Unveiling the Complexity of Yield Determinants through Genetic Variability, Correlation, and Path Analysis across Diverse Bread Wheat [*Triticum aestivum* (L.) em. Thell]Germplasm

Abstract

Wheat feeds billions of people around the world, acting as a dietary staple and crucial source of sustenance for a vast number of global communities.Enhancing wheat yield remains a paramount goal in addressing global food security challenges. The present study aimed to elucidate the genetic variability, correlation, and path analysis of various agronomic and morphological traits among fifty genotypes of bread wheat (*Triticum aestivum* (L.) em. Thell)to facilitate targeted breeding efforts. The genotypes, exhibiting a wide spectrum of variability, were evaluated for thirteen morphological traits during the Rabi season of 2019 at Banaras Hindu University, India. Analysis of variance revealed significant genotypic differences for all the studied traits. Correlation analysis unveiled intricate interrelationships among traits, highlighting both direct and indirect effects on grain yield per plot. Path coefficient analysis further delineated these associations, providing insights into cause-and-effect dynamics. Notably, biomass exhibited the highest positive direct effect on grain yield, followed by harvest index and germination percentage. Conversely, traits such as tillers per meter, days to flowering, and plant height exerted negative direct effects on yield. Genetic variability parameters indicated substantial variability for traits like harvest index and grain yield per plot, with spike length exhibiting the highest heritability. The study underscores the complexity of grain yield determination, influenced by multiple genetic and environmental factors. These findings helpin understanding of the genetic basis of yield-related traits for wheat breeding programs, emphasizing the importance of selecting genotypes with favourable trait combinations to enhance yield potential.

Keywords: Genetic variability,Heritability, correlation, path analysis

1. Introduction

Bread wheat (*Triticum aestivum* (L.) em. Thell), also known as common wheat, is an annual species belonging to the Triticeae tribe of the grasses (Poaceae) family(Levy & Feldman, 2022). It is an allohexaploid species, composed of 21 chromosome pairs organized in three subgenomes, A, B, and D, Genome BBAADD, 2n = 6x = 42(Przewieslik-Allen et al., 2021).It is the world's largest famous energy-rich cereal crop (Dvivedi et al., 2023). Wheat, the first domesticated food crop since 8000 years, is the stable food for various civilizations throughout the world(Poonia et al., 2023). It originated from South-Western Asia and Central Asia and the Mediterranean and Ethiopian regions are centres of diversity for wheat and its related species(Liu et al., 2022). It covers 17% of the total cultivated land in the world(Erenstein et al., 2022). Wheat has been described as the king of cereals because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade, it is a C3 plant grown from temperate irrigated to dry and high rainfall areas and from warm humid to dry cold environment(Verma et al., 2019). In the world, wheat occupies an area of 217 million hectares (Mha) with a total production of 765 million tonnes (Mt) and productivity of 3530 kg/ha(Poonia et al., 2023).It is a monoecious plant with perfect flowers, reproducing sexually as an autogamous crop although limited (3%) cross pollination is possible(Orellana- Torrejon et al., 2022). Wheat grain has a high nutritional value with 70-75% starch, 14% water, 8-20% proteins, 2-3% non-starch polysaccharides, 2% lipids, 1.6% minerals, antioxidants(Sharma et al., 2023). “Grain yield is a complex trait and highly influenced by many genetic factors and environmental fluctuations.Precise knowledge about germplasm variability, heritability and genetic advance is a pre-requisite for crop improvement programs, as it helps in the development of superior recombinants for all traits of interest including yield (Zewdu et al., 2023). The degree of genetic control related to some heritable significant features is referred to as heritability (Abdelghany et al., 2023). In plant breeding programme, direct selection for yield as such could be misleading (P. K. Singh et al., 2022). Therefore, study of genetic variability of grain yield and its component characters among different varieties provides a strong basis for selection of suitable genotypes for enhancing of yield and other agronomic characteristics (Chaudhary et al., 2022). It is vital to investigate the relationships between genotype variation and yield components to make the best use of wheat genetic resources in breeding program initiatives (Abdelghany et al., 2023). Correlation studies along with path analysis provide a better understanding of the association of different characters with grain yield(Sudeepthi et al., 2020). The correlation coefficient measures the mutual relationship between various plant characters and determines the component character on which selection can be based for improvement of yield” (Sharma et al., 2023).The present investigation was conducted in bread wheat to obtain the information on following aspects: 1. To estimate the variability present among the different genotypes in a population. 2. To find out the correlation between the characters and estimating the direct and indirect effects through path analysis for yield and yield contributing traits in wheat.

2. Materials and Methods

2.1. Study sites

The experiment was carried out during *Rabi* 2019 at agricultural farm of Banaras Hindu University of Varanasi-221005 (U.P.).Geographically, Varanasi lies at a latitude of 25° 19' in the North and a longitude of 83° 46' to the east, with an altitude of 264 meters above mean sea level (MSL), representing the Eastern Plain Zone (EPZ). The soil in the experimental field is rich and sandy loam in texture.The experiment was laid out in Randomized Complete Block Design (RCBD) in 2 replications. In each replication genotypes were sown in 6rows of 5-meter length. The row to row and plant to plant distance was maintained at 25 and 10 cm, respectively.

2.2. Method of data collection

Experimental materials comprised of fifty bread wheat genotypes including local check varietyThe Karan Vandana (DBW 187) which was released for irrigated timely sown conditions of North Eastern Plains Zones comprising of Eastern Uttar Pradesh, Bihar, Jharkhand, Assam and West Bengal name and source of fifty bead wheat genotypes were given in supplementary Table 1. These genotypes exhibiting wide spectrum of variability for various agronomic and morphological characters were obtained throughCIMMYTand maintained in the Department of Genetics & Plant Breeding, BHU, Varanasi. The detail of genotypes is given in supplementary Table 1. The observation was recorded on 13 morphological traits viz., germination, days to 50% flowering, days to maturity, canopy temperature, vegetative index, biomass, chlorophyll content, grain yield per plot, plant height (cm), no. of productive tillers per meter, length of the spike, 1000 seed weight (g), and harvest index (%), and all data were analyzed by standard statistical method.Germination percentage was determined in the field by observing the proportion of seeds that successfully sprouted from the total number of seeds planted. Days to maturity, days to 50% flowering, plant height, and the number of tillers per meter were recorded at maturity for each experimental plot. Three measurements of the Normalized Difference Vegetation Index (NDVI) were taken using a GreenSeeker device from the vegetative stage to the dough stage. Chlorophyll content, was measured at the heading and anthesis phases using a Minolta SPAD-502 Chlorophyll meter. Canopy temperature, was measured from the vegetative stage to the dough stages using a handheld infrared thermometer. The 1000 seed weight, was determined by weighing a sample of 1000 wheat grains. At maturity, the biomass was measured by harvesting the total above-ground biomass, while the grain yield per plot, was measured by threshing grains from spikes harvested from each experimental plot. The harvest index, was calculated by dividing the grain yield per plot by the total above-ground biomass harvested from the same plot at maturity.

