

SABRAO Journal of Breeding and Genetics  
 55 (5) 1666-1677, 2023  
<http://doi.org/10.54910/sabrao2023.55.5.19>  
<http://sabraojournal.org/>  
 pISSN 1029-7073; eISSN 2224-8978



## CORRELATION AND PATH ANALYSES IN F<sub>4</sub> SEGREGATING POPULATIONS OF BREAD WHEAT FOR GRAIN YIELD AND ITS ATTRIBUTES

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### SUMMARY

Wheat breeders focus on enhancing the production potential of bread wheat by creating new varieties with acceptable genetic makeup to combat the pressure of rising human population consumption. Research to resolve this issue transpired during the Rabi of November 2021– April 2022 at the Lovely Professional University, Punjab, India. Developing the field trial used an augmented block design, 45 F<sub>4</sub> segregating population genotypes, and five checks. Data on characteristics, such as days to 50% flowering, days to maturity, number of productive tillers, plant height, ear length, and weight, number of spikelets ear<sup>-1</sup> and grains ear<sup>-1</sup>, 1000 grain weight, grain yield plant<sup>-1</sup>, biological yield, harvest index, and chlorophyll index underwent assessment. Highly significant variations between the genotypes for all the traits had the analysis of variance determining these, except 1000 grain weight and chlorophyll index in the treatment test and the test versus check. In this study, the harvest index, biological yield plant<sup>-1</sup>, and grain yield plant<sup>-1</sup> are all higher for the phenotypic and genotypic coefficient of variances (PCV, GCV). The genetic advancement and heritability are highest for days to maturity, ear weight, number of grains ear<sup>-1</sup>, biological yield plant<sup>-1</sup>, grain yield plant<sup>-1</sup>, and harvest index. Studies on the relationships between various traits divulged that the number of productive tillers and harvest index had a positive, strong link and a direct effect with grain yield plant<sup>-1</sup>. These findings support the application of genetic modification to increase seed yield in bread wheat.

**Keywords:** wheat, genetic variability, genotypic coefficient of variance, phenotypic coefficient of variance, heritability, correlation and path analysis

**Key findings:** The results from the study stated that the number of productive tillers and harvest index manifested a positive correlation and a direct effect on grain yield plant<sup>-1</sup>, indicating that further improvement of these traits may indirectly lead to an overall improvement of the crop yield in future breeding programs.

**Citation:** Sharadhi GP, Avinashe H, Dubey N, Danalakoti K, Ghosh S, Sachan S, Choudhary S (2023). Correlation and path analyses in f<sub>4</sub> segregating populations of bread wheat for grain yield and its attributes. *SABRAO J. Breed. Genet.* 55(5): 1666-1677. <http://doi.org/10.54910/sabrao2023.55.5.19>.

Communicating Editor: Dr. A.N. Farhood

Manuscript received: May 9, 2023; Accepted: July 22, 2023.

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## INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is an annual plant with an allohexaploid genome. It is a member of the "Triticeae" tribe and the "Gramineae" family. According to Mergoum *et al.* (2009), it is one of the earliest food crops being domesticated and developed in the Fertile Crescent of the Middle East. It is now a fundamental chief diet for most humans. Three factors distinguish bread wheat from other cultured crops: first, its production has a broader area; second, it contributes more calories to the human diet than any other crop; and third, it comprises global trading more than all other food grains (Mangi *et al.*, 2008). Compared with other food crops, it delivers nutrition in bulk and has the highest area coverage and total output (FAOSTAT, 2019). With a total yield of around 773.5 million tons, the average productivity worldwide was 3.54 t/ha. In terms of production and consumption, wheat is one of the most significant exported grain crops globally. The International Maize and Wheat Improvement Centre (CIMMYT) has selected a wheat spike emblem in their logo with the caption "Let there be bread." The Food and Agriculture Organization of the United Nations or FAO graciously projects worldwide praise by stating wheat as human nourishment (Maqbool *et al.*, 2010; Dutamo *et al.*, 2015).

