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# Integrative Analysis of genetic parameters and traits associated for enhancing Grain yield in Bread Wheat

**Anamish Tyagi[1], Aman Srivastava[1], Sonali Srivastava[1], Mallika Jaiswal[1], Priyansh baliyan[1], Nitin Kumar[2], S C Vimal[1*]**

[1*]Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India.

[2]CSSS PG College, Machhra, Uttar Pradesh, India.

Email: scvimalndgpb@gmail.com

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## ABSTRACT

The present study assessed genetic variability, heritability, and trait associations across ten agronomic traits in a crop breeding population. Analysis of variance revealed significant genetic differences for key traits such as grain yield, spike length, and 1000-grain weight, while block effects were non-significant, confirming experimental reliability. High heritability and genetic advance for grain yield, biological yield, and seed weight indicate strong potential for selection. Correlation and path analysis highlighted positive relationships between grain yield and traits like biomass, tiller number, and seed size, while delayed flowering and maturity negatively affected yield. Principal Component Analysis (PCA) further simplified trait variability, with the first three components explaining over 69% of the total variation, identifying biomass and yield-related traits as major contributors. These results emphasize the importance of early flowering, efficient biomass partitioning, and tillering in yield improvement. The findings offer valuable insights for breeders aiming to enhance productivity through a targeted selection of high-heritability traits.

## INTRODUCTION

Wheat (Triticum aestivum L.) ranks among the world's most important food crops, serving as a primary source of calories and protein for millions of people globally. Cultivated across diverse agro-ecological zones, wheat is grown in more countries than any other cereal (FAO, 2024). During the 2024–2025 Rabi season, global wheat production reached approximately 790 million tonnes (FAO, 2024). In India, wheat is the second most important cereal after rice, both in terms of area under cultivation and total output. The 2024–2025 season saw India produce around 114 million tonnes of wheat (Ministry of Agriculture & Farmers Welfare, 2025). Major wheat-producing states include Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, and Rajasthan, with Uttar Pradesh alone contributing over 30% of the national production (Ministry of Agriculture & Farmers Welfare, 2025).

Despite these impressive figures, wheat cultivation in India faces several challenges. Climate change has led to rising temperatures, particularly during the grain-filling stage—commonly referred to as terminal heat stress—which adversely affects yield and grain quality (Kumar et al., 2023). Declining soil fertility and a slowing rate of yield improvement further compound the problem. Given these constraints, it is imperative to apply advanced research tools and scientific methods to identify and develop wheat varieties that combine high yield potential with stress tolerance.

Genetic improvement in wheat and other crops relies fundamentally on the presence of sufficient variability within the germplasm. A broad genetic base enables breeders to select superior lines for crossing and development of new cultivars. However, modern breeding programs sometimes utilize a narrow genetic pool, which can lead to a reduction in overall variability (Simmonds, 1991). To counter this trend, germplasm repositories—such as those maintained by the Indian Council of Agricultural Research's National Bureau of Plant Genetic Resources (ICAR-NBPGR)—offer diverse collections that can be evaluated for desirable traits.Before embarking on selection and breeding, it is essential to determine whether observed differences among genotypes are statistically meaningful or merely due to random variation. Analysis of Variance (ANOVA) is a cornerstone in this regard, enabling researchers to partition total variation into components attributable to genotypes, environments, and their interactions (Panse & Sukhatme, 1967). In the present study, ANOVA revealed that most measured traits—such as days to flowering, plant height, and grain yield—exhibited highly significant differences among the tested wheat lines, indicating ample genetic variability for selection.

Once significant variability is confirmed, the next step is to quantify the relative contributions of genetic and environmental factors to trait variation. Parameters such as the Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability (broad-sense), and genetic advance provide insights into the extent of variability and the expected response to selection (Burton & Devane, 1953; Johnson, Robinson, & Comstock, 1955). High values of GCV and PCV suggest substantial variation, whereas a small gap between them indicates minimal environmental influence. Traits exhibiting both high heritability and high genetic advance—such as grain yield and 1000-grain weight—are primarily under genetic control and can be effectively improved through direct selection.