2.3. Statistical analysis

GCV and PCV were calculated as per the standard formula suggested by Searle (1961). The formula provided by Allard (1960) was used to calculate genetic advance as percentage of mean (GAM) and broad sense heritability (h^2_b).All the genetic parameters analysis, correlation and path analysis were carried out using R-software.

3. Results and Discussion

3.1.Mean performance

The analysis of variance revealed significant differences for all the 13 characters studied in 50 wheat genotypes(supplementary table 3). The mean performance of different genotypes of wheat for various characters is given in the supplementary table 02. The character-wise results are as follows: Germination Percentage (GP) varied from 90 percent to 95 percent with a mean of 93.924 percent. Wheat, on average, has a germination percentage of 85%. Days to 50% flowering (DFF) varied from 62.01 days to 86.5 days with a mean of 77.8 days. Among all genotypes, GEN 49 (62.01) showed early flowering, while GEN 10 (86.5) showed late flowering. Days to maturity (DM) varied from 111.5 days to 161.885 days with a mean of 116.328 days. The earliest maturity was recorded in GEN 48 (111.5), and late maturity in GEN 49 (161.885). Canopy temperature (CT) ranges between 14.66°C to 26.6°C with a mean value of 25.016°C. The highest canopy temperature was recorded for GEN 27 (26.6°C), and the lowest for GEN 49 (14.66°C). Vegetative index (VI) ranged between 62.5 and 115.74 with a mean value of 65.175. The highest value was recorded for GEN 49 (115.74), and the least value for GEN 24 (62.5). Biomass (BM) ranged from 2.515 to 10.4 with a mean value of 8.979. The highest value was recorded for GEN 41 (10.4), and the least value for GEN 49 (2.515). Chlorophyll content (CC) ranged between 21.8 to 44.2 with a mean value of 42.618. The highest chlorophyll content was recorded for GEN 9 (44.2), and the least value for GEN 49. Grain yield per plot (GYPP) ranges between 0.475 to 3.5 with a mean value of 2.876. The highest value was recorded for GEN 6 (3.5), and the least value for GEN 49 (0.475). 1000 seed weight (TSW) ranged from 30.49 to 54.48 with a mean value of 42.387. The highest 1000-grain weight was recorded for GEN 4 (54.48), and the least value for GEN 49 (30.49). Plant height (PH) in different genotypes ranges from 69.08 cm to 108 cm with a mean of 96.173 cm. Among all, GEN 49 (69.08 cm) was the shortest variety, and GEN 19 (108 cm) was the longest variety. Length of the spike (SL) ranged between 8 cm and 12 cm with a mean of 10.1 cm. The spike length is highest in GEN 48 (12 cm) and lowest in the case of GEN 24 (8 cm). Tillers per plant(TM) ranged between 20.965 and 91 with a mean value of 79.709. The highest value was recorded for GEN 48 (91), and the least value for GEN 49 (20.965). Harvest Index (HI)ranged from 0.235 to 0.37 with a mean of 0.317. GEN 10 (0.235) registered the least harvest index, and GEN 27 (0.37) recorded the highest value of the harvest index.

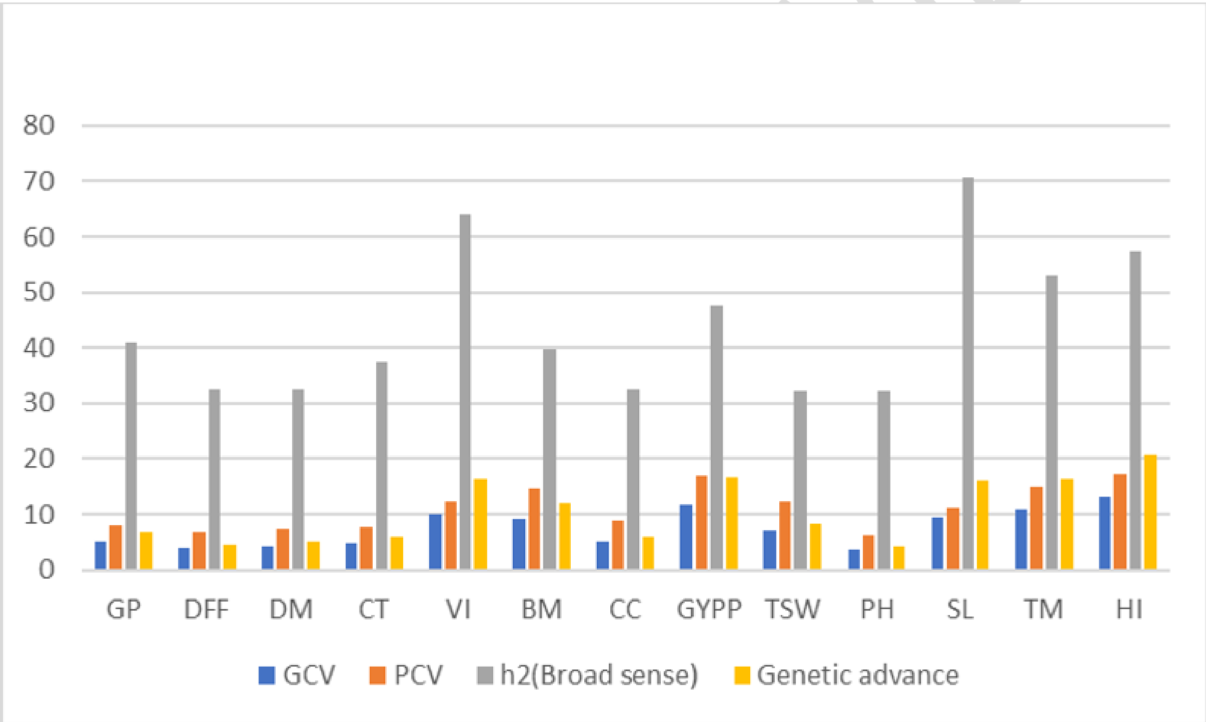

Figure 1. Graphical representation of genetic parameters of variation (GCV, PCV, Genetic Advance (5%), Genetic advance as percent of mean (5%), h^2_b for 13 traits among 50 bread wheat accessions

*Abbreviations: GCV-Genotypic coefficient of variation, PCV-phenotypic coefficient of variation, h^2_b-Broad Sense heritability

3.2.Genetic variability parameters

Genotypicandphenotypiccoefficientsofvariabilityare the two parameters which areusedformeasuringthe variability(Al-Tabbal & Al-Fraihat, 2012). This observed variability is due to both genetic and environmental causes. Hence estimation of heritability will give better insights of genetic transmission to next generation compared to variability(Jaiswal et al., 2020). Heritabilityestimates along with genetic advance are more helpful in predicting the gain underselection than heritability estimates alone(He et al., 2023). However, it is not necessary that a charactershowinghighheritabilitywillalwaysexhibithighgeneticadvance(Johnsonetal.1955).