Currently, India is self-sufficient based on the amount of wheat grain consumed by its people; however, a significant increase in wheat cultivation will be necessary to ensure the food security of the nation's constantly growing population. There is less land for the nation's wheat acreage to plant further; thus, improving productivity is crucial. Most of the world's significant agricultural production takes place in rural regions. Some previous research recently indicated the cultivated farmland in rural areas is decreasing. The economy relies mainly on agricultural production. Agriculture produces food crops but also contributes to the

economy by exporting a wide range of goods. Despite this, farmers often abandon their jobs.

Globally, bread wheat is a significant strategic crop; the utmost goal needed pursuits by plant breeders is the process of producing new crop varieties characterized by high production standards and excellent quality features (Singh *et al.*, 2007). As the industry develops, grain quality becomes an increasingly important component (Javed *et al.*, 2022; Khan *et al.*, 2023). The various industrial wheat products demand distinct parameter criteria for the final product's quality assessment. Therefore, plant breeders must pay equal attention to enhancing grain production metrics and quality parameters (Sajjad *et al.*, 2012). According to Ahmad *et al.* (2022) and Javed *et al.* (2022), the traits positively correlated with yield included the number of ears, ear length, chlorophyll index, and the number of grains ear<sup>-1</sup>. Some researchers found a negative correlation between yield and product quality (O'Brien and Ronalds, 1987; Kaya and Akura, 2014). However, several studies have shown a favorable relationship between quality and yield (Kanwal *et al.*, 2019; Rathod *et al.*, 2019).

Utilizing easily accessible genetic resources with this acquaintance of nature, connotation, and quantification of genetic differences in population is central to organizing an effective breeding strategy. It is essential to know the crop results to practice an efficient selection process; therefore, a comprehensive examination of the significance of genetic variation in crops is also vital in this regard. Since yield is a complicated attribute, factors influencing yield the most require identification. Genetic variability has been a significant component and a necessary prerequisite for a successful hybridization intended to produce high-yielding progeny (Nukasani *et al.*, 2013). Understanding the genetic effects of hybridization may proceed by

studying genetic parameters from segregating populations (Koujalagi *et al.*, 2017).

The availability of genetic variation, high heritability, and genetic gain for the targeted characteristics in segregating generations was essential for the success of any breeding program in a chosen environment. The analysis of variance (ANOVA) determines whether the variation for a given characteristic has genotypic variations or environmental factors causing it. According to Johnson and Frey (1967), heritability is the ratio of phenotypic variation to genotypic variation. Heritability estimation constitutes an essential component of the response to selection for improvement because it reveals the gene interaction in future generations. Selecting secondary target features among breeding lines focusing on heritability and genetic advancement under stressful conditions may lead to genetic improvement of complex traits (Khan *et al.*, 2022).

To provide information about the proper cause-and-effect relationships between yield and specific yield components, correlation and path coefficient analysis requires usage as a key tool, and determining how characteristics relate to one another and how strongly they correlate with one another is crucial in plant breeding. When two attributes are positively connected, one may indirectly achieve augmenting by enhancing the other. The correlation coefficient might be helpful if employing an indirect selection of the secondary trait to boost the fundamental feature (Hussain *et al.*, 2010). A need to figure out the correlation coefficient entails making a selection index.

Wright (1921) developed a path coefficient analysis method to help people understand the correlation. This method helped create criteria for selecting complex traits in many crops (Dewey and Lu, 1959). This study is a better way to know the direct and secondary reasons for relationships.

## MATERIALS AND METHODS

### Experimental area and design

The trial's execution was in November, during Rabi season 2021–2022 in Punjab, India, under the Genetics and Plant Breeding Department, Lovely Professional University, located at an elevation of 243 masl, with the coordinates 31° 19' 32" North, 75° 34' 45" East. The experimental region's careful selection has the basis of geography and fertility. Field trials' implementation used an augmented design with 45 F<sub>4</sub> segregating population genotypes and five checks (Table 1) planted in 12.5 m × 8 m plots with 22.5 cm × 5 cm spacing. The choice of 45 F<sub>4</sub> population genotypes came from three crosses of the F<sub>3</sub> generation. All advised agronomic procedures and plant protection techniques aided in growing a healthy crop. Urea fertilizer application ensued after 45 days of sowing, with four times irrigation given as per the package of practice.

