4.6 | 6967.72 | 16.61 | 0.25 | 51.56 | 0.0025 |
| **PCV** | 5.20 | 23.94 | 42.80 | 39.65 | 20.58 | 12.73 | 28.60 | 11.83 |
| **GCV** | 4.94 | 23.40 | 41.18 | 39.08 | 18.26 | 12.09 | 28.15 | 11.60 |
| **Heritability (Broad sense)** | 0.9 | 0.95 | 0.92 | 0.97 | 0.84 | 0.90 | 0.96 | 0.96 |
| **Expected genetic gain (per cent of mean)** | 9.69 | 47.13 | 81.62 | 79.33 | 36.01 | 23.65 | 57.10 | 23.44 |

**Table 3 :** Genotypic correlation coefficients for morphological, maturity and forage component traits in oats (*Avena sativa* L.)

| **Parameters** | **Day to 50% flowering** | **Plant height (cm)** | **Culm diameter (mm)** | **No. of tillers m$^{-1}$** | **Flag leaf length (cm)** | **Leaf area index** | **Green fodder yield (qha$^{-1}$)** | **Leaf stem ratio** |
|---|---|---|---|---|---|---|---|---|
| Day to 50% flowering | - | -0.0023 | -0.0885 | 0.2552* | -0.3434** | -0.2750* | -0.2923* | 0.1790 |
| Plant height (cm) | | - | -0.2701* | 0.1550 | 0.1685 | 0.0590 | 0.5174** | -0.0381 |
| Culm diameter (mm) | | | - | -0.3430** | 0.1880 | -0.3096** | 0.6342** | -0.1954 |
| No. of tillers m$^{-1}$ | | | | - | -0.0336 | 0.9142** | 0.8386** | 0.0901 |
| Flag leaf length (cm) | | | | | - | 0.3519** | 0.2815* | -0.1120 |
| Leaf area index | | | | | | - | 0.8135** | 0.0204 |
| Green fodder yield (qha$^{-1}$) | | | | | | | - | 0.0657 |
| Leaf stem ratio | | | | | | | | - |

*, **, significant at 5% and 1 % level of significance respectively

**Table 4 :** Analysis of variance for dispersion of oats genotypes

| **Source of variation** | **d.f** | **Mean squares** |
|---|---|---|
| Genotypes | 54 | 8.69** |
| Error | 107 | 4.38 |
| Total | 161 | 0.00 |

**, significant at 1.0 per cent level of significance

Wilk's criterion = 5.76

V Statistics = 5138.59

**Table 5 :** Distribution of different oat genotypes into clusters based on D$^2$ statistics

| **Cluster** | **No. of genotypes in the cluster** | **Detail of genotypes** |
|---|---|---|
| I | 35 | JPO-21, JPO-2, JPO-17, JPO-70, WINTOK, JPO-45, JPO-69, GRAIG, JPO-79, JPO-72, EC-528916, ARFOB, JPO-67, JPO-42, JPO-166, WINTER TURF, JPO-34, JPO-43, FRUGUNATE, JPO-32, JPO-33, AVNA x ASTRIGOSA, JPO-81, DIADEM, MIRABLE, MAJECAR, JPO-40, JPO-37, JPO-18, KINGFISHER, EMPORER, JPO-13, JPO-26, AZUL, JPO-52. |
| II | 1 | JPO-19 |
| III | 1 | MILLENIUM |
| IV | 1 | NORLINE |
| V | 1 | ROSEFFE |
| VI | 1 | JPO-39 |
| VII | 1 | JPO-7 |
| VIII | 10 | JPO-49, JPO-11, JPO-51, JPO-66, JPO-25, SABZAAR, JPO-73, U-ZARK, EC-528874, JPO-31 |
| IX | 1 | JPO-24 |
| X | 1 | JPO-65 |
| XI | 1 | JPO-63 |
| XII | 1 | JPO-23 |