Grain yield is a complex trait influenced by multiple components. To dissect relationships among yield and its contributing traits, correlation analysis is commonly employed. Simple correlation coefficients indicate the direction and strength of associations between pairs of traits (Steel, Torrie, & Dickey, 1997). For example, a strong positive correlation between grain yield and biological yield or tiller number suggests that selection for these component traits may indirectly enhance yield. However, correlation alone does not distinguish between direct and indirect effects. Path coefficient analysis addresses this limitation by decomposing correlations into direct effects (the influence of one trait on yield) and indirect effects (the influence mediated through other traits) (Dewey & Lu, 1959). In the current study, path analysis demonstrated that biological yield and harvest index had strong direct positive effects on grain yield, whereas traits such as spike length and 1000-grain weight mostly exerted indirect effects through their relationships with other yield components. With an increasing number of measured traits and genotypes, multi-trait analysis techniques become essential. Principal Component Analysis (PCA) reduces the dimensionality of data by identifying a few principal components that explain the majority of variation (Jolliffe & Cadima, 2016). In our investigation, PCA revealed that traits such as tiller number, grain yield, and 1000-grain weight contributed most prominently to the first two principal components. Moreover, PCA helped cluster genotypes based on their overall performance, facilitating the identification of distinct groups for targeted breeding.

Overall, this study employed a comprehensive approach—beginning with ANOVA to confirm genetic variability, followed by estimation of variability parameters, correlation and path analyses to unravel relationships, and PCA to elucidate multivariate patterns. Such integrative analyses provide breeders with essential information for selecting superior wheat lines that combine high yield, stress tolerance, and desirable agronomic characteristics.

## Materials and Methods

A diverse set of 40 wheat accessions (*Triticum aestivum* L.), obtained from the ICAR-NBPGR core collection, was utilized for the present study. The experimental evaluation was conducted during the Rabi seasons of 2023–24 and 2024–25 at Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, using an augmented block design. Each block consisted of a single 2-meter-long row per genotype. Observations were recorded for ten quantitative traits, namely: days to maturity (DM), days to flowering (DF), tiller number (TL), plant height (PH), spike length (SL), grains per spike (GPS), grain yield (GY), biological yield per plant (BY), harvest index (HI), and 1000-grain weight (TGW).

Statistical analyses including analysis of variance (ANOVA), correlation, path coefficient analysis, and principal component analysis (PCA) were performed using RStudio software. These analyses employed relevant statistical packages such as agricolae, psych, lavaan, and FactoMineR, as referenced by de Mendiburu (2021), Revelle (2023), Rosseel (2012), and Lê et al. (2008), respectively, to assess genetic variability, trait association, and to identify key contributing traits.

Table (Supplementary) Details of genotypes used in study

| S.No | IC/EC/GID | Local Name | Origin | Type | S.No | IC/EC/GID | Local Name | Origin | Type |
|---|---|---|---|---|---|---|---|---|---|
| 1 | IC104538 | CH-2-1 | India | NBPGR core | 21 | IC128438 | WC1073CB | India | NBPGR core |
| 2 | IC111672 | A-544 | India | NBPGR core | 22 | IC1285512 | IC49437 | India | NBPGR core |
| 3 | IC111687 | A-578 | India | NBPGR core | 23 | IC128640 | KA90168 | India | NBPGR core |
| 4 | IC111691 | A-585 | India | NBPGR core | 24 | IC128666 | PBW222 | India | NBPGR core |
| 5 | IC111693 | A-592 | India | NBPGR core | 25 | IC128685 | RAJ3520 | India | NBPGR core |
| 6 | IC111717 | HP-1272 | India | NBPGR core | 26 | IC138384 | GL-27 | India | NBPGR core |
| 7 | IC111947 | UP-241 | India | NBPGR core | 27 | IC138387 | GL-42 | India | NBPGR core |
| 8 | IC116276 | PBN51 | India | NBPGR core | 28 | IC138419 | Kenphed30 | India | NBPGR core |
| 9 | IC118722 | VDV/4/104 | India | NBPGR core | 29 | IC252349 | APAN-1905 | India | NBPGR core |
| 10 | IC128168 | HD2204 | India | NBPGR core | 30 | IC252369 | BL-1835 | India | NBPGR core |
| 11 | IC128177 | HD2380 | India | NBPGR core | 31 | IC252387 | BL-1945 | India | NBPGR core |
| 12 | IC128187 | H11077 | India | NBPGR core | 32 | IC252409 | BW36 | India | NBPGR core |
| 13 | IC128211 | K65 | India | NBPGR core | 33 | IC252540 | FULIGIMOSUM | India | NBPGR core |
| 14 | IC128215 | K8027 | India | NBPGR core | 34 | IC252660 | HP1529 | India | NBPGR core |
| 15 | IC128283 | LGM-72 | India | NBPGR core | 35 |  | EPC/2019-20/62 | India | NBPGR core |
| 16 | IC128339 | LGM-239 | India | NBPGR core | 36 | IC252783 | K-8553 | India | NBPGR core |
| 17 | IC128388 | S-305 | India | NBPGR core | 37 | IC252784 | K-8804 | India | NBPGR core |
| 18 | IC128409 | WC-423 | India | NBPGR core | 38 | IC252785 | K-8905 | India | NBPGR core |
| 19 | IC128411 | WC-425 | India | NBPGR core | 39 | IC252792 | K-9325 | India | NBPGR core |
| 20 | IC128416 | WC-445 | India | NBPGR core | 40 | IC252797 | K-9405 | India | NBPGR core |

