**Investigation of Various Quantitative Traits Interaction and Genetic Variability in Oats (*Avena Sativa* L)**

**Abstract**

The present study, titled “Investigation of Various Quantitative Traits Interaction and Genetic Variability in Oats (*Avena Sativa* L)” was conducted during the *Rabi* season of 2024–25 at the Agricultural Research Farm, Prof. Rajendra Singh (Rajju Bhaiya) University, Naini, Prayagraj, Uttar Pradesh. The present investigation entitled “Investigation of Various Quantitative Traits Interaction and Genetic Variability in Oats (Avena sativa L.)” was carried out during the Rabi season of 2024–25 at the Agricultural Research Farm, Prof. Rajendra Singh (Rajju Bhaiya) University, Naini, Prayagraj, Uttar Pradesh. Thirteen oat genotypes, including a check variety, were evaluated in a randomized block design with three replications to assess genetic variability, heritability, genetic advance, correlation, and path coefficient analysis across 18 quantitative traits. Analysis of variance revealed highly significant differences among genotypes for all traits, indicating the presence of substantial genetic variability. High genotypic and phenotypic coefficients of variation were observed for seed yield per plot (88.92% and 89.27%), seed yield per plant (18.44% and 18.93%), and number of tillers per plant (12.44% and 16.40%), suggesting the prevalence of additive gene action. Heritability estimates ranged from moderate to high, with the highest values recorded for seed yield per plot (99.21%), days to 75% maturity (95.83%), and seed yield per plant (94.96%). Correspondingly, high genetic advance as percentage of mean was noted for seed yield per plot (182.45%), seed yield per plant (37.03%), and number of tillers per plant (19.42%). Genotypic correlation analysis revealed that seed yield per plot exhibited highly significant and positive associations with harvest index (0.507\*\*), seed yield per plant (0.385\*), biological yield (0.496\*\*), and number of seeds per panicle (0.720\*\*), highlighting their importance in yield improvement. Path coefficient analysis at the genotypic level indicated that biological yield (1.053), harvest index (0.706), and panicle length (0.390) exerted the highest direct positive effects on seed yield per plot, confirming their role as key determinants for enhancing oat productivity.

***Key words:***Oat, Heritability, Genetic advance, Correlation coefficient, Path analysis.

**Introduction**

Oats (*Avena sativa* L*.)* is an important forage annual crop of Rabi season belongs to family Gramineae and ranks sixth in production among all cereal crops next to wheat, maize, rice, barley and sorghum in the world scene. The genus *Avena* is large and diverse containing both wild and cultivated polyploidy series with a basic chromosome number of x=7. Three naturally occurring ploidy levels are known with the genus, diploids (2n=2x=14), tetraploid (2x=4x=28) and hexaploid (2n=6x=42). Differing from other cereal grains such as wheat (*Triticum aestivum* L.) and barley *(Hordeum vulgare* L.), oat is a multipurpose cereal crop grown worldwide for human food and animal feed (Dubey *et al.,* 2014).

It is basically a European and North American crop. It is best grown in temperate regions of the world as they are winter hardy in nature. Oat requires cool and moist climate. It is an important winter season cereal fodder crop (kumari *et al.,* 2019). Oat is sensitive to hot, dry weather. For these reasons, world oat production is concentrated from the 40th latitude in the southern hemisphere to the 60th latitude in the northern hemisphere. Thus, includes mainly Australia, China, North America, Scandinavian, Russia and related countries (Schrickel 1986). The total area under cultivated fodders is 8.6 million ha on individual crop basis. The crop occupies maximum area in Uttar Pradesh (34 %), followed by Punjab (20 %), Bihar (16 %), Haryana (9 %) and Madhya Pradesh (6 %) (Kumar, *et al.,* 2021).

In recent clinical studies on human health benefits, it was found that oat consumption reduces cardiovascular risks like diabetes, blood pressure control, weight management and gastrointestinal health (Anderson and Bridges 1993; Wrick 1993; Wrick 1994; Stark and Madar 1994) where as β glucan found to have cholesterol lowering properties. The consumption of oat meal and oat bran reduces total plasma cholesterol and LDL-cholesterol levels (Saltzman et al. 2001).

Cultivation of oats with legumes such as berseem provides a better opportunity to obtain higher yields of high-quality fodder. Nowadays, the demand for oats for human consumption has increased, especially due to the demonstrated dietary benefits of oats as whole grain products.

Oat is rich in energy, protein, vitamin B, phosphorus and iron. The nutritive value of oat forage is high and showed to have dry matter digestibility in excess of 75% when fed to dairy cattle (Burgess *et al*., 1972).And the Nutritional composition of whole grain oat is Protein 15 - 17 %, Starch and sugars 59 - 70 %, Fat 4.5 %, Total dietary fiber 12 %, Ash 3.5 %, ß-Glucan 2 - 6 %, Cellulose 14 %, Lignin 2.4 %, (Usman *et al*., 2010).

Because of the growing awareness of the public toward healthy eating habits, oat has received increased attention from scientific researchers and industries. Food-based companies are considering better nutritional composition together with the popularity of ancient grains and are developing novel food products by incorporating oats as an ancient grain in breakfast cereals, beverages, bread, and infant foods (Boukid, *et al.,*2018). Although oats are mainly used in breakfast cereals and snack bars, the inclusion of it in different products would greatly benefit consumers because of its health promoting attributes, (Sang, *et al.,*2017and Paudel, *et al.,* 2018).

During the processing of oats for human consumption, the hulls or glumes are eliminated, resulting in the naked caryopsis, commonly referred to as groats, which is typically consumed as whole grain.