**Table 6 :** Average inter-cluster (above diagonal) and intra-cluster (diagonal) D$^2$ values among different oats genotypes

| Cluster | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII | Cluster VIII | Cluster IX | Cluster X | Cluster XI | Cluster XII |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | **53.48** | 89.63 | 88.54 | 97.00 | 84.12 | 81.56 | 109.68 | 129.40 | 97.80 | 82.22 | 93.31 | 218.81 |
| II | | **0.00** | **112.52** | 42.47 | **128.13** | 95.24 | 88.27 | 174.82 | 53.20 | 137.56 | 115.86 | 89.83 |
| III | | | **0.00** | **143.01** | 54.27 | 33.46 | **190.18** | **260.40** | 89.27 | 106.56 | 59.12 | 303.40 |
| IV | | | | **0.00** | 99.21 | **132.99** | 19.79 | 118.11 | 30.13 | **191.76** | 152.00 | 193.34 |
| V | | | | | **0.00** | 101.59 | 130.15 | 225.69 | 71.04 | 146.52 | 55.38 | **356.36** |
| VI | | | | | | **0.00** | 179.46 | 211.76 | 88.72 | 101.66 | 114.39 | 245.18 |
| VII | | | | | | | **0.00** | 88.18 | 82.39 | 210.57 | 184.16 | 217.92 |
| VIII | | | | | | | | **69.95** | **179.84** | 174.19 | **252.91** | 268.66 |
| IX | | | | | | | | | **0.00** | 186.97 | 132.96 | 233.50 |
| X | | | | | | | | | | **0.00** | 59.12 | 197.98 |
| XI | | | | | | | | | | | **0.00** | 241.30 |
| XII | | | | | | | | | | | | **0.00** |

**Table 7 :** Cluster means and (%) contribution for morphological, maturity and forage component traits in different clusters of oats genotypes

| Clusters | Days to 50% flowering | Plant height (cm) | Culm diameter (mm) | Number of tillers $m^{-1}$ | Flag leaf length (cm) | Leaf Area Index | Green fodder yield ($qha^{-1}$) | Leaf stem ratio |
|---|---|---|---|---|---|---|---|---|
| I | 161.70 | 114.98 | 6.93 | 119.33 | 21.29 | 4.02 | 381.37 | 0.42 |
| II | 166.33 | 169.00 | 3.63 | 171.33 | 26.00 | 3.56 | 436.15 | 0.48 |
| III | 162.00 | 99.00 | 8.30 | 129.08 | 16.67 | 3.54 | 398.10 | 0.42 |
| IV | 163.67 | 133.00 | 5.13 | 149.67 | 24.17 | 4.37 | 421.22 | 0.55 |
| V | 159.33 | 85.67 | 9.27 | 107.00 | 23.17 | 4.20 | 369.09 | 0.48 |
| VI | 174.00 | 110.33 | 8.10 | 184.77 | 21.50 | 4.22 | 444.45 | 0.39 |
| VII | 165.00 | 133.33 | 4.73 | 162.67 | 16.50 | 4.91 | 430.39 | 0.55 |
| VIII | 156.00 | 113.25 | 8.10 | 99.67 | 21.12 | 4.94 | 351.01 | 0.46 |
| IX | 163.33 | 120.33 | 5.53 | 144.00 | 24.83 | 3.96 | 417.12 | 0.52 |
| X | 140.33 | 130.90 | 5.43 | 84.33 | 26.67 | 4.31 | 327.05 | 0.33 |
| XI | 143.00 | 131.67 | 5.32 | 91.33 | 23.67 | 4.11 | 345.27 | 0.41 |
| XII | 162.67 | 152.67 | 3.79 | 135.00 | 22.50 | 4.21 | 408.68 | 0.41 |
| (%) contribution | 5.93 | 12.59 | 10.17 | 28.55 | 2.29 | 4.18 | 23.29 | 13.0 |