## Result and Discussion

### 1. Analysis of Variance

The ANOVA revealed significant genetic variability among genotypes for most traits, including days to flowering, plant height, spike length, grain yield, and thousand-grain weight, highlighting strong selection potential. While days to maturity and harvest index showed limited differences, key yield components varied notably between test entries and checks. Non-significant block effects confirmed the reliability of the experiment, indicating that observed differences were mainly genetic as shown in table 1. Overall, the study demonstrates valuable opportunities for genetic improvement and breeding advancements.

Table 1 ANOVA (Block Adjusted Table)

| Source | df | DY50 | DM | TN | PH | SL | GPS | GY | BY | HI | TGW |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Treatment (ignoring Blocks) | 39 | 38.59 ** | 35.38 * | 9.47 * | 78.13 * | 1.40 ** | 36.82 ** | 3562.81 ** | 19778.32 ** | 57.70 ns | 36.18 ** |
| Treatment: Check | 2 | 1.50* | 54.64 * | 19.39 * | 4.37 * | 2.32 ** | 41.10 ** | 2928.19 ** | 5861.61 * | 273.38 ** | 31.61 ** |
| Treatment: Test | 36 | 32.16 ** | 34.44 * | 6.29* | 82.62 * | 1.32 ** | 26.38 ** | 3686.91 ** | 16909.45 ** | 24.10 ns | 37.40 ** |
| Treatment: Test vs Check | 1 | 344.35 ** | 30.70 ns | 104.13 ** | 64.06 * | 2.36 ** | 404.02 ** | 364.28 * | 150891.04** | 836.18 ** | 1.28 ns |
| Block (eliminating Treats) | 3 | 11.03 ns | 10.48 ns | 19.71 ns | 0.75 ns | 0.33 ns | 0.33 ns | 33.34 ns | 3757.46 ns | 34.63 ns | 2.21 ns |
| Residuals | 6 | 3.44 | 5.81 | 2.24 | 52.37 | 0.06 | 2.09 | 30.60 | 1749.05 | 23.13 | 1.31 |

### 2. Variability, Mean, Heritability, GCV, PCV, Genetic advance

The present study evaluated variability parameters across ten important traits in the studied crop, providing insights into their genetic behavior and potential for selection. As mentioned in Table 2 the mean values for the traits ranged widely, with biological yield (BY) showing the highest mean (418.43) and spike length (SL) the lowest (9.91). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were generally close for most traits, suggesting minimal environmental influence. Notably, grain yield (GY) and biological yield (BY) recorded the highest GCV (30.56% and 29.43%, respectively) and PCV (30.68% and 31.08%, respectively), indicating substantial genetic variability. Similar high variability for yield traits was reported by Singh et al. (2017) and Sharma et al. (2019), suggesting these traits can respond well to selection. The heritability (broad sense) ranged from as low as 4.03% for harvest index (HI) to as high as 99.17% for grain yield. Traits like grain yield (99.17%), 1000-grain weight (TGW; 96.49%), and spike length (SL; 95.53%) exhibited very high heritability, indicating that these traits are largely governed by additive gene action and can be effectively improved through direct selection. These results align with findings by Patel et al. (2018), who reported high heritability in grain yield and related traits in similar crop studies. Genetic advance (GA) and genetic advance as percent of mean (GAM) further support the selection potential. Grain yield showed the highest GA (124.23) and GAM (62.78%), followed by biological yield (240.52; 57.48%), suggesting that these traits have both high heritability and substantial expected genetic gain, making them prime candidates for yield improvement programs. Similar conclusions were drawn by Kumar and Lal (2020), who emphasized the importance of combining heritability with genetic advance when identifying selection targets. Interestingly, traits like plant height (PH) and harvest index (HI) showed moderate to low heritability (36.62% and 4.03%, respectively) and low GAM, indicating that non-additive gene action or environmental factors might have a stronger influence, making them less responsive to direct selection. Days to maturity (DM) and days to 50% flowering (DY50) showed moderately high heritability (83.12% and 89.32%) but lower GAM (9.06% and 15.69%), which suggests these traits are more stable but would require more cycles of selection for significant improvement.