According to the USDA Foreign Agricultural Service's April 2025 report, global oat production for the 2024/2025 marketing year is projected at approximately 22.62 million metric tons, marking a 16% increase from the previous year.​The leading countries in oat production were as follows European Union (7.75-34%), Canada (3.36-15%), Russia (3.00-13%), Australia (1.31-6%),Brazil (1.04-5%), United Kingdom (1.00-4%), United States (0.98-4%), China (0.85-4%)Argentina (0.60-3%), Chile (0.48-2%), The European Union leads global oat production, contributing over a third of the total output, followed by Canada and Russia.

Enhancing oat yield and quality characteristics significantly relies on a comprehensive understanding of genetic variability and the interrelationships among different quantitative traits. Evaluating genetic variability is an essential component of any crop enhancement initiative, as it lays the groundwork for selection and hybridization processes. Quantitative traits, including plant height, tiller count, leaf quantity, spikelets per panicle, test weight, and grain yield, are influenced by numerous genes and environmental factors. An estimation of genetic variability is beneficial for determining appropriate selection criteria for the genetic enhancement of crop yield.The analysis of variance, along with genotypic and phenotypic coefficients of variation (GCV & PCV), heritability, and genetic advance, are commonly utilized parameters for estimating variability. These parameters assist in identifying traits that are predominantly influenced by genetic factors rather than environmental conditions. Additionally, correlation and path coefficient analyses contribute to a deeper understanding of the nature and extent of relationships among traits, as well as their direct or indirect impacts on yield, which is crucial for effective selection. Numerous studies have indicated significant variation among oat genotypes concerning yield and its components, suggesting the possibility for genetic enhancement (Saleh, 2017; Surje & De, 2014). Investigating the relationship between yield and its component traits can assist breeders in creating high-yielding and nutritionally superior oat varieties that are appropriate for various agro-ecological environments.

**Material and methods**

The present investigation entitled “**Investigation of Various Quantitative Traits Interaction and Genetic Variability in Oats (*Avena Sativa* L.)**” was conducted at agriculture research field Department of Genetics and plant breeding, Prof. Rajendra Singh(Rajju Bhaiya) University Naini Prayagraj during *Rabi* season 2024-25, in the experimental Design fallowed by Randomized block designmethod with three replications. And 2 m2 plot size. The experimental material used in the research work comprises of 13 diverse oats genotypes one check variety NDO-952. The genotypes were procured from ANDAUT Ayodhya.

The observation were recorded for five randomly superior selected plant for eighteen different characters viz., Plant Height 30 ,60,90 DAS ,Number of tillers Per Plant ,Days To 50% Flowering ,Leaves Per Plant ,Leaf Length in (cm ),leaf width (cm) ,Length of Panicle in (cm) ,DAS To 75% Maturity Number of Seed Per spikelet, Seed Yield Per Plant in (g), seed yield per plot(kg)1000 Seed Weight in (g), Biological Yield (kg) , Harvest Index ,For the experiment's design, an analysis of variance was carried out separately for every character.

**Result and discussion**

Analysis of variance showed significant differences among 13 genotypes for 18 characters studied. It shows the significant difference among all genotype at 1% and 5% level of significance. The mean sum of square given in table (4.1) for different character. The highly mean sum of square is recorded for the trait viz., DAS to 50% flowering, plant height at 30, 60, 90, DAS, No. Of leaves per plant, Leaf length, Leaf width, Das to 75% maturity, No. Of seed per panicle, Pedicle length, Panicle length, No. Of tillers per plant, Number of spikelets per panicle. Test weight(1000g), biological yield, Harvest index, Seed yield per plant(g), Seed yield per plot(kg). Similar finding is recorded by

**Sofi *et al.* (2012)** conducted an analysis of variance across various traits and found that genotypes differed significantly for seed yield per hectare, seed breadth, tillers per m², seed length, and green fodder yield—along with high genotypic coefficients of variation (GCV), high heritability, and high genetic advance—demonstrating strong additive genetic control and effective selection potential

**Dubey *et al*. (2014)** similarly carried out ANOVA on oat genotypes and recorded that genotypic mean squares were significant for traits such as number of tillers per plant and leaf length, indicating notable genetic variability

**Bind *et al*. (2016)** reported that in their ANOVA, the mean squares due to genotype were significant for all 11 traits studied, reinforcing the presence of sufficient genetic variance suitable for selection

**Kumari, T *et al.,* (2019)** The analysis of variance investigated during the study indicated significant differences among the genotypes for all the characters studied. seed yield. flag leaf length. leaf width.

**Table 1: Analysis of variance of different eighteen characters of oat genotype**

|  |  |  |  |
| --- | --- | --- | --- |
| Genotypes | Mean sum of squares | | |
| Replications | Treatment | Error |
| (d.f=2) | (d.f=12) | (d.f=24) |
| 30 das plant height | 5.392 | 18.385\*\* | 5.140 |
| 60 das plant height | 3.620 | 5.380\*\* | 1.691 |
| 90 das plant height | 1.33 | 3.88\* | 0.88 |
| no. of leaves per plant | 0.081 | 0.245\* | 0.084 |
| leaf length | 4.947 | 20.540\*\* | 2.695 |
| leaf width | 0.004 | 0.012\* | 0.005 |
| das to 50% flowering | 0.077 | 28.000\*\* | 1.244 |
| das to 75% maturity | 18.487 | 39.923\*\* | 0.571 |
| no. of seed per panicle | 1.103 | 21.706\*\* | 6.880 |
| pedicle length | 0.467 | 4.886\*\* | 0.776 |
| penicle length | 0.148 | 4.420\*\* | 0.635 |
| no. of tillers per plant | 0.048 | 0.304\* | 0.060 |
| number of spiklets per penicle | 5.846 | 46.632\*\* | 4.068 |
| test weight | 0.39 | 3.47\* | 0.23 |
| Biological yield | 43293.9487 | 76421.419\*\* | 12100.643 |
| Harvest index | 296.9679 | 65.0587\*\* | 24.5866 |
| Seed yield per plant | 0.004 | 0.398\* | 0.021 |
| Seed yield per plot | 21262.259 | 419971.282\*\* | 3343.772 |

**Estimation of coefficient of variation, heritability and genetic advance.**

The estimates of variability parameters for 18 different characters in thirteen genotypes of oat are presented in table 2.