Genotypiccoefficientofvariation(GCV)wasrecordedhighest for harvest index (13.162), indicating substantial genetic variability within the population for this trait, followed by Grain yield per plot (11.659), tillers per meter (10.8), and spike length (10.67). Traits like days to 50% flowering (3.828) exhibit low GCV, suggesting limited genetic diversity for this trait. The phenotypic coefficientof variation(PCV) washigher inmagnitudethanthat of genotypic coefficient of variation for all characters under study. The highest PCVwas recorded for harvest index (17.357) followed by grain yield per plot (16.894), no. oftillers permeter (14.908), biomass (14.596), vegetative index (12.426), 1000seed weight (12.415) spike length (11.775), and days to 50% flowering (6.703) exhibited low phenotypic coefficientofvariation.

Broadsenseheritabilitywasestimatedforallthecharactersunderstudy.Heritability was recorded high for spike length (70.8) and least for plant height(32.3). The high genetic advance as percent of mean was recorded forharvestindex(20.56)followedbygrainyieldperplot(16.574),vegetativeindex(16.435), tillers per meter (16.311), spike length (16.171) and least genetic advance as percent mean forplant height(4.2).

3.3.Correlationstudies

Germination percentage has significant positive correlation with spike length (0.2548), indicating that higher germination rates may result in longer spikes. This finding suggests that seed quality and viability could influence plant growth and development(Finch-Savage, 2020). There is a significant negative correlation between Grain yield per plot (-0.1013), tillers per meter (-0.0802), plant height (-0.1441), days to 50% flowering (-0.1061). implying that higher germination rates do not necessarily lead to higher grain yields. Days to 50% Flowering has significant negative correlation with Canopy temperature (-0.1378) and harvest index (-0.47504).). suggesting that earlier flowering may result in a lower harvest index(Ronga et al., 2020). This result could indicate that early-flowering cultivars might not efficiently utilize resources, impacting overall yield. There is a significant positive correlation between days to 50% flowering and tillers per meter (0.1795), implying that delayed flowering could be associated with increased tiller production. Days to maturity has Significant negative correlations with Canopy temperature (-0.03918) and harvest index (-0.0303). Canopy Temperature has significant positive correlation with Grain yield per plot (0.4161), tillers per meter (0.1942) and days to 50% flowering (0.1942). indicating that higher canopy temperatures may be linked to increased yields(Sohail et al., 2020). There is a significant negative correlation between canopy temperature and germination (-0.00176), suggesting that higher temperatures may negatively impact germination rates. This finding highlights the potential vulnerability of germination processes to temperature extremes. Vegetative Index has significant positive correlation with spike length (0.0771), indicating that higher vegetative indices may be associated with longer spikes(Panek et al., 2020). There is a significant negative correlation with Chlorophyll content (-0.0729), grain yield per plot (-0.0729), biomass (-0.12278), tillers per meter (-0.1330), days to 50% flowering (-0.2465).). implying that higher vegetative indices may be associated with lower chlorophyll levels. Biomass has significant positive correlation with grain yield per plot (0.2711), indicating that higher biomass production may lead to increased yields. There is a significant negative correlation between biomass and the vegetative index (-0.12278), suggesting that higher biomass may be associated with lower vegetative indices. Chlorophyll Content has significant positive correlation with grain yield per plot (0.579), suggesting that higher chlorophyll levels may be associated with increased yields. There is a significant negative correlation between chlorophyll content and the vegetative index (-0.0729), indicating that higher chlorophyll levels may be associated with lower vegetative indices. Grain Yield per Plot has significant positive with and canopy temperature (0.41606), indicating that higher yields may be associated with higher canopy temperatures(S. K. Singh et al., 2022). There is a significant negative correlation with Germination (-0.10135), days to maturity (-0.2223). suggesting that higher yields may not necessarily be associated with higher germination rates. 1000-Grain Weight has significant positive correlation with Canopy temperature (0.40518), harvest index (0.55414). indicating that higher temperatures may be associated with larger grain sizes. This result suggests the potential influence of temperature stress on grain development and filling. There is a significant negative correlation between 1000-grain weight and days to 50% flowering (-0.08017), suggesting that earlier flowering may be associated with smaller grain sizes. Plant Height has significant positive correlation with tillers per meter (0.1270), indicating that taller plants may have more tillers per meter. There is a significant negative correlation between plant height and the harvest index (-0.00453), suggesting that taller plants may have lower harvest indices. Spike length has Significant negative correlations with Grain yield per plot (-0.2794). Tillers per meter has Significant negative correlation with Vegetative index (-0.1330). Harvest index has Significant negative correlations with Days to 50% flowering (-0.47504).Similar results were shown by Abdulhamed et al., 2021;Baye et al., 2020; Poudel et al., 2021**.**

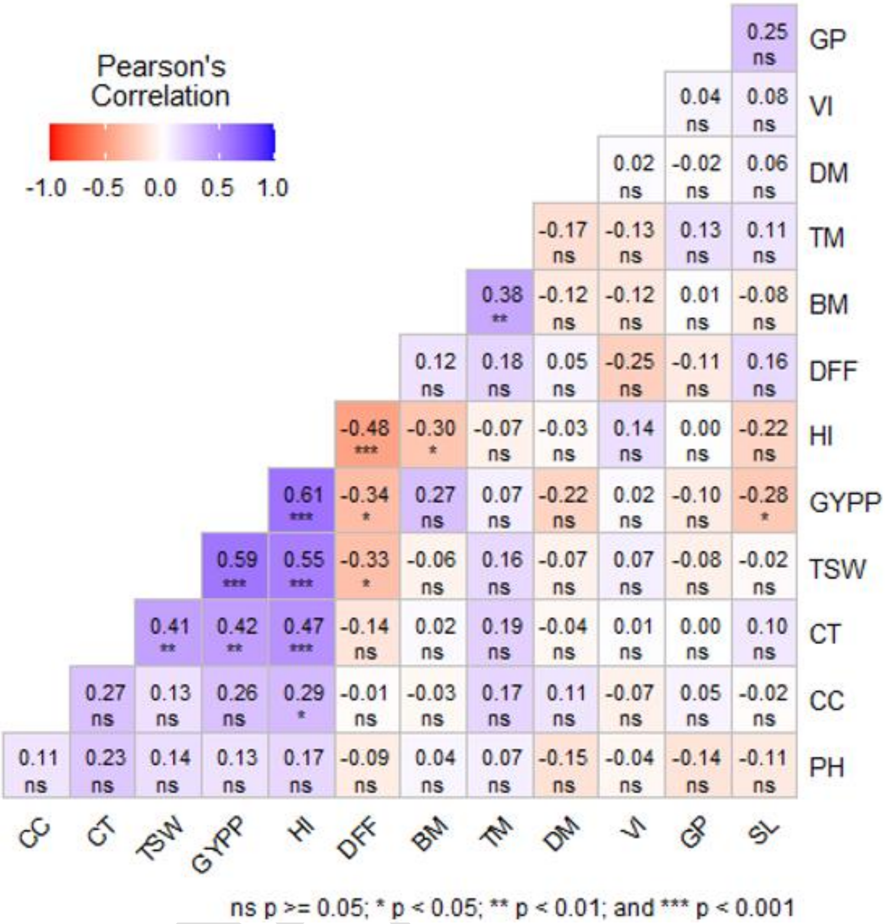

Figure 2. Phenotypiccorrelationstudiesamong 12charactersfor 50genotypesofbreadwheat