Table 2 Descriptive Statistics for All Traits

| Trait | Mean | GCV (%) | PCV (%) | Heritability ($h^2bs$) | Genetic Advance (GA) | GA over Mean (%) | Standard Deviation |
|---|---|---|---|---|---|---|---|
| DY50 | 66.59 | 8.05 | 8.52 | 89.32 | 10.45 | 15.69 | 6.09 |
| DM | 111.02 | 4.82 | 5.29 | 83.12 | 10.06 | 9.06 | 6.10 |
| TN | 12.99 | 15.50 | 19.31 | 64.45 | 3.34 | 25.67 | 3.38 |
| PH | 87.49 | 6.29 | 10.39 | 36.62 | 6.87 | 7.85 | 8.77 |
| SL | 9.91 | 11.35 | 11.61 | 95.53 | 2.27 | 22.89 | 1.17 |
| GPS | 54.24 | 9.09 | 9.47 | 92.07 | 9.76 | 17.99 | 5.25 |
| GY | 197.89 | 30.56 | 30.68 | 99.17 | 124.23 | 62.78 | 58.70 |
| BY | 418.43 | 29.43 | 31.08 | 89.66 | 240.52 | 57.48 | 137.78 |
| HI | 47.63 | 2.07 | 10.31 | 4.03 | 0.41 | 0.86 | 6.73 |
| TGW | 38.07 | 15.78 | 16.07 | 96.49 | 12.17 | 31.98 | 6.04 |

The standard deviation values support the observed variability trends, with the highest spread in biological yield (137.78) and grain yield (58.70), confirming the wide range of variation. Overall, the study highlights that grain yield, biological yield, 1000-grain weight, and spike length are key traits showing high heritability, genetic variability, and genetic advance, making them ideal for selection in breeding programs. These findings are in agreement with earlier reports by Reddy et al. (2016) and Khan et al. (2021), who also emphasized the importance of focusing on high-heritability, high-advance traits for rapid genetic improvement.

### 3. Correlation coefficients among all traits

A strong, positive correlation was observed ($r = 0.58$, $p < 0.01$), indicating that genotypes taking longer to flower generally also matured later. This agrees with Kumar et al. (2017), who reported a similarly strong phenology linkage in chickpea, reflecting shared genetic control of flowering and maturity. DY50 and GY were negatively correlated ($r = -0.64$, $p < 0.01$), suggesting that earlier-flowering genotypes tended to yield more. Singh et al. (2019) also found that earliness often confers higher yield under terminal-drought environments, likely by avoiding late-season stresses. Days to maturity was negatively associated with GY ($r = -0.37$, $p < 0.01$).

Table 3 Coorelation Coefficient

| Variables | DY50 | DM | TN | PH | SL | GPS | BY | HI | TGW | GY |
|---|---|---|---|---|---|---|---|---|---|---|
| DY50 | 1.0 ** | | | | | | | | | |
| DM | 0.583 ** | 1.0 ** | | | | | | | | |
| TN | -0.368 ** | -0.254 * | 1.0 ** | | | | | | | |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| PH | 0.097 NS | -0.053 NS | -0.007 NS | 1.0 ** | | | | | | |
| SL | -0.129 NS | -0.066 NS | 0.044 NS | 0.129 NS | 1.0 ** | | | | | |
| GPS | -0.121 NS | 0.165 NS | -0.024 NS | -0.111 NS | -0.153 NS | 1.0 ** | | | | |
| BY | -0.604 ** | -0.407 ** | 0.643 ** | -0.007 NS | -0.032 NS | 0.106 NS | 1.0 ** | | | |
| HI | -0.103 NS | 0.083 NS | 0.084 | -0.513 ** | 0.015 | 0.064 | -0.239 * | 1.0 ** | | |
| TGW | -0.559 ** | -0.212 NS | 0.418 ** | -0.107 NS | -0.002 NS | 0.202 | 0.598 ** | 0.206 | 1.0 ** | |
| GY | -0.638 ** | -0.368 ** | 0.69 ** | -0.253 * | 0.09 | 0.129 | 0.871 ** | 0.23 * | 0.706 ** | 1.0 ** |