**Genotypic coefficient of variability:**

The highest genotypic coefficient of variation (GCV) was recorded for seed yield per plot (88.92%), followed by seed yield per plant (18.44%), pedicle length (12.57%), and number of tillers per plant (12.44%), indicating high genetic variability in these traits. Moderate GCV was observed in number of pods per panicle (7.98%), leaf length (8.41%), biological yield kg (8.10%), and harvest index (9.03%), suggesting reasonable genetic diversity. However, low GCV was noted for panicle length (3.96%), number of leaves per plant (3.96%), DAS to 50% flowering (3.89%), DAS to 75% maturity (3.01%), test weight (2.86%), leaf width (5.64%), and all stages of plant height (30 DAS: 4.45%, 60 DAS: 1.12%, 90 DAS: 0.70%), indicating limited genetic variation in these traits. Similar finding is recorded by Bind *et al*., (2016), Singh *et al.,* (2019), Rawat, *et al****.,*** (2022).

**Phenotypic coefficient of variability:**

Highest phenotypic coefficient of variation (PCV) was exhibited by seed yield per plot (89.27%), followed by seed yield per plant (18.93%), pedicle length (15.73%), and number of tillers per plant (16.40%), reflecting substantial total variability influenced by both genetic and environmental factors. Moderate PCV was observed in leaf length (10.14%), harvest index (15.17%), biological yield (10.13%), and number of pods per panicle (9.05%), indicating moderate variability. Traits such as test weight (3.16%), panicle length (4.85%), number of leaves per plant (6.35%), leaf width (9.60%), DAS to 50% flowering (4.12%), DAS to 75% maturity (3.07%), and plant height at 30 DAS (6.55%), 60 DAS (1.72%), and 90 DAS (0.96%) showed low PCV, suggesting these traits are more stable with less environmental influence. Similar finding is recorded by Bind *et al*., (2016), Singh *et al.,* (2019), Rawat, *et al****.,*** (2022).

**Heritability and genetic advance**

High heritability in broad sense was observed for seed yield per plot (99.21%), seed yield per plant (94.96%), DAS to 75% maturity (95.83%), DAS to 50% flowering (89.23%), and test weight (82.30%), indicating a strong genetic control over these traits. Other traits with high heritability included number of pods per panicle (77.72%), leaf length (68.82%), panicle length (66.53%), biological yield (63.92%), pedicle length (63.84%), and number of tillers per plant (57.48%). Moderate heritability was recorded for plant height 90 DAS (53.24%), plant height 30 DAS (46.21%), and plant height 60 DAS (42.10%), while number of leaves per plant (38.86%) and leaf width (34.57%). Similar finding is recorded by Bind *et al*., (2016), Jaiswal *et al.,* (2022), Mathavaraj *et al*.,(2024).

**Table 2: Estimation of components of variance and genetic parameters for different eighteen characters of oat genotype**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Genotypes | Vg | Vp | **GCV** | **PCV** | **HERTI** | **GA** | **GA AS %** |
| 30 das plant height | 4.42 | 9.55 | 4.45 | 6.55 | 46.21 | 2.94 | 6.24 |
| 60 das plant height | 1.23 | 2.92 | 1.12 | 1.72 | 42.10 | 1.48 | 1.49 |
| 90 das plant height | 1.00 | 1.88 | 0.70 | 0.96 | 53.24 | 1.50 | 1.05 |
| No. Of leaves per plant | 0.05 | 0.14 | 3.96 | 6.35 | 38.86 | 0.30 | 5.08 |
| Leaf length | 5.95 | 8.64 | 8.41 | 10.14 | 68.82 | 4.17 | 14.37 |
| Leaf width | 0.00 | 0.01 | 5.64 | 9.60 | 34.57 | 0.06 | 6.84 |
| Das to 50% flowering | 8.97 | 10.06 | 3.89 | 4.12 | 89.23 | 5.83 | 7.57 |
| Das to 75% maturity | 13.12 | 13.69 | 3.01 | 3.07 | 95.83 | 7.30 | 6.06 |
| No. Of seed per panicle | 4.94 | 11.82 | 1.76 | 2.72 | 41.80 | 2.96 | 2.34 |
| Pedicle length | 1.37 | 2.15 | 12.57 | 15.73 | 63.84 | 1.93 | 20.69 |
| Penicle length | 1.26 | 1.90 | 3.96 | 4.85 | 66.53 | 1.89 | 6.65 |
| No. Of tillers per plant | 0.08 | 0.14 | 12.44 | 16.40 | 57.48 | 0.45 | 19.42 |
| Number ofspiklets per penicle | 14.19 | 18.26 | 7.98 | 9.05 | 77.72 | 6.84 | 14.48 |
| Test weight | 1.08 | 1.31 | 2.86 | 3.16 | 82.30 | 1.94 | 5.35 |
| Biological yield | 21440.26 | 33540.90 | 8.10 | 10.13 | 63.92 | 241.16 | 13.34 |
| Harvest index | 13.4907 | 38.0773 | 9.03 | 15.17 | 35.43 | 4.50 | 11.07 |
| Seed yield per plant | 0.391 | 0.412 | 18.44 | 18.93 | 94.96 | 1.26 | 37.03 |
| Seed yield per plot | 418856.69 | 422200.46 | 88.92 | 89.27 | 99.21 | 1327.92 | 182.45 |

