



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

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Aims: 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.

Study Design: The experiment was laid out in Randomized Complete Block Design (RCBD) in 2 replications.

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Place and Duration of Study: The study was conducted during the Rabi season of 2019 at Banaras Hindu University, India.

Methodology: Fifty genotypes of bread wheat were evaluated for thirteen morphological traits. Analysis of variance (ANOVA), correlation analysis, direct and indirect effects on grain yield per plot through path coefficient analysis were calculated. Assessed traits included biomass, harvest index, germination percentage, tillers per meter, days to flowering, plant height, and spike length. Genetic variability and heritability parameters were calculated for these traits. Genetic variability parameters were also calculated to determine the extent of variability and heritability for these traits.

Results: The analysis of variance revealed significant genotypic differences for all studied traits. Correlation analysis highlighted intricate interrelationships among traits, with biomass exhibiting the highest positive direct effect on grain yield, followed by harvest index and germination percentage. In contrast, tillers per meter, days to flowering, and plant height had negative direct effects on yield. Genetic variability parameters indicated substantial variability for traits like harvest index and grain yield per plot, with spike length showing the highest heritability.

Conclusion: The study highlights the complexity of grain yield determination, which is affected by various genetic and environmental factors. The results offer deeper insights into the genetic basis of yield-related traits in wheat, stressing the importance of selecting genotypes with beneficial trait combinations to boost yield potential.

Keywords: Variability parameters; heritability; genetic advance; direct effects; indirect effects.

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 [1]. It is an allohexaploid species, composed of 21 chromosome pairs organized in three subgenomes, A, B, and D, Genome BBAADD, $2n = 6x = 42$ [2]. It is the world's largest famous energy-rich cereal crop [3]. Wheat, the first domesticated food crop since 8000 years, is the stable food for various civilizations throughout the world [4]. 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 [5]. It covers 17% of the total cultivated land in the world [6]. 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 [7]. 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 [4]. It is a monoecious plant with perfect flowers, reproducing sexually as an autogamous crop although limited (3%) cross pollination is possible [8]. 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 [9]. "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 [10]. The degree of genetic control related to some heritable significant features is referred to as heritability [11]. In plant breeding programme, direct selection for yield as such could be misleading [12]. 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 [13]. 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 [11]. Correlation studies along with path analysis provide a better understanding of the association of different characters with grain yield [14]. 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" [9]. 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 6 rows 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 variety The 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 bread wheat genotypes were given in supplementary Table 1. These genotypes exhibiting wide spectrum of variability for various agronomic and morphological characters were obtained through CIMMYT and 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 [15]. The formula provided by Allard ([16] was used to calculate genetic advance as percentage of mean (GAM) and broad sense heritability (h^2_b). The correlation coefficients were calculated based on the analysis of variance and covariance, as recommended by Searle [15]. The path coefficient analysis was performed using the method proposed by Wright [17] and further explained by Dewey and Lu [18]. All the genetic parameters analysis, correlation analysis was done using R-software. Path coefficients were estimated using INDOSTAT 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.

3.2 Genetic Variability Parameters

Genotypic and phenotypic coefficients of variability are the two parameters which are used for measuring the variability [19]. 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 [20]. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone [21]. However, it is not necessary that a character showing high heritability will always exhibit high genetic advance [22]. Genotypic coefficient of variation (GCV) was recorded highest 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 coefficient of variation (PCV) was higher in magnitude than that of genotypic coefficient of variation for all characters under study. The highest PCV was recorded for harvest index (17.357) followed by grain yield per plot (16.894), no. of tillers per meter (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 coefficient of variation. Similar findings for PCV and GCV were reported by many researchers in bread wheat [23]. Broad sense heritability was estimated for all the characters under study. 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 for harvest index (20.56) followed by grain yield per plot (16.574), vegetative index (16.435), tillers per meter (16.311), spike length (16.171) and least genetic advance as percent mean for plant height (4.2). For heritability and genetic advance similar findings were reported by earlier researchers [24].

3.3 Correlation Studies

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 [25]. 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 [26]. 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 [27]. 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 [28]. 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 [29]. 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., [30]; Baye et al., [31]; Poudel et al., [32].