### Data recorded

Data collection on the number of days until 50 percent flowering (DTF) and days to maturity (DTM) per plot progressed. Plant height (cm, PH), number of productive tillers (NPT), ear weight (g, EW), ear length (cm, EL), number of spikelets ear<sup>-1</sup> (NSE), number of grains ear<sup>-1</sup> (NGE), 1000-grain weight (GW), grain yield plant<sup>-1</sup> (g, GYP), biological yield plant<sup>-1</sup> (g, BYP), harvest index (HI), and chlorophyll index (CI) gained measuring on a sample of five plants each.

### Statistical analysis

Analysis and coefficient of variances, heritability, and genetic advance for augmented design ran on the data gathered for each quantitative trait using R Studio software.

**Table 1.** List of crosses and checks.

No.	Checks	Genotypes
1	IC-57578	HD-2932 × GW-273 (16 entries)
2	IC-532283	MP-3137 × LOK-1 (14 entries)
3	IC-82264	HD-2932 × LOK-1 (15 entries)
4	IC-73570	-
5	IC-82555	-

The correlation coefficient's analysis examined positively and negatively associated features with yield and other characters. Path coefficient analysis helped examine the attributes' direct and indirect impact on the correlations. Both parameters' evaluation used INDOSTAT 9.3 version software.

## RESULTS AND DISCUSSION

### Analysis of variance (ANOVA)

The 13 yield and attributing characters' investigation determined the genetic variability among 45 genotypes of three crosses of segregating F<sub>4</sub> population with five wheat checks (Table 1) in the presented research. The results of an analysis of variance for augmented design for 13 characters appear in Table 2, investigating the importance of divergences across various treatments (checks). Since there is variation across segregating populations, the best pure lines can proceed with propagation following selection. Treatment tests on DTF, DTM, EL, NSE, EW, NGE, BYP, NGE, and HI characters showed significant variations. Evidence of substantial variations occurred across tests and checks for DTF, DTM, PH, NPT, EL, NSE, EW, NGE, BYP, and GYP for 50 bread wheat genotypes. It is a sign of variability that may be advantageous in subsequent breeding programs via selection. Kalimullah *et al.* (2012) and Dutamo *et al.* (2015) found statistically significant variations in 11 morphological variables, including DTF, DTM, PH, NPT, and GW.

### Estimation of genetic variability

The phenotypic and genotypic coefficients of variance, heritability, and genetic advance mean underwent scrutiny (Table 3). PCV is higher than GCV in all traits, and high heritability coupled with high genetic gain was evident in DM, EW, and NGE. Figure 1 indicates the value of the coefficient of variance of each trait. Prasad *et al.* (2021) also studied 50 wheat genotypes for the following features: DTF, DTM, PH, NPT, NSE, EL, EW, NGE, GW, GYP, BYP, and HI. In Table 3, the PCV and GCV are higher in BYP (31.38, 27.52), GYP (27.51, 23.17), and harvest index (47.9, 45.07). These outcomes are comparable to the report of Swelam *et al.* (2022) for GW and GYP in F<sub>2</sub> segregating population under optimum irrigation, Malbhage *et al.* (2020) for PH, BYP, and GYP, and Kumar *et al.* (2019) for EW, BYP, GYP, and HI. Moderate PCV and GCV emerged in DTM (12.64, 12.63), EW (17.59, 14.05), and NGE (16.3, 14.26). Medium PCV and low GCV occurred in EL (10.05, 8.31), GW (12.21, 6.75), and CI (16.92, 9.43). Low ranges in PCV and GCV surfaced in DTF (4.82, 4.32), PH (8.2, 5.32), and NSE (8.87, 7.5) (Figure 1). Sharma *et al.* (2018) revealed a similar result type in NSE and DTF. The heritable component of the variance cannot be calculable with only these numbers. Heritability reflects the contingency of genetic diversity, especially passed down from the parents to all offspring. Heritability estimations ranged from 30.54% for GW to 99.78% for DTM (Figure 2). DTM (99.78%) has the highest heritability estimate recorded among all traits, followed by HI (88.54%), DTF (80.35%), BYP (76.91%), NGE (76.54%), NSE