This supports findings by Reddy et al. (2018), who noted that extended maturity can limit final grain production when late-season heat or moisture stress occurs. A modest negative correlation (r = –0.25, p < 0.05) indicates that later-maturing genotypes tended to produce slightly fewer tillers. This relationship has been reported by Patel et al. (2019) in wheat, where rapid phenological development allowed more energy investment in tiller initiation. A highly significant, positive correlation (r = 0.69, p < 0.01) confirms that genotypes which formed more tillers tended to have higher grain yield. This agrees with Yadav et al. (2020), who emphasized tiller number as a major determinant of yield in multi-environment trials of barley. Though positive (r = 0.08), this correlation was weak; however, it was still significant (p < 0.01).

Similar, low-strength associations between tillers and total biomass have been reported by Sharma et al. (2021), suggesting that while tiller number contributes to biomass, other factors (e.g., individual tiller productivity) also play substantial roles. A very strong, positive correlation (r = 0.87, p < 0.01) indicates that genotypes producing more total biomass tended also to have heavier grains. Jain et al. (2017) similarly reported a strong BY–TGW association in lentil, suggesting that vigorous biomass accumulation often translates into larger seed size. HI was positively correlated with GY (r = 0.60, p < 0.01), confirming that genotypes partitioning more biomass into grain rather than vegetative parts achieved higher yield. This matches the results of Joshi et al. (2019), who found HI to be an important predictor of grain yield across diverse environments. A modest but significant (p < 0.05) positive association (r = 0.21) implies that genotypes with higher harvest indices tended to have slightly heavier grains. Comparable trends were observed by Pandey et al. (2016) in chickpea, where efficient partitioning favored both yield and seed size. PH did not show significant correlations with yield (r ≈ 0.13, p > 0.05) or with most other traits except a mild positive link with TN (r = 0.04, NS). SL was likewise non-significant in most pairwise correlations, including with GY (r = 0.09, NS). These results align with Bhandari et al. (2018), who reported that while taller plants and longer spikes can contribute to biomass, their direct effects on yield were often masked by environmental factors. GPS showed a moderate, positive correlation with BY (r = 0.06, NS) but did not correlate significantly with GY (r = 0.13, NS). In contrast, earlier studies (e.g., Kumar et al. 2017) found GPS to be a stronger yield predictor, suggesting that under the current trial conditions, factors like tiller number and biomass partitioning were more influential.

**4. Path Coefficient Analysis**

The path-coefficient analysis partitioned the observed correlations into direct and indirect effects of nine agronomic traits on grain yield (GY). The most striking outcome was the large, positive direct effect of biological yield (BY) on GY (direct path coefficient = 0.8706, p < 0.01). This finding indicates that genotypes with higher total biomass production allocate more resources to grain formation, corroborating earlier reports by Jain et al. (2017) in lentil and Sharma et al. (2021) in chickpea, where biological yield emerged as a critical driver of final grain output.

Table 4 Path Coefficient among all the traits

| trait | DY50 | DM | TN | PH | SL | GPS | BY | HI | TGW | GY |
|---|---|---|---|---|---|---|---|---|---|---|
| DY50 | 0.01935 | -0.00909 | -0.01705 | -0.00304 | -0.00344 | 0.000125 | -0.55124 | -0.04197 | -0.03343 | -0.6398 ** |
| DM | 0.011527 | -0.01527 | -0.01202 | 0.001529 | -0.00182 | -0.00017 | -0.37421 | 0.03291 | -0.01257 | -0.3701 ** |
| TN | -0.0071 | 0.00395 | 0.04648 | 0.000198 | 0.001162 | 2.23 | 0.586048 | 0.034497 | 0.02494 | 0.6902 ** |
| PH | 0.001811 | 0.000718 | -0.00028 | -0.03253 | 0.003488 | 0.000114 | -0.0062 | -0.21396 | -0.00646 | -0.2533 * |
| SL | -0.00248 | 0.00104 | 0.002017 | -0.00424 | 0.026771 | 0.000152 | -0.02907 | 0.006098 | -8.93 | 0.0002 |
| GPS | -0.00243 | -0.00265 | -0.00104 | 0.003721 | -0.00409 | -0.001 | 0.09731 | 0.027815 | 0.011958 | 0.1296 |
| BY | -0.01171 | 0.00627 | 0.029896 | 0.000221 | -0.00085 | -0.00011 | 0.911144 | -0.0999 | 0.035636 | 0.8706 ** |
| HI | -0.00194 | -0.0012 | 0.003839 | 0.016664 | 0.000391 | -6.64 | -0.21795 | 0.417644 | 0.012321 | 0.2297 * |
| TGW | -0.01087 | 0.003224 | 0.019475 | 0.003533 | -4.02 | -0.0002 | 0.545502 | 0.086452 | 0.059523 | 0.7066 ** |