3.4.Path coefficient analysis

The observed correlation between yield and its component characters is the netresult of the direct and indirect effects of the component character through other yieldattributes(Rangare et al., 2010). The total correlation coefficient between yield and its component charactersmay sometimes be misleading, as it may be an over or under estimate of its associationwith other characters. In these cases, direct selection on the basis of correlated responsemay not be fruitful(Okuyama et al., 2004). For critical evaluation, the correlation coefficient needs to be splitinto direct and indirect effects using path coefficient analysis since, many charactersaffect a given trait(Devesh et al., 2021). Thus, the correlation and path coefficients in combination can give abetter insight into cause-and-effect relationship between different pairs of characters(Abrar Yasin et al., 2020). Ifthe correlation coefficient is positive, but the direct effect is negative or negligible, theindirect effects seem to be the cause of positive correlation(Shrivastava et al., 2023). In such situations, theindirectcausal factorsareto beconsideredsimultaneouslyforselection. Correlation coefficient may be negative but the direct effect is positive and high. Underthese circumstances,arestrictedsimultaneousselectionmodelistobefollowed. i.e., restrictionsaretobe imposed tonullifytheundesirableindirecteffectsinorderto make use of the direct effect. If correlation coefficient is negative and directeffect is also negative, then the character cannot be considered as a selection criterion(Usman et al., 2017). In the present study, path analysis was used to work out the direct and indirecteffectsof yield contributing characters onyield in50 genotypes. The directand indirecteffects of various characters towards grain yield perplant are presented in table number 1. At phenotypic level highest positive direct effect towardsgrainyieldwasobservedbybiomass(0.868)followedbyharvestindex(0.686),germination percentage (0.0436), vegetative index (0.0334), days to maturity (0.0292),canopy temperature (0.0229), while negative direct effect was exerted by no. of tillersper meter (-0.0467), days to flowering (-0.0332),length of spike (-0.0287), plant height(-0.0179),chlorophyll content (-0.0141). Germination percentage has phenotypic positive indirect effect via no. of tillersper meter (0.0258) and prominent negative indirect effect through biomass (-0.5799)and the remaining had negligible indirect negative and positive effects at the phenotypiclevel. Days to 50% flowering has indirect positive effect via biomass (0.3577) and itwas revealed negative indirect effect via harvest index (-0.1171) and the remaining hasnegligibleindirectnegativeandpositiveeffectsatthephenotypiclevel. Days to maturity has indirect positive effect on germination percentage (0.0267)and it was revealed negative indirect effect via biomass (-0.4354) and the remaining has negligible indirectnegativeandpositiveeffectsatthephenotypiclevel.Canopy temperature has indirect positive effect via biomass (0.5184) and it wasrevealed negative indirect effect via no. of tillers per meter (-0.0293) and the remaininghasnegligibleindirectnegativeandpositiveeffectsatthephenotypiclevel. Vegetativeindexhasindirectpositiveeffectviagerminationpercentage(0.0308) and it was revealed negative indirect effect via biomass (-0.5696) and theremaining has negligible indirect negative and positive effects at the phenotypic level.Biomass has indirect positive effect via canopy temperature (0.0137) and it wasrevealed negative indirect effect via harvest index (-0.0497) and the remaining hasnegligibleindirectnegativeandpositiveeffectsatthephenotypiclevel.Chlorophyll content has indirect positive effect via biomass (0.5058) and it wasrevealednegativeindirecteffectviagerminationpercentage(-0.0286)andtheremaining has negligible indirect negative and positive effects at the phenotypic level.1000-grain weight has indirect positive effect via harvest index (0.3353) and itwas revealed negative indirect effect via vegetative index (-0.0116) and the remaininghasnegligibleindirectnegativeandpositiveeffectsatthephenotypiclevel.Plantheighthas indirectpositiveeffectviabiomass(0.3725)anditwasrevealed negative indirect effect via no. of tillers/m (-0.0263) and the remaining has negligibleindirectnegativeandpositiveeffectsatthephenotypiclevel.Length of spike has indirect positive effect via germination percentage (0.0033)and it was revealed negative indirect effect via biomass (-0.0365) and the remaining hasnegligible indirect negative and positive effects at the phenotypic level. No. of tillers per meter has indirect positive effect via biomass (0.4856) and itwas revealed negative indirect effect via germination percentage (-0.0241) and theremaining has negligible indirect negative and positive effects at the phenotypic level. Harvest index has indirect positive effect via days to maturity (0.072) and it wasrevealed negative indirect effect via biomass (-0.0629) and the remaining has negligibleindirectnegativeandpositiveeffectsatthephenotypiclevel.Similar results were shown by Kumar et al., 2023;Abo-Elwafa et al., 2023;Bhardwaj et al., 2023

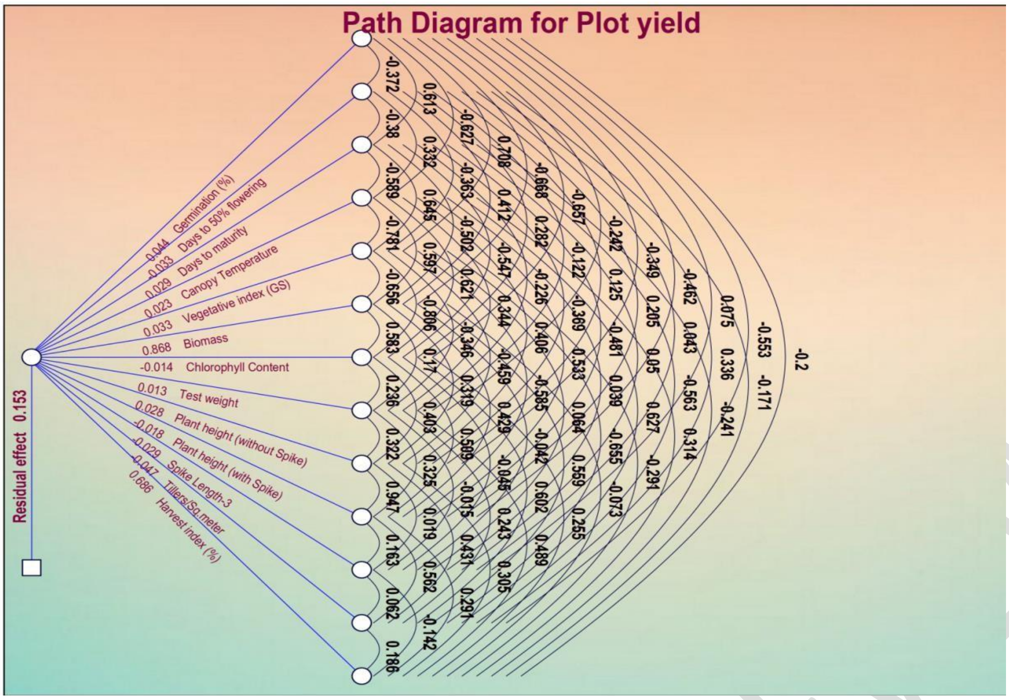

Figure 3.Path diagram for grain yield per plotamong 50 bread wheat genotypes

Table 1. Pathcoefficientanalysisforgrainyieldperplotamong50 bread wheat genotypes