**Genetic advance**

The highest genetic advance (GA as % of mean) was recorded for seed yield per plant (37.03%), followed by seed yield per plot (182.45%), harvest index (11.07%), number of tillers per plant (19.42%), and pedicle length (20.69%), indicating good potential for improvement through selection. Other traits with moderately high genetic advance included leaf length (14.37%), number of pods per panicle (14.48%), biological yield (13.34%), and leaf width (6.84%). Lower values of genetic advance as percent of mean were noted for panicle length (6.65%), DAS to 75% maturity (6.06%), DAS to 50% flowering (7.57%), test weight (5.35%), and plant height at 30 DAS (6.24%), 60 DAS (1.49%), and 90 DAS (1.05%). Similar finding is recorded by Bind *et al*., (2016), Chauhan *et al*., (2019).

**Estimation of correlation coefficients**

**Genotypic correlation**

Seed yield per plot (kg) exhibited a positive and significant genotypic correlation with seed yield per plant (0.385\*), biological yield (0.496\*\*), and harvest index (0.507\*\*), indicating these traits are strongly associated with higher plot yield and can be considered key contributors. It also showed positive and non-significant correlation with plant height 30 DAS (0.279), plant height 60 DAS (0.359\*), plant height 90 DAS (0.916\*\*), number of leaves per plant (0.112), number of grains per panicle (0.720\*\*), panicle length (0.185), test weight (0.356\*), and DAS to 50% flowering (0.507\*\*). whereas negative and significant genotypic correlation was observed with leaf width (-0.605\*\*). The trait also showed negative and non-significant correlation with leaf length (-0.116), DAS to 75% maturity (0.572\*\*), pedicle length (0.108), number of tillers per plant (-0.072), and number of pods per panicle (0.194). Similar finding are recorded by Vaisi *et al.,* (2013),Krishna, A. *et al.,* (2014), Kumar *et al.,* (2016), Paonia *et al*., (2017), Madosa, *et al.,* (2021).

**Phenotypic correlation between grain yield per plot (g) and its attributing characters:**

Seed yield per plot (kg) showed a positive and significant phenotypic correlation with harvest index (0.719\*\*),It also showed positive and non-significant correlations with plant height 30 DAS (0.153), plant height 60 DAS (0.157), plant height 90 DAS (0.308\*), number of leaves per plant (-0.206), leaf length (-0.014), DAS to 50% flowering (0.280), DAS to 75% maturity (0.329\*), number of grains per spike (0.241), pedicle length (0.035), panicle length (0.336\*), number of tillers per plant (-0.045), number of pods per panicle (0.240), test weight (0.253), biological yield (0.199), and seed yield per plant (0.196). leaf width (-0.176) and number of tillers per plant (-0.045) showed negative and non-significant associations. Similar finding are recorded by Vaisi *et al.,* (2013),Krishna, A. *et al.,* (2014), Kumar *et al.,* (2016), Paonia *et al*., (2017), Madosa, *et al.,* (2021).

**Path analysis (Genotypic path):**

**Direct effect of yield contributing characters on grain yield:**

Out of eighteen characters, nine showed positive and direct effect on grain yield at genotypic level viz.,biological yield (kg) exerted the highest positive direct effect on grain yield per plot , followed by pedicle length (cm) (0.9721), harvest index (%) (0.7057), plant height 30 DAS (cm) (0.4542), plant height 90 DAS (cm) (0.3555), plant height 60 DAS (cm) (0.3325), panicle length (cm) (0.3899), number of spikelet per panicle (0.3051), and number of grains per panicle (0.1284). And character shows negative direct effects on grain yield per plot, including number of tillers per plant (–0.9644), DAS to 50% flowering (–0.8481), test weight (g) (–0.7500), number of leaves per plant (–0.5052), leaf width (cm) (–0.2622), seed yield per plant (g) (–0.1671), and DAS to 75% maturity (–0.0624). These negative effects suggest that higher expression of these traits may reduce grain yield, and they should be carefully considered in selection strategies. Similar finding is recorded by Beyene *et al.,* (2015), Kumar, *et al*., (2016),Singh, *et al*., (2018) Madosa, *et al*., (2021),Nagesh *et al*., (2022).