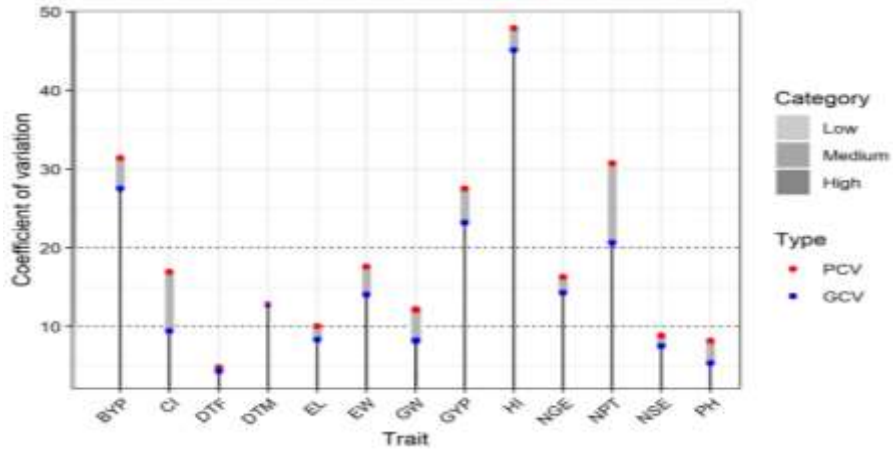
**Table 2.** Analysis of variance among the bread wheat genotypes for all the traits.

Source of variation	d.f.	DTF	DTM	PH	NPT	EL	NSE	EW	NGE	GW	BYP	GYP	HI	CI
Treatment (ignoring Blocks)	49	28.62**	243.9**	258.37**	4.3 <sup>NS</sup>	1.2**	1.92**	0.15**	49.16**	24.51 <sup>NS</sup>	69.18**	9**	319.2**	40.48 <sup>NS</sup>
Treatment: Check	4	66.07**	7.25 **	794.71**	8.45*	1.08*	2.09*	0.02 <sup>NS</sup>	127.47**	71.92 <sup>NS</sup>	8.12 <sup>NS</sup>	4.48 <sup>NS</sup>	45.55 <sup>NS</sup>	60.49 <sup>NS</sup>
Treatment: Test vs. Check	1	232.75**	1461.03**	6961.24**	11.72*	18.78**	6.98**	2.51**	321.68**	67.83 <sup>NS</sup>	180.79**	155.91**	2094.82**	9.29 <sup>NS</sup>
Treatment: Test	44	20.57**	237.75**	57.28 <sup>NS</sup>	3.75 <sup>NS</sup>	0.81*	1.79*	0.11*	35.85**	19.22 <sup>NS</sup>	72.19**	6.07*	303.72**	39.37 <sup>NS</sup>
Block (Eliminating Treatments)	3	3.00 <sup>NS</sup>	0.85 <sup>NS</sup>	12.04 <sup>NS</sup>	0.06 <sup>NS</sup>	0.32 <sup>NS</sup>	0.59 <sup>NS</sup>	0.07 <sup>NS</sup>	23.15 <sup>NS</sup>	7.07 <sup>NS</sup>	36.43 <sup>NS</sup>	0.88 <sup>NS</sup>	76.85 <sup>NS</sup>	11.54 <sup>NS</sup>
Residuals	12	4.04	0.52	33.14	2.06	0.26	0.51	0.04	8.41	25.09	16.67	1.76	34.8	27.14
CV %		2.11	0.58	5.94	23.49	5.52	4.7	11.12	8.13	14.13	15.52	16.08	17.44	14.1