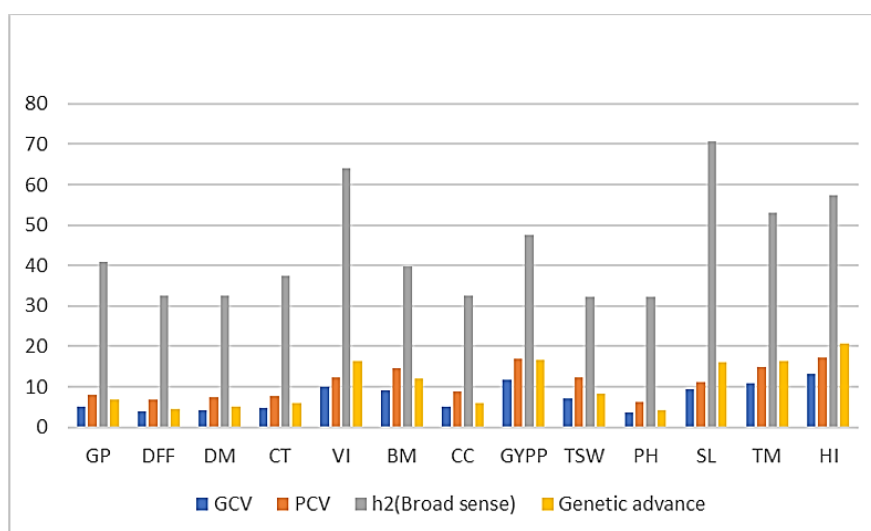


Fig. 1. Graphical representation of genetic parameters of variation (GCV, PCV, Genetic Advance (5%), Genetic advance as percent of mean (5%), h²_b for 13 traits among 50 bread wheat accessions

*Abbreviations: GCV-Genotypic coefficient of variation, PCV-phenotypic coefficient of variation, h²_b-Broad Sense heritability

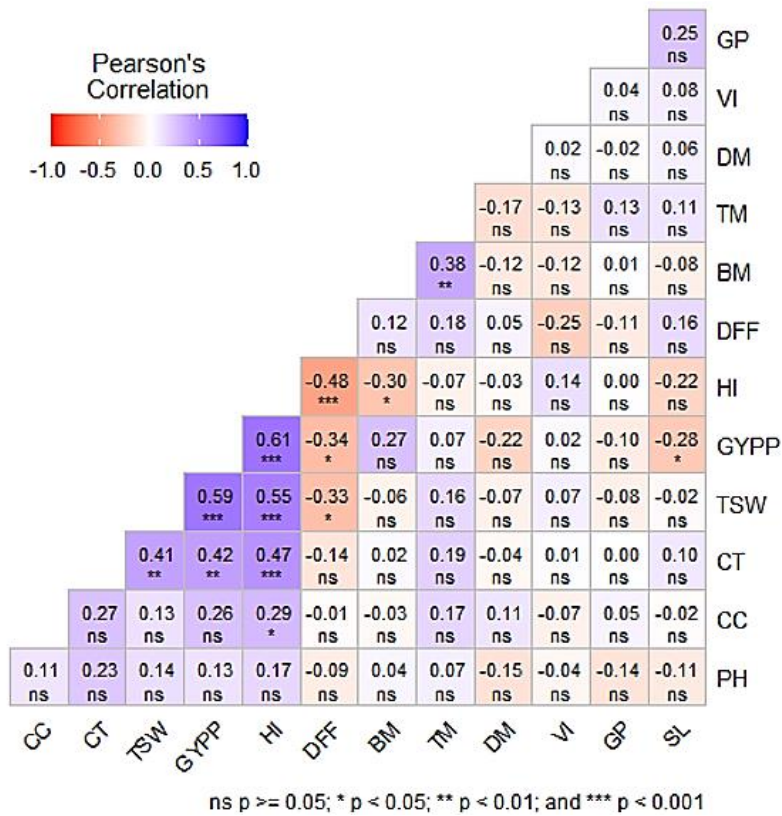


Fig. 2. Phenotypic correlation studies among 12 characters for 50 genotypes of bread wheat