Trait	Germination(%)	Days to50% flowering	Days tomaturity	Canopytemperature	Vegetativeindex(GS)	Biomass	Chlorophyllcontent	1000-grainweight	Plantheight(without Spike)	Planthe Spike)
Germination (%)	**0.0436**	-0.0162	0.0267	-0.0273	0.0308	-0.0291	-0.0286	-0.0105	-0.0152	-0.0201
Daysto 50% flowering	0.0123	**-0.0332**	0.0126	-0.011	0.012	-0.0137	-0.0093	0.0041	-0.0041	-0.0068
Daysto maturity	0.0179	-0.0111	**0.0292**	-0.0172	0.0188	-0.0146	-0.016	-0.0066	-0.0108	-0.014
Canopy Temperature	-0.0144	0.0076	-0.0135	**0.0229**	-0.0179	0.0137	0.0142	0.0079	0.0093	0.0122
Vegetative index(GS)	0.0236	-0.0121	0.0216	-0.0261	**0.0334**	-0.0219	-0.0269	-0.0116	-0.0153	-0.0196
Biomass	-0.5799	0.3577	-0.4354	0.5184	-0.5696	**0.868**	0.5058	0.1479	0.277	0.3725
Chlorophyll content	0.0092	-0.004	0.0077	-0.0087	0.0114	-0.0082	**-0.0141**	-0.0033	-0.0057	-0.0072
1000-grain weight	-0.0031	-0.0016	-0.0029	0.0044	-0.0044	0.0022	0.003	**0.0127**	0.0041	0.0041
Plantheight (Without spike)	-0.0099	0.0035	-0.0104	0.0115	-0.013	0.009	0.0114	0.0091	**0.0283**	0.0268
Plantheight (withSpike)	0.0083	-0.0037	0.0086	-0.0095	0.0105	-0.0077	-0.0091	-0.0058	-0.017	**-0.0179**
Spikelength	-0.0022	-0.0012	-0.0014	-0.0011	-0.0018	0.0012	0.0013	0.0004	-0.0006	-0.0047
tillers/meter	0.0258	-0.0157	0.0263	-0.0293	0.0306	-0.0262	-0.0281	-0.0113	-0.0201	-0.0263
Harvest index(%)	-0.1369	-0.1171	-0.1656	0.2153	-0.1995	-0.0497	0.175	0.3353	0.2092	0.1998
grainyield perplot	-0.606**	0.153	-0.497**	0.642**	-0.659**	0.723**	0.579**	0.468**	0.439**	0.499**

PartialR^2	-0.0264	-0.0051	-0.0145	0.0147	-0.022	0.6276	-0.0081	0.006	0.0124	-0.0089

***Significant atP = 0.05,** Significant atP = 0.01**

Conclusion

The findings of this study highlight the intricate interplay and complex relationships among various morphological and agronomic traits that influence grain yield per plot in bread wheat. Notably, traits such as biomass, harvest index, and germination percentage emerged as key positive contributors to yield enhancement, exhibiting significant positive correlations with grain yield. On the other hand, traits like tillers per meter and days to flowering exerted negative impacts on grain yield, underscoring the complex nature of yield determination in wheat. Additionally, the observed genetic variability for critical traits such as harvest index and grain yield per plot itself, emphasizes the potential for targeted improvement of these traits through wheat breeding programs. Furthermore, the heritability estimates shed light on the genetic basis of these traits, with spike length exhibiting notable heritability. Collectively, this study provides valuable insights into the genetic architecture and underlying components that govern grain yield in wheat.

References

Abdelghany, M., Makhmer, K., Zayed, E., Salama, Y., & Amer, K. (2023). Genetic Variability, Principle Components and Cluster Analysis of Twenty-eight Egyptian Wheat Genotypes. *Scientific Journal of Agricultural Sciences*, *5*(1), 107-118.

Abdulhamed, Z. A., Abood, N. M., & Noaman, A. H. (2021, May). Genetic path analysis and correlation studies of yield and its components of some bread wheat varieties. In *IOP Conference Series: Earth and Environmental Science* (Vol. 761, No. 1, p. 012066). IOP Publishing.

Abo-Elwafa, A., Taib, A., Abo-Sapra, H. M., &Bakheit, B. R. (2023). Path Coefficient Analysis for Grain Yield and Some of its Attributes in Bread wheat (Triticum aestivum L.). *Assiut Journal of Agricultural Sciences*, *54*(1), 1-18.

Abrar Yasin, B., Kumar, M., & Kumar, R. (2020). Assessment of Cause-and-Effect Relationship between Different Character Combinations on Yield and Quality of Bread Wheat (Triticum aestivum L.). https://www.academia.edu/download/79853701/6378-6382_206291.pdf

Allard, R.W. (1960). *Principles of Plant Breeding*. John Wiley and Sons. Inc, New York

Al-Tabbal, J. A., & Al-Fraihat, A. H. (2012). Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *Journal of Agricultural Science*, *4*(3), 193.

Baye, A., Berihun, B., Bantayehu, M., &Derebe, B. (2020). Genotypic and phenotypic correlation and path coefficient analysis for yield and yield-related traits in advanced bread wheat (Triticum aestivum L.) lines. *Cogent Food & Agriculture*, *6*(1), 1752603.

Bhardwaj, R., Thakur, S., & Mushtaq, M. (2023). Assessment of Yield Criteria in Bread Wheat through Correlation and Path Analysis. *International Journal of Environment and Climate Change*, *13*(11), 2329-2336.

Chaudhary, H., Jaiswal, J. P., Kumar, A., & Joshi, S. (2022). Determination of genetic variability and diversity in bread wheat for yield and Yield contributing traits. *International Journal of Plant & Soil Science*, *34*(19), 16-23.

Devesh, P., Moitra, P. K., & Shukla, R. S. (2021). Correlation and path coefficient analysis for yield, yield components and quality traits in wheat. Electronic Journal of Plant Breeding, 12(2), 388–395.

Dvivedi, R. S., Singh, B., Pathak, V. N., Verma, S. P., & Pandey, K. K. (2023). Genetic variability, character association and component analysis in wheat: Genetic variability in wheat. *Journal of AgriSearch*, *10*(3), 151-157.

Erenstein, O., Jaleta, M., Mottaleb, K. A., Sonder, K., Donovan, J., & Braun, H.-J. (2022). Global trends in wheat production, consumption and trade. In Wheat improvement: Food security in a changing climate (pp. 47–66). Springer International Publishing Cham. https://library.oapen.org/bitstream/handle/20.500.12657/57013/978-3-030-90673-3.pdf#page=90

Finch-Savage, W. E. (2020). Influence of seed quality on crop establishment, growth, and yield. In Seed quality (pp. 361–384). CRC Press. https://www.taylorfrancis.com/chapters/edit/10.1201/9781003075226-11/influence-seed-quality-crop-establishment-growth-yield-finch-savage

He, Z. H., Xiao, Y., Lv, Y. W., Yeh, F. C., Wang, X., & Hu, X. S. (2023). Prediction of Genetic Gains from Selection in Tree Breeding. *Forests*, *14*(3), 520.