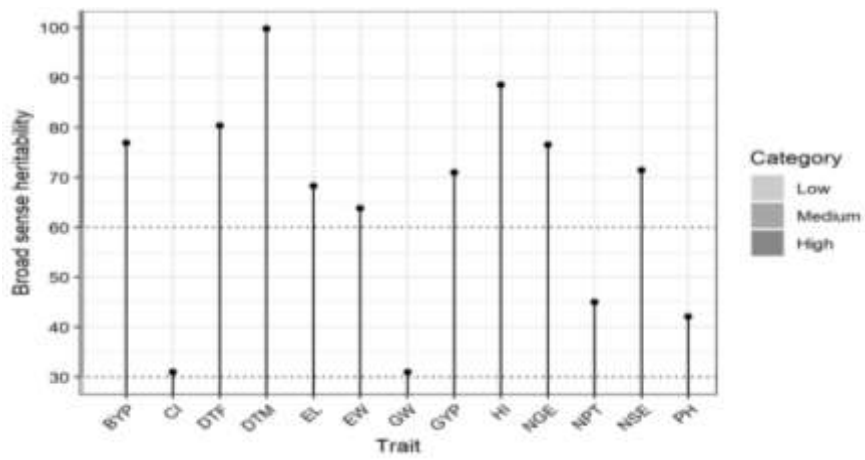
DTF: days to 50% flowering, DTM: days to maturity, PH: plant height, NPT: number of productive tillers, EL: ear length, NSE: number of spikelets ear<sup>-1</sup>, EW: ear weight, NGE: number of grains ear<sup>-1</sup>, GW: 1000 grain weight, BYP: biological yield plant<sup>-1</sup>, GYP: grain yield plant<sup>-1</sup>, HI: harvest index, CI: chlorophyll index.

**Table 3.** Genetic variability parameters for grain yield and its components in bread wheat.

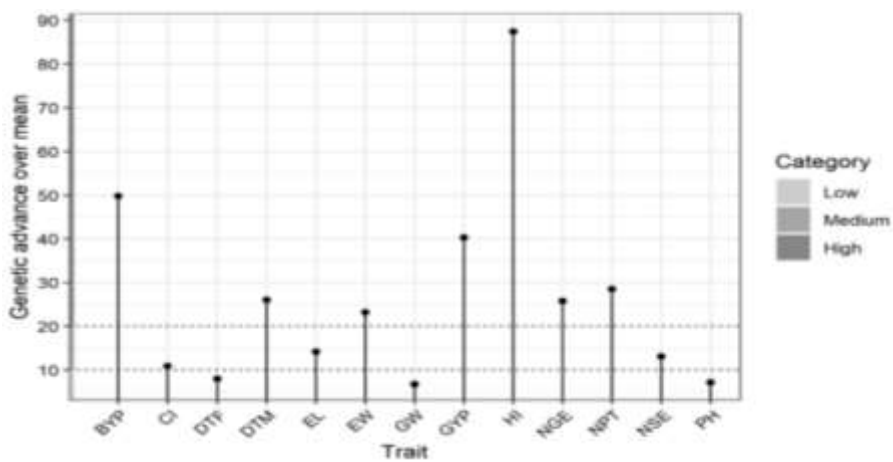
Traits	Minimum range	Maximum range	Mean	GCV %	PCV %	ECV %	Heritability (hBS) %	Genetic advance	Genetic % mean	advance
Days to 50% flowering	85.9	104.3	94.19	4.32	4.82	2.13	80.35	7.52	7.98	
Days to maturity	95.05	138.45	121.99	12.63	12.64	0.59	99.78	31.74	26.02	
Plant height	71.16	120.95	92.31	5.32	8.2	6.24	42.13	6.58	7.13	
Number of productive tillers	3.4	11	6.31	20.61	30.71	22.77	45.03	1.8	28.53	
Ear length	7.73	10.91	8.95	8.31	10.05	5.66	68.27	1.27	14.16	
Number of spikelets ear <sup>-1</sup>	12.39	18.23	15.08	7.5	8.87	4.74	71.46	1.97	13.08	
Ear weight	0.99	2.8	1.88	14.05	17.59	10.58	63.82	0.44	23.16	
Number of grains ear <sup>-1</sup>	24.1	54.34	36.73	14.26	16.3	7.9	76.54	9.45	25.74	
1000 grain weight	26.94	46.4	35.89	6.75	12.21	13.96	30.54	2.75	7.66	
Biological yield plant <sup>-1</sup>	11.5	47.58	27.08	27.52	31.38	15.08	76.91	13.48	49.78	
Grain yield plant <sup>-1</sup>	4.39	15.46	8.96	23.17	27.51	14.82	70.96	3.61	40.27	
Harvest index	13.37	92.52	36.38	45.07	47.9	16.21	88.54	31.83	87.49	
Chlorophyll index	17.4	55.66	37.08	9.43	16.92	14.05	31.05	4.02	10.84	