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genotypes | 30 das plant height | 60 das plant height | 90 das plant height | No. Of leaves per plant | Leaf length | Leaf width | Das to 50% flowering | Das to 75% maturity | No. Of seed per panicle | Pedicle length | Penicle length | No. Of tillers per plant | Number of spiklets per penicle | Test weight | Biological yield | Harvest index | Seed yield per plant | Seed yield per plot |
| 30 das plant height | 1.00 | 0.073 | 0.400\*\* | 0.203 | -0.258 | -1.052\*\* | 0.277 | 0.304 | -0.184 | -0.410\*\* | -0.018 | -0.428\*\* | -0.047 | 0.249 | 0.193 | 0.069 | 0.117 | 0.279 |
| 60 das plant height |  | 1.00 | -0.510\*\* | 0.096 | -0.091 | -0.328\* | 0.716\*\* | 0.707\*\* | 0.549\*\* | -0.127 | -0.227 | -0.625\*\* | 0.693\*\* | 0.188 | 0.553\*\* | -0.227 | 0.415\*\* | 0.359\* |
| 90 das plant height |  |  | 1.00 | 0.319\* | 0.067 | -0.713\*\* | -0.148 | -0.157 | 0.665\*\* | 0.016 | 0.335\* | 0.333\* | -0.011 | 0.440\*\* | 0.238 | 0.633\*\* | -0.243 | 0.916\*\* |
| no. of leaves per plant |  |  |  | 1.00 | 1.020\*\* | 0.430\*\* | -0.503\*\* | -0.489\*\* | -0.304 | -0.870\*\* | 0.107 | -0.219 | -0.355\* | 0.586\*\* | -0.127 | 0.203 | -0.674\*\* | 0.112 |
| leaf length |  |  |  |  | 1.00 | 0.490\*\* | -0.276 | -0.323\* | -0.088 | -0.523\*\* | 0.013 | -0.060 | -0.236 | 0.147 | -0.078 | -0.053 | -0.508\*\* | -0.116 |
| leaf width |  |  |  |  |  | 1.00 | -0.470\*\* | -0.567\*\* | 0.653\*\* | 0.167 | -0.448\*\* | -0.150 | 0.017 | -0.242 | -0.761\*\* | 0.128 | -0.378\* | -0.605\*\* |
| das to 50% flowering |  |  |  |  |  |  | 1.00 | 1.013\*\* | -0.071 | -0.096 | -0.064 | -0.330\* | 0.259 | -0.378\* | 0.567\*\* | -0.058 | 0.501\*\* | 0.507\*\* |
| das to 75% maturity |  |  |  |  |  |  |  | 1.00 | 0.028 | 0.016 | 0.015 | -0.322\* | 0.251 | -0.263 | 0.542\*\* | 0.033 | 0.466\*\* | 0.572\*\* |
| no. of seed per panicle |  |  |  |  |  |  |  |  | 1.00 | -0.466\*\* | 0.236 | 0.097 | 0.511\*\* | -0.035 | 0.197 | 0.501\*\* | -0.139 | 0.720\*\* |
| pedicle length |  |  |  |  |  |  |  |  |  | 1.00 | 0.100 | 0.197 | -0.214 | 0.235 | -0.518\*\* | 0.642\*\* | 0.068 | 0.108 |
| penicle length |  |  |  |  |  |  |  |  |  |  | 1.00 | 0.896\*\* | -0.109 | -0.060 | 0.445\*\* | -0.224 | -0.259 | 0.185 |
| no. of tillers per plant |  |  |  |  |  |  |  |  |  |  |  | 1.00 | 0.051 | -0.157 | 0.094 | -0.118 | -0.527\*\* | -0.072 |
| number of spikelets per penicle |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 | -0.049 | 0.412\*\* | -0.214 | 0.530\*\* | 0.194 |
| test weight |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 | -0.142 | 0.469\*\* | 0.033 | 0.356\* |
| Biological yield |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 | -0.500\*\* | 0.373\* | 0.496\*\* |
| Harvest index |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 | 0.027 | 0.507\*\* |
| Seed yield per plant |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 | 0.385\* |
| Seed yield per plot |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 |

**Table no: 3 .Genotypic correlation coefficient of different eighteen characters of oat genotype**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genotypes | 30 das plant height | 60 das plant height | 90 das plant height | No. Of leaves per plant | Leaf length | Leaf width | Das to 50% flowering | Das to 75% maturity | No. Of seed per panicle | Pedicle length | Penicle length | No. Of tillers per plant | Number of spiklets per penicle | Test weight | Biological yield | Harvest index | Seed yield per plant | Seed yield per plot |
| 30 das plant height | 1.00 | -0.005 | 0.095 | 0.180 | -0.124 | -0.519\*\* | 0.158 | 0.207 | 0.063 | -0.109 | -0.007 | -0.135 | 0.001 | 0.212 | 0.069 | 0.063 | 0.107 | 0.153 |
| 60 das plant height |  | 1.00 | 0.089 | -0.187 | 0.262 | 0.286 | 0.378\* | 0.444\*\* | 0.240 | -0.258 | -0.163 | -0.154 | 0.231 | -0.057 | 0.400\*\* | -0.167 | 0.354\* | 0.157 |
| 90 das plant height |  |  | 1.00 | -0.072 | 0.085 | 0.046 | -0.136 | -0.063 | 0.089 | -0.296 | 0.026 | 0.255 | -0.165 | 0.137 | 0.222 | 0.110 | -0.209 | 0.308\* |
| no. of leaves per plant |  |  |  | 1.00 | 0.456\*\* | -0.105 | -0.311\* | -0.295 | 0.141 | -0.121 | -0.139 | -0.224 | -0.183 | 0.373\* | -0.141 | -0.104 | -0.223 | -0.206 |
| leaf length |  |  |  |  | 1.00 | 0.325\* | -0.254 | -0.297 | 0.086 | -0.378\* | 0.109 | 0.013 | -0.212 | 0.060 | -0.023 | -0.001 | -0.290 | -0.014 |
| leaf width |  |  |  |  |  | 1.00 | -0.315\* | -0.305 | -0.072 | -0.188 | -0.279 | -0.031 | -0.111 | -0.254 | -0.214 | -0.001 | -0.158 | -0.176 |
| das to 50% flowering |  |  |  |  |  |  | 1.00 | 0.940\*\* | 0.010 | -0.030 | -0.060 | -0.247 | 0.246 | -0.294 | 0.452\*\* | -0.075 | 0.397\* | 0.280 |
| das to 75% maturity |  |  |  |  |  |  |  | 1.00 | 0.013 | -0.037 | -0.062 | -0.217 | 0.223 | -0.225 | 0.468\*\* | -0.046 | 0.393\* | 0.329\* |
| no. of seed per panicle |  |  |  |  |  |  |  |  | 1.00 | 0.073 | 0.028 | 0.187 | 0.324\* | 0.016 | 0.135 | 0.087 | 0.001 | 0.241 |
| pedicle length |  |  |  |  |  |  |  |  |  | 1.00 | 0.068 | 0.106 | -0.082 | 0.228 | -0.380\* | 0.307 | 0.144 | 0.035 |
| penicle length |  |  |  |  |  |  |  |  |  |  | 1.00 | 0.491\*\* | 0.017 | 0.008 | 0.225 | 0.161 | -0.203 | 0.336\* |
| no. of tillers per plant |  |  |  |  |  |  |  |  |  |  |  | 1.00 | 0.034 | -0.164 | 0.230 | -0.174 | -0.393\* | -0.045 |
| number of spiklets per penicle |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 | 0.048 | 0.285 | 0.001 | 0.398\*\* | 0.240 |
| test weight |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 | -0.063 | 0.257 | -0.006 | 0.253 |
| Biological yield |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 | -0.527\*\* | 0.260 | 0.199 |
| Harvest index |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 | -0.011 | 0.719\*\* |
| Seed yield per plant |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 | 0.196 |
| Seed yield per plot |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 1.00 |