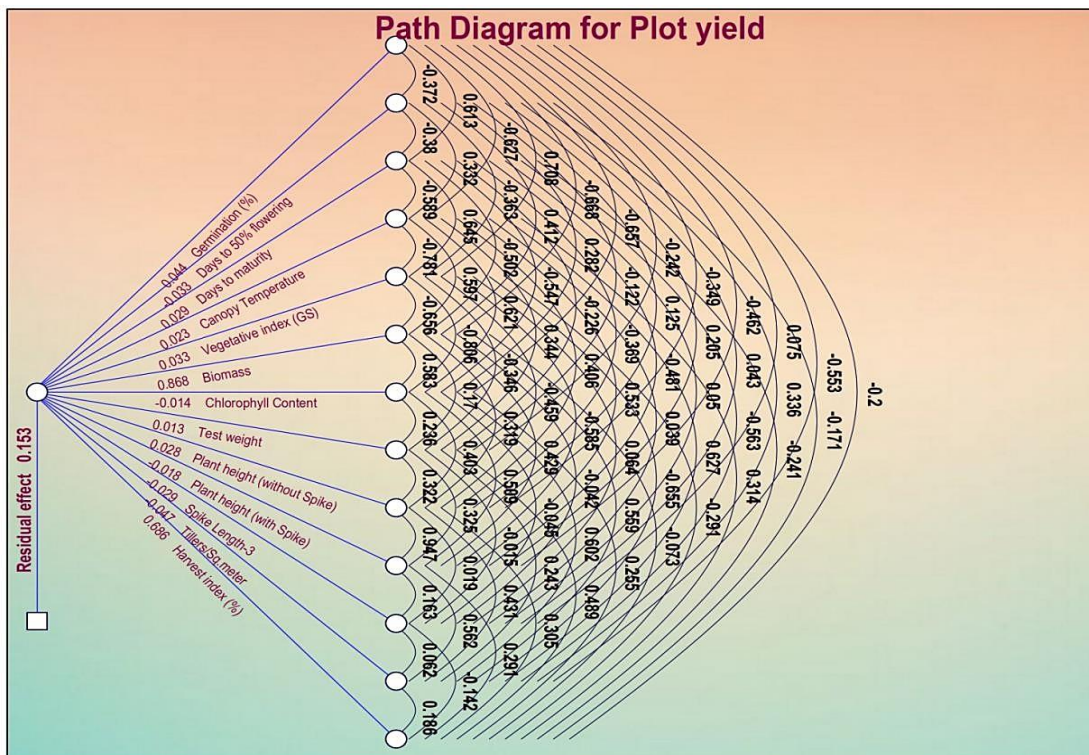


Fig. 3. Path diagram for grain yield per plot among 50 bread wheat genotypes

Table 1. Path coefficient analysis for grain yield per plot among 50 bread wheat genotypes

Trait	Germination (%)	Days to 50% flowering	Days to maturity	Canopy temperature	Vegetative index (GS)	Biomass	Chlorophyll content	1000-grain weight	Plant height (without Spike)	Plant height (with Spike)	Spike length	tillers/meter ¹	Harvest index (%)	grain yield per plot
Germination (%)	0.0436	-0.0162	0.0267	-0.0273	0.0308	-0.0291	-0.0286	-0.0105	-0.0152	-0.0201	0.0033	-0.0241	-0.0087	-0.606**
Days to 50% flowering	0.0123	-0.0332	0.0126	-0.011	0.012	-0.0137	-0.0093	0.0041	-0.0041	-0.0068	-0.0014	-0.0111	0.0057	0.153
Days to maturity	0.0179	-0.0111	0.0292	-0.0172	0.0188	-0.0146	-0.016	-0.0066	-0.0108	-0.014	0.0015	-0.0164	-0.007	-0.497**
Canopy Temperature	-0.0144	0.0076	-0.0135	0.0229	-0.0179	0.0137	0.0142	0.0079	0.0093	0.0122	0.0009	0.0144	0.0072	0.642**
Vegetative index (GS)	0.0236	-0.0121	0.0216	-0.0261	0.0334	-0.0219	-0.0269	-0.0116	-0.0153	-0.0196	0.0021	-0.0219	-0.0097	-0.659**
Biomass	-0.5799	0.3577	-0.4354	0.5184	-0.5696	0.868	0.5058	0.1479	0.277	0.3725	-0.0365	0.4856	-0.0629	0.723**
Chlorophyll content	0.0092	-0.004	0.0077	-0.0087	0.0114	-0.0082	-0.0141	-0.0033	-0.0057	-0.0072	0.0006	-0.0085	-0.0036	0.579**
1000-grain weight	-0.0031	-0.0016	-0.0029	0.0044	-0.0044	0.0022	0.003	0.0127	0.0041	0.0041	-0.0002	0.0031	0.0062	0.468**
Plant height (Without spike)	-0.0099	0.0035	-0.0104	0.0115	-0.013	0.009	0.0114	0.0091	0.0283	0.0268	0.0005	0.0122	0.0086	0.439**
Plant height (with Spike)	0.0083	-0.0037	0.0086	-0.0095	0.0105	-0.0077	-0.0091	-0.0058	-0.017	-0.0179	-0.0029	-0.0101	-0.0052	0.499**
Spike length	-0.0022	-0.0012	-0.0014	-0.0011	-0.0018	0.0012	0.0013	0.0004	-0.0006	-0.0047	-0.0287	-0.0018	0.0041	-0.161
tillers/meter	0.0258	-0.0157	0.0263	-0.0293	0.0306	-0.0262	-0.0281	-0.0113	-0.0201	-0.0263	-0.0029	-0.0467	-0.0087	0.503**
Harvest index (%)	-0.1369	-0.1171	-0.1656	0.2153	-0.1995	-0.0497	0.175	0.3353	0.2092	0.1998	-0.0975	0.1278	0.686	0.612**
grain yield per plot	-0.606**	0.153	-0.497**	0.642**	-0.659**	0.723**	0.579**	0.468**	0.439**	0.499**	-0.161	0.503**	0.612**	1
Partial R ²	-0.0264	-0.0051	-0.0145	0.0147	-0.022	0.6276	-0.0081	0.006	0.0124	-0.0089	0.0046	-0.0235	0.4197	