**Figure 1.** Coefficient of variation for all the 13 traits.



**Figure 2.** Heritability (broad sense) for all the 13 traits.



**Figure 3.** Genetic advance over mean for all the 13 traits.

(71.46%), GYP (70.96%), EL (68.27%), and EW (63.82%) (Table 3). Dagade *et al.* (2020) revealed similar consequences for NGE, DTF, DTM, GW, and GYP. The moderate estimation of heritability is NPT (45.03%) and PH (42.13%). Similar results also came from Sharma *et al.* (2018) for EL, NPT, GW, and GYP. The lowest heritability estimates were notable in CI (31.05%) and GW (30.54%). The highest heritability and elevated genetic advance resulted in DTM, EW, NGE, BYP, GYP, and HI. Figure 3 indicates the range of genetic diversity for all traits. The high genetic advance and heritability assessment suggested that direct selection could improve these traits. High heritability is present in EL and NSE with moderate genetic advance, indicating the influence of environment upon genotype. Several characters were not advantageous to simple selection in this case.

### Genotypic and phenotypic correlation

According to Lamara *et al.* (2022), due to the robust and positive connection between the features, selection for one trait would directly affect the expression of another; it promotes fast choosing and breeding program progress. Analyzing correlation coefficients can determine which attributes are most strongly related and in which directions. Table 4 lists the phenotypic correlation (P) and genotypic correlation (G) for the wheat attributes recorded for this study. The HI (0.54, 0.541) and NPT (0.39, 0.391) showed a highly significant positive correlation, and GW (0.28, 0.273) showed significant positive correlations with GYP. DTM (-0.391, -0.391) and NSE (-0.182, -0.78) had soaring significant negative correlations, and EL (-0.281, 0.281) showed significant negative correlations with GYP at both levels. These results are in line with the reports of Khan *et al.* (2023) that GW has a significant positive correlation with GYP and Kaur *et al.* (2019) that HI and NPT have considerable positive correlations and NSE, EL, and EW have significant negative correlations with GYP. The DTF showed a highly significant positive correlation with DTM (0.53, 0.53) and a significant positive correlation with NGE (0.342, 0.342). DTM showed a significant

positive correlation with NGE (0.603, 0.596), BYP (0.571, 0.567), and CI (0.488, 0.486), a highly significant negative correlation with NPT (-0.466, -0.466) and HI (-0.748, -0.746), and significant negative correlation with PH (-0.295, -0.294) at the phenotypic and genotypic level. A similar result from Singh *et al.* (2021) stated that DTF had a highly significant positive correlation with DTM, HI, and BYP.