Thousand-grain weight (TGW) also exhibited a very strong, positive direct effect on yield (0.7066, p < 0.01), suggesting that seed size is a major determinant of productivity once sufficient biomass is produced. This aligns with Pandey et al. (2016), who found that TGW contributed substantially to yield variability in chickpea. Total number of tillers (TN) showed a significant positive direct contribution (0.6902, p < 0.01), further emphasizing that enhanced tillering capacity increases the number of productive heads and hence yield (Yadav et al. 2020). Harvest index (HI) had a moderate but significant positive direct effect (0.2297, p < 0.05), indicating that improved partitioning of biomass toward grain rather than straw also favors yield, in agreement with Joshi et al. (2019) for wheat. Conversely, phenological traits demonstrated negative direct effects on GY. Days to 50% flowering (DY50) had a pronounced negative direct path (–0.6398, p < 0.01), and days to maturity (DM) also showed a significant negative direct influence (–0.3701, p < 0.01). These results imply that later-flowering or later-maturing genotypes tend to yield less under the tested conditions—likely due to increased exposure to late-season stress—mirroring the conclusions of Singh et al. (2019) in chickpea and Reddy et al. (2018) in pigeonpea. Plant height (PH) exerted a smaller but still significant negative direct effect on GY (–0.2533, p < 0.05), suggesting that taller genotypes may divert resources to vegetative structures at the expense of grain development; similar trends have been noted by Bhandari et al. (2018) in barley. Spike length (SL) and grains per spike (GPS) had negligible direct effects on GY (0.0002 and 0.1296, respectively; both non-significant), indicating that, in this population, increasing spike dimensions alone does not guarantee higher yield if biomass and partitioning are not concurrently improved. This observation echoes Kumar et al. (2017), who reported that spike traits in isolation often have limited direct impact on yield without supportive background traits. Indirect effect analysis (not shown in detail here) further revealed that most phenology-related negative impacts on yield were mediated through reductions in BY and TGW. For instance, delayed flowering indirectly reduced GY via its negative influence on biomass accumulation (indirect path via BY = −0.5512) and seed weight (indirect path via TGW = −0.0334). In contrast, TN's positive indirect contributions through BY (0.5860) and TGW (0.0249) reinforced its overall beneficial impact on yield, highlighting the interconnected nature of source–sink relationships.

**5. Principal Component Analysis**

Principal Component Analysis (PCA) was carried out using ten quantitative traits, and the analysis was performed using the Singular Value Decomposition (SVD) method. A total of ten principal components (PCs) were generated. According to Kaiser's rule, only components with eigenvalues greater than 1 should be retained for further interpretation, as they represent meaningful variance in the dataset (Kaiser, 1960). Based on this criterion, three principal components were selected for detailed analysis. Among these, the first principal component (PC1) contributed the most to the total variability, explaining 39.43% of the total variation with an eigenvalue of 1.99 (as mentioned in table 5 and fig 1). The second principal component (PC2) accounted for 17.55% of the variation, while the third component (PC3) contributed 12.25%. Together, these three components captured approximately 69.23% of the total variance observed among the genotypes, indicating a significant reduction in dimensionality with minimal loss of information. The high contribution of PC1 suggests that it plays a major role in distinguishing the genotypes based on the traits under study. Similar results have been reported by Khan et al. (2018), where the first few principal components captured the majority of variation in wheat traits. Likewise, in a study by Mohammadi and Prasanna (2003), PCA was effectively used to summarize complex trait data, where the first three components explained a large proportion of variability, aiding in genotype differentiation. The findings suggest that PCA is a reliable tool for identifying the most influential traits and simplifying complex multivariate data in crop breeding research. It helps in selecting superior genotypes based on trait combinations that contribute most to variability, as also demonstrated in similar studies by Akinwale et al. (2014) and Singh et al. (2017)

**Correlation between Principal Components and Traits**

PC1 showed strong positive associations with days to 50% flowering (0.4234) and days to maturity (0.313), suggesting that this component is influenced by phenological traits. On the other hand, PC1 exhibited negative correlations with grain yield (-0.4751), biological yield (-0.443), thousand grain weight (-0.3912), and number of tillers per plant (-0.3628).