* Significant at P = 0.05, ** Significant at P = 0.01

3.4 Path Coefficient Analysis

The observed correlation between yield and its component characters is the net result of the direct and indirect effects of the component character through other yield attributes [33]. The total correlation coefficient between yield and its component characters may sometimes be misleading, as it may be an over or under estimate of its association with other characters. In these cases, direct selection on the basis of correlated response may not be fruitful [34]. For critical evaluation, the correlation coefficient needs to be split into direct and indirect effects using path coefficient analysis since, many characters affect a given trait [35]. Thus, the correlation and path coefficients in combination can give a better insight into cause-and-effect relationship between different pairs of characters [36]. If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation [37]. In such situations, the indirect causal factors are to be considered simultaneously for selection. Correlation coefficient may be negative but the direct effect is positive and high. Under these circumstances, a restricted simultaneous selection model is to be followed. i.e., restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect. If correlation coefficient is negative and direct effect is also negative, then the character cannot be considered as a selection criterion [38]. In the present study, path analysis was used to work out the direct and indirect effects of yield contributing characters on yield in 50 genotypes. The direct and indirect effects of various characters towards grain yield per plant are presented in Table number 1. At phenotypic level highest positive direct effect towards grain yield was observed by biomass (0.868) followed by harvest index (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 tillers per 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 tillers per meter (0.0258) and prominent negative indirect effect through biomass (-0.5799) and the remaining had negligible indirect negative and positive effects at the phenotypic level. Days to 50% flowering has indirect positive effect via biomass (0.3577) and it was revealed negative indirect effect via

harvest index (-0.1171) and the remaining has negligible indirect negative and positive effects at the phenotypic level. 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 indirect negative and positive effects at the phenotypic level. Canopy temperature has indirect positive effect via biomass (0.5184) and it was revealed negative indirect effect via no. of tillers per meter (-0.0293) and the remaining has negligible indirect negative and positive effects at the phenotypic level. Vegetative index has indirect positive effect via germination percentage (0.0308) and it was revealed negative indirect effect via biomass (-0.5696) and the remaining has negligible indirect negative and positive effects at the phenotypic level. Biomass has indirect positive effect via canopy temperature (0.0137) and it was revealed negative indirect effect via harvest index (-0.0497) and the remaining has negligible indirect negative and positive effects at the phenotypic level. Chlorophyll content has indirect positive effect via biomass (0.5058) and it was revealed negative indirect effect via germination percentage (-0.0286) and the remaining has negligible indirect negative and positive effects at the phenotypic level. 1000-grain weight has indirect positive effect via harvest index (0.3353) and it was revealed negative indirect effect via vegetative index (-0.0116) and the remaining has negligible indirect negative and positive effects at the phenotypic level. Plant height has indirect positive effect via biomass (0.3725) and it was revealed negative indirect effect via no. of tillers/m (-0.0263) and the remaining has negligible indirect negative and positive effects at the phenotypic level. 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 has negligible indirect negative and positive effects at the phenotypic level. No. of tillers per meter has indirect positive effect via biomass (0.4856) and it was revealed negative indirect effect via germination percentage (-0.0241) and the remaining 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 was revealed negative indirect effect via biomass (-0.0629) and the remaining has negligible indirect negative and positive effects at the phenotypic level. Similar results were shown by Kumar et al., [39]; Abo-Elwafa et al., [40]; Bhardwaj et al., [41].