**Table no: 4. Phenotypic Correlation Coefficient of different eighteen characters of oat genotypes**

**Indirect effect of different independent traits on oat yield**

Leaf length exhibited a negative and non-significant correlation with seed yield per plot at both the genotypic (–0.116) and phenotypic (–0.014) levels. Number of pods per panicle showed a non-significant positive correlation at the genotypic level (0.194), but a significant positive correlation at the phenotypic level (0.240). Number of seeds per panicle showed a strong genotypic correlation (0.720), but its phenotypic correlation (0.241) with seed yield per plot was not statistically significant. Similar finding is recorded by Kumar, *et al*., (2016),Singh, *et al*., (2018) Madosa, *et al*., (2021)Nagesh *et al*., (2022).

**Phenotypic path analysis among different genotype**

Positive and direct effects on grain yield at the phenotypic level, viz., biological yield (kg) shows the highest positive direct effect on grain yield per plot (0.8519), followed by harvest index (%) (1.1682), number of pod per panicle (0.0261), number of grains per panicle (0.0053), DAS to 75% maturity (0.0015), and pedicle length (cm) (0.0397).Whereas the characters like plant height 30 DAS (cm) (–0.0200), plant height 60 DAS (cm) (–0.0630), plant height 90 DAS (cm) (–0.0070), number of leaves per plant (–0.0270), leaf length (cm) (–0.0170), leaf width (cm) (–0.0320), DAS to 50% flowering (–0.0410), seed yield per plant (g) (–0.0600), test weight (g) (–0.0500), number of tillers per plant (–0.0610), and panicle length (cm) (–0.0250) had negative direct effects on grain yield per plot. Similar finding is recorded by Beyene *et al.,* (2015), Kumar, *et al*., (2016),Singh, *et al*., (2018) Madosa, *et al*., (2021)Nagesh *et al*., (2022).