Jaiswal, R., Gaur, S., Jaiswal, S., & Kumar, A. (2020). An Estimate of Variability, Heritability and Genetic Advance for Grain Yield and Yield Components in Bread Wheat (Triticum aestivum L.). Current Journal of Applied Science and Technology, 1–6. https://doi.org/10.9734/cjast/2020/v39i1230657

Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy journal. 1955;47(7):314-8

Kumar, D., Rana, V., Rana, A., &Guleria, P. (2023). Genetic variability, correlation and path analysis studies for grain yield and morpho-physiological traits under moisture-stress conditions in bread wheat (Triticum aestivum L.) under north-western Himalayan conditions. *Journal of Cereal Research 15 (1): 92-102. http://doi. org/10.25174/2582-2675/2023, 124000*.

Levy, A. A., & Feldman, M. (2022). Evolution and origin of bread wheat. *The Plant Cell*, *34*(7), 2549-2567.

Liu, J., Yao, Y., Xin, M., Peng, H., Ni, Z., & Sun, Q. (2022). Shaping polyploid wheat for success: Origins, domestication, and the genetic improvement of agronomic traits. Journal of Integrative Plant Biology, 64(2), 536–563. https://doi.org/10.1111/jipb.13210

Okuyama, L. A., Federizzi, L. C., & Barbosa Neto, J. F. (2004). Correlation and path analysis of yield and its components and plant traits in wheat. Ciência Rural, 34, 1701–1708.

Orellana- Torrejon, C., Vidal, T., Saint- Jean, S., &Suffert, F. (2022). The impact of wheat cultivar mixtures on virulence dynamics in Zymoseptoria tritici populations persists after interseason sexual reproduction. *Plant Pathology*, *71*(7), 1537-1549.

Orellana- Torrejon, C., Vidal, T., Saint- Jean, S., &Suffert, F. (2022). The impact of wheat cultivar mixtures on virulence dynamics in Zymoseptoria tritici populations persists after interseason sexual reproduction. Plant Pathology, 71(7), 1537–1549. https://doi.org/10.1111/ppa.13577

Panek, E., Gozdowski, D., Stępień, M., Samborski, S., Ruciński, D., &Buszke, B. (2020). Within-field relationships between satellite-derived vegetation indices, grain yield and spike number of winter wheat and triticale. Agronomy, 10(11), 1842.

Poonia, M. K., Kumar, A., Kumar, V., Bhanu, A. N., & Kumar, S. (2023). Genetic Variability and Character Association Analysis for Seed Yield and its Attributes in Wheat (Triticum aestivum L.). International Journal of Plant & Soil Science, 35(9), 123–131. https://doi.org/10.9734/ijpss/2023/v35i92912

Poudel, M. R., Poudel, P. B., Puri, R. R., & Paudel, H. K. (2021). Variability, correlation and path coefficient analysis for agro-morphological traits in wheat genotypes (Triticum aestivum L.) under normal and heat stress conditions.

Przewieslik-Allen, A. M., Wilkinson, P. A., Burridge, A. J., Winfield, M. O., Dai, X., Beaumont, M., King, J., Yang, C., Griffiths, S., Wingen, L. U., Horsnell, R., Bentley, A. R., Shewry, P., Barker, G. L. A., & Edwards, K. J. (2021). The role of gene flow and chromosomal instability in shaping the bread wheat genome. Nature Plants, 7(2), 172–183. https://doi.org/10.1038/s41477-020-00845-2

Rangare, N. R., Krupakar, A., Kumar, A., & Singh, S. (2010). Character association and component analysis in wheat (Triticum aestivum L.). Electronic Journal of Plant Breeding, 1(3), 231–238.

Ronga, D., Dal Prà, A., Immovilli, A., Ruozzi, F., Davolio, R., & Pacchioli, M. T. (2020). Effects of harvest time on the yield and quality of winter wheat hay produced in Northern Italy. Agronomy, 10(6), 917.

Searle, S.R. (1961). Phenotypic, genotypic and environmental correlations. *Biometrics.* 17: 474-480.

Sharma, S., Tripathi, M. K., Tiwari, S., Solanki, R. S., Chauhan, S., Tripathi, N., ... &Kandalkar, V. S. (2023). The Exploitation of genetic variability and trait association analysis for diverse quantitative traits in bread wheat (Triticum aestivum L.). *Curr. J. Appl. Sci. Technol*, *42*(8), 19-33.

Shrivastava, A., Tripathi, M. K., Solanki, R. S., Tiwari, S., Tripathi, N., Singh, J., & Yadav, R. (2023). Genetic correlation and path coefficient analysis of yield attributing parameters in Indian mustard. Current Journal of Applied Science and Technology, 42(7), 42–58.

Singh, P. K., Sushma, B., & Kumari, N. (2022). Character association and path analysis for yield components and biochemical traits in maize (Zea mays L.) genotypes. *Indian Journal of Agricultural Research*, *56*(2), 135-140.

Singh, S. K., Barman, M., Prasad, J. P., & Bahuguna, R. N. (2022). Phenotyping diverse wheat genotypes under terminal heat stress reveal canopy temperature as critical determinant of grain yield. *Plant Physiology Reports*, *27*(2), 335-344.

Sohail, M., Hussain, I., Qamar, M., Tanveer, S. K., Abbas, S. H., Ali, Z., & Imtiaz, M. (2020). Evaluation of spring wheat genotypes for climatic adaptability using canopy temperature as physiological indicator. Pakistan Journal of Agricultural Research, 33(1), 89–96.

Sudeepthi, K., Srinivas, T., Kumar, B. R., Jyothula, D. P. B., & Umar, S. N. (2020). Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (Oryza sativa L.). Electronic Journal of Plant Breeding, 11(01), 144–148.

Usman, M. G., Rafii, M. Y., Martini, M. Y., Oladosu, Y., &Kashiani, P. (2017). Genotypic character relationship and phenotypic path coefficient analysis in chili pepper genotypes grown under tropical condition. *Journal of the Science of Food and Agriculture*, *97*(4), 1164-1171.

Verma, S. P., Pathak, V. N., & Verma, O. P. (2019). Interrelationship between yield and its contributing traits in wheat (Triticum aestivum L.). *Int. J Curr. Microbiol. App. Sci*, *8*(2), 3209-3215.

Zewdu, D., Mekonnen, F., Geleta, N., & Abebe, K. (2023). Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits of Bread Wheat (Triticum aestivum L.) Genotypes.