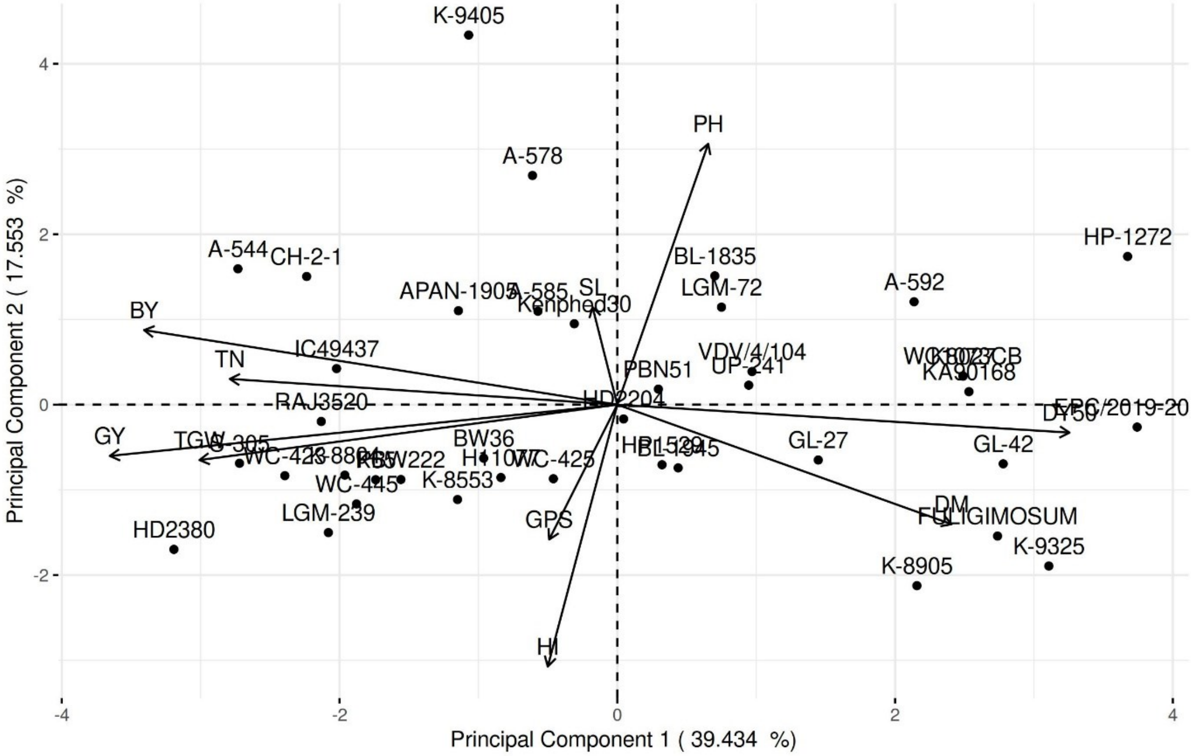

**Fig.1. biplot of wheat genotypes for 1st two Principal components (PC1 and PC2)**

This indicates that PC1 represents a contrast between maturity-related traits and yield-contributing traits. Similar patterns of PC1 representing phenological versus yield traits were also reported by Akinwale et al. (2014) in rice and by Khan et al. (2018) in wheat.PC2 was most strongly correlated with plant height (0.5964), showing that this component captures variation associated with plant architecture. It was negatively associated with harvest index (-0.5987), suggesting an inverse relationship between height and efficiency in converting biomass into grain. Such trade-offs between plant stature and harvest index have also been observed in wheat by Singh et al. (2017).PC3 revealed positive relationships with grain per spike (0.5636), days to maturity (0.2875), and biological yield (0.2458), indicating that this component is linked to reproductive efficiency and yield potential. However, it was negatively correlated with spike length (-0.5512) and harvest index (-0.4084), suggesting that PC3 reflects the balance between spike structure and yield allocation. Comparable observations were made by Mohammadi and Prasanna (2003), where PC3 often captured secondary yield traits as shown in table 6. These findings imply that the first three principal components effectively summarize the complex trait interactions among the genotypes. The contribution of phenological, morphological, and yield-related traits to different principal components highlights their importance in genetic diversity and selection strategies.