**Table no: 5. Genotypic Path Analysis of different eighteen characters of oat genotype**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genotypes | 30 das plant height | 60 das plant height | 90 das plant height | No. Of leaves per plant | Leaf length | Leaf width | Das to 50% flowering | Das to 75% maturity | No. Of seed per panicle | Pedicle length | Penicle length | No. Of tillers per plant | Number of spikelets per penicle | Test weight | Biological yield | Harvest index | Seed yield per plant | Seed yield per plot |
| 30 das plant height | **0.4542** | 0.0244 | 0.1424 | -0.1025 | -0.2764 | 0.2758 | -0.2347 | -0.0190 | -0.0236 | -0.3983 | -0.0071 | 0.4132 | -0.0144 | -0.1871 | 0.2031 | 0.0488 | -0.0196 | 0.4540 |
| 60 das plant height | 0.0334 | **0.3325** | -0.1814 | -0.0483 | -0.0974 | 0.0860 | -0.6071 | -0.0442 | 0.0705 | -0.1230 | -0.0883 | 0.6031 | 0.2114 | -0.1411 | 0.5824 | -0.1604 | -0.0694 | 0.3330 |
| 90 das plant height | 0.1819 | -0.1696 | **0.3555** | -0.1612 | 0.0722 | 0.1869 | 0.1253 | 0.0098 | 0.0854 | 0.0155 | 0.1307 | -0.3207 | -0.0032 | -0.3297 | 0.2506 | 0.4464 | 0.0407 | 0.3560 |
| no. of leaves per plant | 0.0922 | 0.0318 | 0.1134 | **-0.5052** | 1.0930 | -0.1126 | 0.4270 | 0.0305 | -0.0390 | -0.8462 | 0.0417 | 0.2115 | -0.1083 | -0.4398 | -0.1342 | 0.1434 | 0.1127 | -0.5050 |
| leaf length | -0.1172 | -0.0302 | 0.0240 | -0.5155 | **1.0712** | -0.1285 | 0.2343 | 0.0201 | -0.0113 | -0.5087 | 0.0052 | 0.0578 | -0.0719 | -0.1104 | -0.0824 | -0.0374 | 0.0850 | 1.0710 |
| leaf width | -0.4779 | -0.1090 | -0.2535 | -0.2171 | 0.5250 | **-0.2622** | 0.3982 | 0.0354 | 0.0839 | 0.1621 | -0.1746 | 0.1450 | 0.0053 | 0.1817 | -0.8011 | 0.0902 | 0.0632 | -0.2620 |
| das to 50% flowering | 0.1257 | 0.2381 | -0.0525 | 0.2543 | -0.2959 | 0.1231 | **-0.8481** | -0.0632 | -0.0091 | -0.0929 | -0.0249 | 0.3184 | 0.0789 | 0.2832 | 0.5967 | -0.0412 | -0.0837 | -0.8480 |
| das to 75% maturity | 0.1380 | 0.2352 | -0.0559 | 0.2472 | -0.3455 | 0.1487 | -0.8588 | **-0.0624** | 0.0035 | 0.0153 | 0.0060 | 0.3109 | 0.0765 | 0.1975 | 0.5707 | 0.0236 | -0.0779 | -0.0620 |
| no. of seed per panicle | -0.0836 | 0.1827 | 0.2364 | 0.1536 | -0.0945 | -0.1713 | 0.0598 | -0.0017 | **0.1284** | -0.4533 | 0.0919 | -0.0938 | 0.1559 | 0.0260 | 0.2072 | 0.3533 | 0.0232 | 0.1280 |
| pedicle length | -0.1861 | -0.0421 | 0.0057 | 0.4398 | -0.5606 | -0.0437 | 0.0810 | -0.0010 | -0.0599 | **0.9721** | 0.0391 | -0.1901 | -0.0654 | -0.1760 | -0.5458 | 0.4529 | -0.0115 | 0.9720 |
| penicle length | -0.0083 | -0.0753 | 0.1192 | -0.0540 | 0.0142 | 0.1174 | 0.0541 | -0.0010 | 0.0303 | 0.0974 | **0.3899** | -0.8641 | -0.0333 | 0.0450 | 0.4683 | -0.1584 | 0.0433 | 0.3900 |
| no. of tillers per plant | -0.1946 | -0.2079 | 0.1182 | 0.1108 | -0.0642 | 0.0394 | 0.2800 | 0.0201 | 0.0125 | 0.1916 | 0.3494 | **-0.9644** | 0.0155 | 0.1176 | 0.0993 | -0.0832 | 0.0881 | -0.9640 |
| number of spiklets per penicle | -0.0215 | 0.2304 | -0.0038 | 0.1794 | -0.2524 | -0.0046 | -0.2192 | -0.0157 | 0.0656 | -0.2085 | -0.0426 | -0.0489 | **0.3051** | 0.0367 | 0.4339 | -0.1508 | -0.0886 | 0.3050 |
| test weight | 0.1133 | 0.0626 | 0.1563 | -0.2963 | 0.1577 | 0.0635 | 0.3202 | 0.0164 | -0.0045 | 0.2282 | -0.0234 | 0.1513 | -0.0149 | **-0.7500** | -0.1499 | 0.3311 | -0.0056 | -0.7500 |
| Biological yield | 0.0876 | 0.1839 | 0.0846 | 0.0644 | -0.0838 | 0.1994 | -0.4805 | -0.0338 | 0.0253 | -0.5038 | 0.1734 | -0.0909 | 0.1257 | 0.1067 | **1.0532** | -0.3527 | -0.0624 | 1.0530 |
| Harvest index | 0.0314 | -0.0756 | 0.2249 | -0.1026 | -0.0567 | -0.0335 | 0.0495 | -0.0021 | 0.0643 | 0.6239 | -0.0875 | 0.1136 | -0.0652 | -0.3519 | -0.5264 | **0.7057** | -0.0045 | 0.7060 |
| Seed yield per plant | 0.0531 | 0.1380 | -0.0865 | 0.3407 | -0.5446 | 0.0991 | -0.4247 | -0.0291 | -0.0178 | 0.0666 | -0.1009 | 0.5085 | 0.1618 | -0.0249 | 0.3933 | 0.0189 | **-0.1671** | -0.1670 |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genotypes | 30 das plant height | 60 das plant height | 90 das plant height | No. Of leaves per plant | Leaf length | Leaf width | Das to 50% flowering | Das to 75% maturity | No. Of seed per panicle | Pedicle length | Penicle length | No. Of tillers per plant | Number of spiklets per penicle | Test weight | Biological yield | Harvest index | Seed yield per plant | Seed yield per plot |
| 30 das plant height | **0.0204** | -0.0003 | 0.0007 | 0.0049 | 0.0022 | 0.0165 | -0.0064 | -0.0049 | 0.0003 | -0.0043 | 0.0002 | 0.0083 | 0.0000 | -0.0105 | 0.0584 | 0.0740 | -0.0064 | 0.0200 |
| 60 das plant height | -0.0001 | **0.0633** | 0.0007 | -0.0050 | -0.0046 | -0.0091 | -0.0154 | -0.0104 | 0.0013 | -0.0102 | 0.0040 | 0.0094 | 0.0060 | 0.0028 | 0.3405 | -0.1945 | -0.0212 | 0.0630 |