4. 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. Future research should enhance traits like biomass, harvest index, and germination percentage due to their positive impact on yield. Investigating the negative effects of tillers per meter and days to flowering is crucial for overall yield improvement. Significant genetic variability in traits like harvest index and grain yield per plot suggests potential for selective breeding. Promising genotypes should be identified and utilized in breeding programs. The high heritability of spike length warrants further genetic studies to integrate this trait into high-yielding genotypes. Combining traditional breeding with modern genomic tools can optimize trait combinations and accelerate yield improvements. Environmental interactions should be considered to develop resilient varieties. Multi-location trials are essential to validate trait performance across different environments.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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Supplementary Table 1. List of 50 bread wheat genotypes and their sources

Sr. No.	Genotype code	Cross Name
1	GEN 1	DBW187
2	GEN 2	FITIS
3	GEN 3	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//SUP152
12	GEN 12	WBLL1*2/KURUKU//HEILO/3/KANCHAN*2/JUCHI/4/PARUS/FRANCOLIN #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*KACHU/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/KIRITATI
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/KUKU	
		NA*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	GEN 46	ELVIRA/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI/6/VEE/PJN//KAU	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	

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

S.No	Genotypes	Germination (%)	Days to 50% flowering	Days to maturity	Canopy Temperature	Vegetative index (GS)	Biomass	Chlorophyll Content	grain yield per plot	1000-grain weight	Plantheight (with Spike)	Spike Length	Tillers/ meter	Harvest index (%)
1	Gen 1	92.500	75.000	111.500	26.300	65.500	9.500	43.150	3.000	45.650	105.500	11.000	84.000	0.320
2	Gen 2	92.500	75.500	116.000	25.450	65.500	9.465	42.550	3.100	42.390	101.000	10.000	72.000	0.330
3	Gen 3	90.000	77.500	115.000	24.600	63.500	8.900	43.300	3.000	48.260	95.500	8.500	78.000	0.340
4	Gen 4	92.500	73.000	116.000	25.600	65.000	9.965	42.200	3.300	54.480	100.000	10.500	81.500	0.340
5	Gen 5	95.000	78.000	116.000	25.100	63.000	9.130	42.850	2.950	44.600	91.000	8.500	72.000	0.325
6	Gen 6	90.000	72.000	114.000	24.800	63.500	9.700	43.050	3.500	46.890	100.000	9.500	86.000	0.365
7	Gen 7	95.000	73.000	115.000	24.800	64.000	8.500	43.200	3.000	42.830	90.500	10.000	72.000	0.350
8	Gen 8	95.000	75.500	116.000	26.000	65.500	9.100	43.300	2.950	44.735	89.500	12.000	78.000	0.330
9	Gen 9	92.500	72.000	118.000	25.000	64.000	8.000	44.200	2.800	40.120	93.500	11.500	72.000	0.355
10	Gen 10	90.000	86.500	122.000	24.600	63.000	10.300	43.150	2.350	38.290	94.500	10.500	84.000	0.230
11	Gen 11	95.000	79.000	118.000	25.750	64.500	9.300	43.950	2.850	43.430	98.000	11.000	87.000	0.310
12	Gen 12	90.000	81.000	114.500	25.000	64.000	8.600	42.650	2.650	37.060	99.000	8.500	79.000	0.310
13	Gen 13	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
14	Gen 14	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	Gen 15	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	Gen 16	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	Gen 17	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	Gen 18	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	Gen 19	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	Gen 20	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	Gen 21	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	Gen 22	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	Gen 23	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	Gen 24	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	Gen 25	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	Gen 26	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	Gen 27	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
28	Gen 28	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
29	Gen 29	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	Gen 30	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	Gen 31	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	Gen 32	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	Gen 33	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	Gen 34	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	Gen 35	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	Gen 36	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	Gen 37	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	Gen 38	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	Gen 39	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

S.No	Genotypes	Germination (%)	Days to 50% flowering	Days to maturity	Canopy Temperature	Vegetative index (GS)	Biomass	Chlorophyll Content	grain yield per plot	1000-grain weight	Plant height (with Spike)	Spike Length	Tillers/ meter	Harvest index (%)
40	Gen 40	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	Gen 41	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	Gen 42	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	Gen 43	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
44	Gen 44	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
45	Gen 45	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	Gen 46	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	Gen 47	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	Gen 48	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	Gen 49	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	Gen 50	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
	Range	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
	Lowest													
	Range	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
	Highest													

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

source of variation	df	Mean sum of s (MSS)												
		Germination%	Days to 50% flowering	Days to maturity	Canopy temperature	Vegetative index	Chlorophyll content	Biological yield/plot	Grain yield/plot	1000 grain weight	Tiller/m	Plant height	Spike length	Harvest index
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

* Significant at P = 0.05, ** Significant at P = 0.01

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