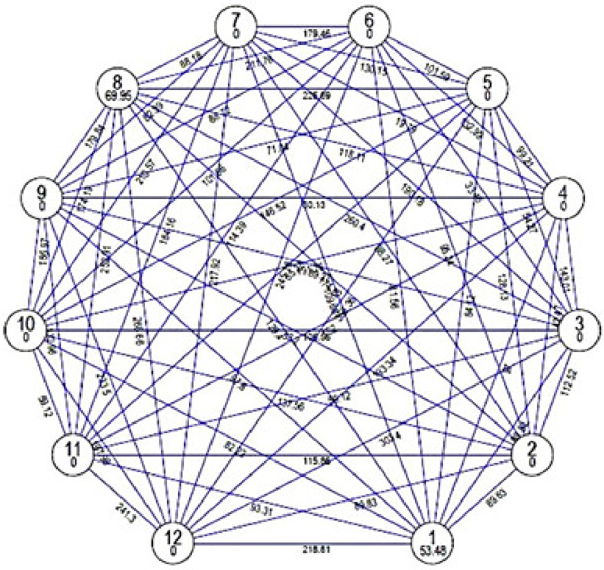

**Fig. 1:** Mahalanobis Euclidean Distance (Not to the Scale)

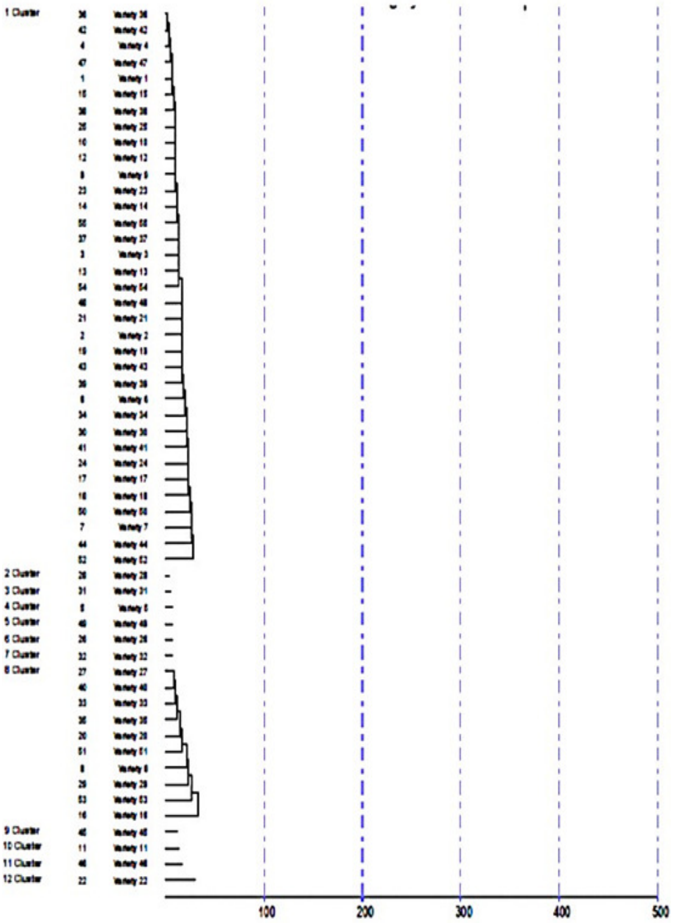

**Fig. 2:** Clustering by Tocher Method

## Conclusion

From the present study, it was concluded that the plant height, culm diameter, no. of tillers $m^{-1}$ and green fodder yield showed high GCV, PCV, heritability as well as GAM. Hence, these traits should be taken into consideration at the time of selecting the genotypes for enhancing the fodder yield of oat. Based on the diversity studies, the traits viz., no. of tillers $m^{-1}$, plant height, leaf stem ratio and green fodder yield were important traits that contributed maximum divergence to the genotypes. As a result, the current study can be used to identify the variables that contribute to the variability and choose the varieties to use as donors for the enhancement of characters in the future breeding programme.

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