| 90 das plant height | 0.0019 | 0.0057 | **0.0073** | -0.0019 | -0.0015 | -0.0015 | 0.0056 | 0.0015 | 0.0005 | -0.0118 | -0.0006 | -0.0156 | -0.0043 | -0.0068 | 0.1891 | 0.1283 | 0.0125 | 0.0070 |
| no. of leaves per plant | 0.0037 | -0.0119 | -0.0005 | **0.0269** | -0.0080 | 0.0033 | 0.0126 | 0.0069 | 0.0007 | -0.0048 | 0.0034 | 0.0138 | -0.0048 | -0.0185 | -0.1205 | -0.1215 | 0.0133 | 0.0270 |
| leaf length | -0.0025 | 0.0166 | 0.0006 | 0.0123 | **-0.0175** | -0.0103 | 0.0104 | 0.0070 | 0.0005 | -0.0150 | -0.0027 | -0.0008 | -0.0055 | -0.0030 | -0.0198 | -0.0012 | 0.0173 | -0.0170 |
| leaf width | -0.0106 | 0.0181 | 0.0003 | -0.0028 | -0.0057 | **-0.0318** | 0.0128 | 0.0072 | -0.0004 | -0.0074 | 0.0069 | 0.0019 | -0.0029 | 0.0126 | -0.1820 | -0.0015 | 0.0095 | -0.0320 |
| das to 50% flowering | 0.0032 | 0.0239 | -0.0010 | -0.0084 | 0.0045 | 0.0100 | **-0.0407** | -0.0221 | 0.0001 | -0.0012 | 0.0015 | 0.0151 | 0.0064 | 0.0146 | 0.3853 | -0.0876 | -0.0237 | -0.0410 |
| das to 75% maturity | 0.0042 | 0.0281 | -0.0005 | -0.0080 | 0.0052 | 0.0097 | -0.0383 | **-0.0235** | 0.0001 | -0.0015 | 0.0015 | 0.0133 | 0.0058 | 0.0112 | 0.3990 | -0.0535 | -0.0235 | -0.0240 |
| no. of seed per panicle | 0.0013 | 0.0152 | 0.0006 | 0.0038 | -0.0015 | 0.0023 | -0.0004 | -0.0003 | **0.0053** | 0.0029 | -0.0007 | -0.0114 | 0.0084 | -0.0008 | 0.1153 | 0.1012 | -0.0001 | 0.0050 |
| pedicle length | -0.0022 | -0.0164 | -0.0022 | -0.0033 | 0.0066 | 0.0060 | 0.0012 | 0.0009 | 0.0004 | **0.0397** | -0.0017 | -0.0065 | -0.0021 | -0.0113 | -0.3237 | 0.3583 | -0.0086 | 0.0400 |
| penicle length | -0.0001 | -0.0103 | 0.0002 | -0.0037 | -0.0019 | 0.0089 | 0.0024 | 0.0015 | 0.0002 | 0.0027 | **-0.0246** | -0.0301 | 0.0004 | -0.0004 | 0.1916 | 0.1875 | 0.0121 | -0.0250 |
| no. of tillers per plant | -0.0028 | -0.0098 | 0.0019 | -0.0060 | -0.0002 | 0.0010 | 0.0101 | 0.0051 | 0.0010 | 0.0042 | -0.0121 | **-0.0613** | 0.0009 | 0.0081 | 0.1956 | -0.2037 | 0.0234 | -0.0610 |
| number of spiklets per penicle | 0.0000 | 0.0146 | -0.0012 | -0.0049 | 0.0037 | 0.0035 | -0.0100 | -0.0052 | 0.0017 | -0.0033 | -0.0004 | -0.0021 | **0.0261** | -0.0024 | 0.2427 | 0.0014 | -0.0237 | 0.0260 |
| test weight | 0.0043 | -0.0036 | 0.0010 | 0.0101 | -0.0011 | 0.0081 | 0.0120 | 0.0053 | 0.0001 | 0.0090 | -0.0002 | 0.0100 | 0.0013 | **-0.0497** | -0.0535 | 0.2997 | 0.0004 | -0.0500 |
| Biological yield | 0.0014 | 0.0253 | 0.0016 | -0.0038 | 0.0004 | 0.0068 | -0.0184 | -0.0110 | 0.0007 | -0.0151 | -0.0055 | -0.0141 | 0.0074 | 0.0031 | **0.8519** | -0.6162 | -0.0155 | 0.8520 |
| Harvest index | 0.0013 | -0.0105 | 0.0008 | -0.0028 | 0.0000 | 0.0000 | 0.0031 | 0.0011 | 0.0005 | 0.0122 | -0.0040 | 0.0107 | 0.0000 | -0.0128 | -0.4493 | **1.1682** | 0.0007 | 1.1680 |
| Seed yield per plant | 0.0022 | 0.0224 | -0.0015 | -0.0060 | 0.0051 | 0.0050 | -0.0162 | -0.0093 | 0.0000 | 0.0057 | 0.0050 | 0.0241 | 0.0104 | 0.0003 | 0.2214 | -0.0132 | **-0.0597** | -0.0600 |

**Table no: 6. Phenotypic Path Analysis of different eighteen characters of oat genotypes**

**CONCLUSION**

The analysis of variance confirmed the presence of significant genetic diversity among the studied oat genotypes. High GCV, PCV, and heritability with genetic advance for seed yield per plot, seed yield per plant, and biological yield highlight the predominance of additive genetic variance, making these traits suitable for direct selection. Correlation studies indicated that improving biological yield, harvest index, and plant height will positively influence seed yield per plot, whereas excessive tillering or leaf width might reduce yield. Path analysis identified biological yield and harvest index as the most critical contributors to seed yield, both directly and indirectly, emphasizing their importance in breeding programs.

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**ACKNOWLEDGEMENT**

All necessary facilities and resources are provided by the authors and Prof. Rajendra Singh (Rajju Bhaiya) University Prayagraj, UP, India and are gratefully Acknowledged.

**CONFLICTS OF INTEREST STATEMENT**

The authors declare that they have no conflicts of interest to disclose. This research was conducted independently without any financial support or external funding.

The authors contributed to the conception and design of this analysis paper, collected and analysed the data, and prepared the manuscript. They also reviewed and evaluated the final version of the paper and recommended it for publication in this journal.

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