Supplementary table 1.Listof50 bread Wheat genotypesand theirsources

Sr. No.	Genotype code	Cross Name
1	GEN1	DBW187
2	GEN2	FITIS
3	GEN3	SOKOLL/3/PASTOR//HXL7573/2*BAU*2/6/OASIS/5*BORL95/5/CNDO/R143 //ENTE/MEXI75/3/AE.SQ/4/2*OCI

4	GEN 4	NADI/COPIO//NADI#2
5	GEN 5	KUTZ//KFA/2*KACHU
6	GEN 6	BOKOTA//KFA/2*KACHU
7	GEN 7	ND643/2*TRCH//MUTUS/3/SUP152/4/KACHU #1/KIRITATI//KACHU
8	GEN 8	SLVS/ATTILA//WBLL1*2/3/GONDO/CBRD/4/BORL14
9	GEN 9	SLVS/ATTILA//WBLL1*2/3/GONDO/CBRD/4/BORL14
10	GEN 10	WBLL1*2/SHAMA//KACHU/3/SUP152*2/TECUE #1/4/WBLL1/KUKUNA//TACUPETO F2001/3/BAJ #1
11	GEN 11	ROLF07*2/3/PRINIA/PASTOR//HUITES/4/2*SUP152/AKURI//SUP1 52
12	GEN 12	WBLL1*2/KURUKU//HEILO/3/KANCHAN*2/JUCHI/4/PARUS/FRA NCOLIN #1
13	GEN 13	BORL14*2/7/MUU/5/WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP// KAUZ/6/ WBLL1*2/SHAMA
14	GEN 14	TILILA/TUKURU/4/SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/KFA/2*K ACHU/6/T ILILA/JUCHI/4/SERI.1B//KAUZ/HEVO/3/AMAD
15	GEN 15	WAXWING*2/TUKURU//KBIRD/3/2*BORL14
16	GEN 16	GRACK/TECUE #1//FRNCLN*2/5/SITE/MO//PASTOR/3/TILHI/4/WAXWING/KIRIT ATI
17	GEN 17	FRET2*2/SHAMA//KIRITATI/2*TRCH/3/KFA/2*KACHU/4/FRET2* 2/SHAMA/ /PARUS/3/FRET2*2/KUKUNA

18	GEN 18	MUU/KBIRD//2*KACHU/KIRITATI
19	GEN 19	WBLL1*2/BRAMBLING//VORB/FISCAL/3/BECARD/4/MUCUY/5/ MUCUY
20	GEN 20	FRET2*2/SHAMA//KACHU/3/MUTUS*2/MUU
21	GEN 21	ATTILA*2/PBW65*2//MURGA/3/KACHU/KIRITATI
22	GEN 22	WBLL1*2/CHAPIO*2//MURGA/3/MUTUS/AKURI
23	GEN 23	MUTUS/ROLF07//MUCUY
24	GEN 24	ALTAR 84/AE.SQUARROSA (221)//3*BORL95/3/URES/JUN//KAUZ/4/WBLL1/5/MUTUS/6/SUP152/BAJ #1
25	GEN 25	CHRZ//BOW/CROW/3/WBLL1/4/CROC_1/AE.SQUARROSA (213) //PGO/5/BORL14
26	GEN 26	PREMIO/4/CROC_1/AE.SQUARROSA (205) //KAUZ/3/PIFED/5/BORL14
27	GEN 27	SNTL/3/KACHU//WBLL1*2/BRAMBLING
28	GEN 28	BORL14*2//BECARD/QUAIU #1
29	GEN 29	BORL14*2//BECARD/QUAIU #1
30	GEN 30	COPIO*2/MUCUY
31	GEN 31	KUTZ*2//KFA/2*KACHU
32	GEN 32	FRANCOLIN #1//WBLL1*2/BRAMBLING/3/WBLL1*2/BRAMBLING/4/2*NADI#1

33	GEN 33	KACHU #1//WBLL1*2/KUKUNA/3/BRBT1*2/KIRITATI/6/ROLF07*2/5/REH/HARE// 2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES/7/BORL14
34	GEN 34	BECARD/FRNCLN//BORL14
35	GEN 35	MUTUS*2/HARIL #1/3/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
36	GEN 36	WBLL1*2/BRAMBLING*2//BAVIS/4/SWSR22T.B.//TACUPETO F2001*2/BRAMBLING/3/2*TACUPETO F2001*2/BRAMBLING
37	GEN 37	TRCH*2//ND643/2*WBLL1/3/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
38	GEN 38	BORL14*2/NAVJ07
39	GEN 39	MUTUS*2/MUU/6/ATTILA/3*BCN//BAV92/3/PASTOR/4/TACUPETO F2001*2/BRAMBLING/5/PAURAQ/7/MUCUY
40	GEN 40	WBLL1*2/VIVITSI//AKURI/3/WBLL1*2/BRAMBLING*2/4/PBW343*2/KUKUNA*2//FRTL/PIFED
41	GEN 41	KACHU/BECARD//WBLL1*2/BRAMBLING*2/3/FRNCLN*2/TECUE #1
42	GEN 42	KENYA SUNBIRD/KACHU//KIDEA
43	GEN 43	MUTUS*2/CHONTE//SUP152/BAJ #1
44	GEN 44	WBLL1*2/BRAMBLING*2//BAVIS/3/BORL14
45	GEN 45	WBLL1*2/BRAMBLING*2//BAVIS/3/KACHU #1/KIRITATI//KACHU
46		ELVIRA/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI/6/VEE/PJN//KAU

	GEN 46	Z/3/PASTOR/7/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ/8/ELVIR A/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI/6/VEE/PJN//KAUZ/3/P ASTOR/9/BORL14

S.No	Genotypes	Germination(%)	Days to50 % flowering	Days tomaturity	CanopyTemperature	Vegetative index(GS)	Biomass	ChlorophyllContent	grainyieldperplot	100 grainwt
1	Gen1	92.500	75.000	111.500	26.300	65.500	9.500	43.150	3.000	45.65
2	Gen2	92.500	75.500	116.000	25.450	65.500	9.465	42.550	3.100	42.39
3	Gen3	90.000	77.500	115.000	24.600	63.500	8.900	43.300	3.000	48.26
4	Gen4	92.500	73.000	116.000	25.600	65.000	9.965	42.200	3.300	54.48
5	Gen5	95.000	78.000	116.000	25.100	63.000	9.130	42.850	2.950	44.60
6	Gen6	90.000	72.000	114.000	24.800	63.500	9.700	43.050	3.500	46.89
7	Gen7	95.000	73.000	115.000	24.800	64.000	8.500	43.200	3.000	42.83
8	Gen8	95.000	75.500	116.000	26.000	65.500	9.100	43.300	2.950	44.73
9	Gen9	92.500	72.000	118.000	25.000	64.000	8.000	44.200	2.800	40.12
10	Gen10	90.000	86.500	122.000	24.600	63.000	10.300	43.150	2.350	38.29
11	Gen11	95.000	79.000	118.000	25.750	64.500	9.300	43.950	2.850	43.43
12	Gen12	90.000	81.000	114.500	25.000	64.000	8.600	42.650	2.650	37.06

13	Gen13	92.500	80.500	116.000	25.800	64.500	8.000	42.150	2.650	45.260	97.000	10.000	86.000	0.330

Supplementary table 2. Mean performance and range for 13 traits studied in 50 bread wheat genotypes