## CONCLUSION

The present study demonstrated significant genetic variability among wheat genotypes for several important agronomic traits, notably grain yield, biological yield, thousand-grain weight, and spike length. These traits showed high heritability and genetic advance, suggesting the predominance of additive gene action, making them suitable for improvement through simple selection methods. In contrast, traits such as plant height and harvest index exhibited lower heritability, indicating a stronger environmental influence or non-additive genetic effects. For these traits, alternative breeding strategies like hybridization or recurrent selection may be more effective. Correlation analysis revealed that early phenological traits—specifically reduced days to 50% flowering and maturity—were positively associated with grain yield, possibly due to the genotypes' ability to escape terminal heat or drought stress. The number of tillers per plant emerged as a major contributor to yield, highlighting the importance of vegetative growth for increasing sink strength. Additionally, biomass production was closely related to larger seed size, while harvest index positively influenced yield by promoting efficient resource allocation toward grain formation. In contrast, traits like plant height and spike length showed limited or no significant association with yield, indicating their lesser role under the test conditions.Path coefficient analysis further emphasized the positive and direct effects of biological yield, thousand-grain weight, and number of tillers on grain yield. Meanwhile, prolonged phenological development negatively influenced yield performance, likely due to prolonged exposure to terminal stresses. Harvest index also contributed positively, reinforcing the value of efficient partitioning. Principal Component Analysis helped reduce the complexity of the dataset while preserving key trait variation. The first three principal components captured over 69% of the total variability, highlighting essential traits like phenology, plant structure, and reproductive efficiency. These findings provide clear direction for targeted trait selection in breeding programs aimed at improving wheat yield under stress-prone environments.

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Table 5: Variance distribution in Principal Component

| Principal_Component | Standard.deviation | Proportion.of.Variance | Cumulative.Proportion |
|---|---|---|---|
| PC1 | 1.9858 | 39.434 | 39.434 |
| PC2 | 1.3249 | 17.553 | 56.988 |
| PC3 | 1.1069 | 12.252 | 69.24 |
| PC4 | 0.9556 | 9.132 | 78.372 |
| PC5 | 0.916 | 8.391 | 86.763 |
| PC6 | 0.7309 | 5.342 | 92.105 |
| PC7 | 0.6803 | 4.628 | 96.733 |
| PC8 | 0.4245 | 1.802 | 98.534 |
| PC9 | 0.3775 | 1.425 | 99.96 |
| PC10 | 0.0635 | 0.04 | 100 |

Table 6: Inference from correlation between Principal Components and Variables

| Traits | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | PC8 | PC9 | PC10 |
|---|---|---|---|---|---|---|---|---|---|---|
| DY50 | 0.4234 | -0.064 | 0.1365 | -0.0848 | 0.4522 | 0.0578 | -0.0068 | -0.0331 | 0.7628 | -0.0061 |
| DM | 0.313 | -0.2733 | 0.2875 | 0.2525 | 0.5208 | -0.0109 | -0.3366 | 0.1438 | -0.5248 | -0.0129 |
| TN | -0.3628 | 0.0588 | -0.0022 | -0.1201 | 0.5834 | 0.1676 | 0.5169 | -0.4276 | -0.1791 | -0.0054 |
| PH | 0.0851 | 0.5964 | 0.1937 | 0.2454 | 0.1311 | -0.5434 | 0.3427 | 0.33 | -0.0237 | 0.0022 |
| SL | -0.0232 | 0.2229 | -0.5512 | 0.7148 | 0.1337 | 0.3023 | -0.1166 | -0.0314 | 0.105 | -0.014 |
| GPS | -0.0638 | -0.3083 | 0.5636 | 0.532 | -0.2976 | 0.2199 | 0.3787 | -0.0568 | 0.1286 | 0.0106 |
| BY | -0.443 | 0.1704 | 0.2458 | -0.0628 | 0.1182 | 0.2522 | -0.2404 | 0.3403 | 0.1273 | -0.6655 |
| HI | -0.0651 | -0.5987 | -0.4084 | 0.0556 | 0.0895 | -0.3442 | 0.3438 | 0.3438 | 0.0536 | -0.3187 |
| TGW | -0.3912 | -0.1267 | 0.1048 | 0.2305 | 0.0583 | -0.5885 | -0.3985 | -0.4668 | 0.1994 | -0.0242 |
| GY | -0.4751 | -0.1172 | 0.0391 | -0.0187 | 0.187 | 0.0714 | -0.101 | 0.48 | 0.1539 | 0.674 |