28	Gen28	92.500	77.000	117.000	25.200	64.500	8.600	43.250	3.000	44.670	94.500	9.000	86.000	0.350
14	Gen14	92.500	79.500	115.000	24.700	64.500	9.000	42.200	2.450	39.990	95.500	9.500	79.000	0.275
15	Gen15	90.000	78.500	112.000	24.650	64.500	9.100	43.050	3.100	39.380	93.000	8.500	79.000	0.345
16	Gen16	95.000	80.500	118.000	25.150	63.000	8.800	43.300	2.600	38.260	91.500	11.000	72.000	0.300
17	Gen17	90.000	75.000	114.000	25.200	64.000	8.600	42.850	2.800	43.800	101.500	11.500	79.000	0.330
18	Gen18	95.000	81.000	120.000	24.750	64.000	8.665	42.700	2.800	37.810	100.000	10.500	79.000	0.325
19	Gen19	95.000	81.500	113.000	25.600	65.000	8.500	43.800	2.750	46.025	108.000	12.000	84.000	0.330
20	Gen20	95.000	76.000	117.500	25.950	65.000	8.600	43.300	2.900	42.100	96.000	11.000	79.000	0.340
21	Gen21	92.500	84.000	115.500	25.150	62.500	9.165	43.450	2.800	38.270	92.500	9.500	86.000	0.305
22	Gen22	95.000	80.500	113.000	24.600	63.500	9.600	42.250	2.800	40.770	100.000	11.500	72.000	0.290
23	Gen23	95.000	82.000	115.000	25.600	65.000	9.600	43.450	3.200	40.300	89.500	9.000	81.500	0.335
24	Gen24	92.500	77.000	116.000	24.650	62.500	9.300	44.000	3.250	42.550	97.500	8.500	79.000	0.350
25	Gen25	92.500	75.000	115.000	25.750	64.000	8.500	44.000	2.950	45.240	102.000	9.500	79.000	0.345
26	Gen26	92.500	76.000	116.000	24.900	65.000	10.400	42.700	3.250	44.310	100.500	9.500	86.000	0.310
27	Gen27	95.000	73.000	120.000	26.600	64.500	8.765	43.150	3.250	48.690	96.500	9.500	72.000	0.370

44	Gen44	92.500	80.000	113.000	25.100	62.500	8.900	42.900	3.000	43.050	94.000	11.000	86.500	0.335
29	Gen29	95.000	76.000	117.000	24.850	64.500	8.400	42.750	2.800	44.550	94.000	9.500	79.000	0.335
30	Gen30	95.000	81.500	112.000	25.200	65.500	9.600	43.100	2.650	33.390	92.500	10.000	79.000	0.280
31	Gen31	92.500	80.000	114.000	25.200	63.500	8.100	42.700	2.850	44.510	98.000	10.500	87.500	0.350
32	Gen32	92.500	75.500	112.000	25.150	64.000	9.300	42.700	2.950	40.570	99.500	10.000	80.500	0.320
33	Gen33	92.500	75.500	112.000	25.150	64.000	9.300	42.700	2.950	40.570	99.500	9.990	80.500	0.320
34	Gen34	90.000	80.000	118.000	26.100	64.000	8.500	43.350	2.900	46.120	94.500	9.500	72.000	0.345
35	Gen35	95.000	75.000	112.500	26.200	64.000	9.500	43.300	3.100	41.240	96.500	8.500	89.000	0.325
36	Gen36	92.500	79.000	119.000	25.950	64.500	8.800	43.100	3.000	42.550	97.500	10.000	90.000	0.340
37	Gen37	92.500	79.000	115.500	25.400	64.500	9.000	42.850	3.150	38.850	95.000	8.000	71.000	0.350
38	Gen38	92.500	72.000	112.000	25.700	64.000	9.200	43.300	2.900	43.800	98.000	10.500	91.000	0.315
39	Gen39	90.000	75.500	117.000	24.500	64.000	9.400	43.700	3.200	48.480	99.000	9.500	81.500	0.340
40	Gen40	95.000	85.500	113.000	24.450	65.000	9.200	42.050	2.700	43.850	93.000	11.000	86.000	0.295
41	Gen41	95.000	81.500	114.500	24.000	63.500	10.400	43.050	2.950	43.250	95.000	10.000	72.000	0.280
42	Gen42	92.500	80.000	112.000	25.950	64.000	8.500	42.250	2.450	39.200	97.000	10.500	86.000	0.285
43	Gen43	95.000	75.500	112.500	24.600	65.500	9.200	43.100	3.000	39.570	95.000	9.000	84.000	0.325

45	Gen45	92.500	81.500	114.000	25.800	64.000	8.800	42.200	3.000	38.450	97.000	11.500	72.000	0.345
46	Gen46	95.000	78.000	117.000	25.750	64.000	9.800	43.300	3.300	47.480	93.000	11.500	91.000	0.335
47	Gen47	92.500	81.000	118.000	24.700	64.000	9.500	43.300	2.950	47.680	98.500	11.000	86.500	0.315
48	Gen48	95.000	85.500	115.500	24.450	64.000	9.600	43.250	2.650	33.950	101.500	11.500	91.000	0.275
49	Gen49	95.000	62.010	161.885	14.660	115.740	2.515	21.800	0.475	30.490	75.135	10.525	20.965	0.283
50	Gen50	92.500	75.500	119.000	24.700	63.000	9.800	43.000	2.850	41.610	92.000	10.000	84.500	0.290
	Mean	93.924	77.800	116.328	25.016	65.175	8.979	42.618	2.876	42.387	96.173	10.100	79.709	0.317
	RangeLowest	90.000	62.010	111.500	14.660	62.500	2.515	21.800	0.475	30.490	75.135	8.000	20.965	0.235
	RangeHighest	95.000	86.500	161.885	26.600	115.740	10.400	44.200	3.500	54.480	108.000	12.000	91.000	0.370

source ofvariation	**df**	**Meansumofs(MSS)**

		Germination %	Days to 50%flowering	Days tomaturity	Canopy temperature	Vegetativeindex	Chlorophyllcontent	Biologicalyield/plot	Grain yield/plot	1000 grainweight	Tiller/m	Plantheight	Spikelength	Harvestindex
Replications	**1**	**0.23**	**7.23**	**76.26**	**0.36**	**7.246**	**7.81**	**0.0338**	**0.087**	**26.29**	**62.39**	**23.90**	**2.289**	**0.0025**
Genotypes	**49**	**80.76****	**36.06****	**98.58****	**5.137****	**107.73****	**18.55****	**2.40****	**0.348****	**36.67****	**216.21****	**48.75****	**2.143****	**0.0047****
Error	**49**	**33.93**	**18.32**	**50.22**	**2.33**	**23.49**	**9.43**	**1.03**	**0.123**	**18.71**	**66.20**	**24.95**	**0.367**	**0.00129**

Supplementary table 3. Analysis of variance for yield and its component traits in 50 bread wheat genotypes

***Significant atP = 0.05,** Significant atP = 0.01**