DTM had a significant positive correlation with BYP, HI, and NPT. The PH showed a highly significant positive correlation with EL (0.599, 0.587) and a significant positive correlation with NSE (0.3339, 0.3336). PH showed a highly significant negative correlation with NGE (-0.577, -0.573) and BYP (-0.399, -0.402). The correlation of NPT is highly substantial with GW (0.90, 0.92) and negatively significant with NGE (-0.324, -0.321). The EL showed a significant positive correlation with NSE (0.38, 0.38). EL showed a highly significant negative correlation with NGE (-0.406, -0.391) and a significant negative correlation with BYP (-0.355, -0.335). NGE has a highly significant positive correlation with BYP (0.582, 0.574) and a significant positive correlation with CI (0.355, 0.335). NGE has a highly significant negative correlation with HI (-0.487, -0.481). The BYP has a highly significant negative correlation with HI (-0.637, -0.639). Kumar *et al.* (2019) revealed PH had an upper significant positive correlation with EL while negatively correlated with BYP. EL showing a negative correlation with BYP also resulted in many researchers' reports (Burio *et al.*, 2004; Bhushan *et al.*, 2013; Avinash *et al.*, 2017; Ahmed *et al.*, 2018). BYP has a significant negative correlation with HI. HI had a highly significant negative correlation with CI (-0.380, -0.377) at both levels.

### Genotypic path analysis on grain yield plant<sup>-1</sup>

Path analysis made possible the segmentation of indirect and direct sources of correlation and comparing the component elements based on relative contributions. In Table 5, HI (1.0157) noted a highly positive straight effect tracked by NPT (0.8238), BYP (0.7543), NGE (0.0517), PH (0.0374), DTM (0.0265), CI (0.1098), and

**Table 4.** Genotypic (G) and Phenotypic (P) correlation coefficient among the traits.

Traits		DTF	DTM	PH	NPT	EL	NSE	EW	NGE	GW	BYP	HI	CI	GYP
DTF	G	1.000	0.532**	-0.126	-0.214	-0.210	-0.257	-0.099	0.342*	-0.049	0.223	-0.264	0.151	-0.173
	P	1.000	0.531**	-0.122	-0.214	-0.213	-0.253	-0.105	0.335*	-0.049	0.215	-0.261	0.153	-0.175
DTM	G		1.000	-0.295*	-0.466**	-0.148	-0.293*	-0.260	0.603**	-0.312*	0.571**	-0.748**	0.488**	-0.391**
	P		1.000	-0.294*	-0.466**	-0.142	-0.292*	-0.258	0.596**	-0.309*	0.567**	-0.746**	0.486**	-0.391**
PH	G			1.000	0.021	0.599**	0.333*	-0.031	-0.577**	-0.060	-0.399**	0.121	-0.085	-0.224
	P			1.000	0.021	0.587**	0.333*	-0.036	-0.573**	-0.062	-0.402**	0.124	-0.083	-0.223
NPT	G				1.000	0.154	0.080	0.076	-0.324*	0.935**	0.054	0.164	-0.152	0.390**
	P				1.000	0.158	0.080	0.077	-0.321*	0.928**	0.053	0.165	-0.152	0.391**
EL	G					1.000	0.387**	0.025	-0.406**	0.107	-0.355*	0.038	0.228	-0.281*
	P					1.000	0.380**	0.036	-0.391**	0.109	-0.335*	0.029	0.219	-0.281*
NSE	G						1.000	0.049	0.059	0.117	-0.157	0.070	-0.110	-0.182
	P						1.000	0.057	0.070	0.104	-0.162	0.075	-0.118	-0.783**
EW	G							1.000	0.079	-0.002	-0.107	0.218	0.106	0.227
	P							1.000	0.095	-0.011	-0.098	0.214	0.089	0.229
NGE	G								1.000	-0.189	0.582**	-0.487**	0.355*	-0.086
	P								1.000	-0.197	0.574**	-0.481**	0.335*	-0.084
GW	G									1.000	0.139	0.075	-0.124	0.280*
	P									1.000	0.145	0.067	-0.113	0.273*
BYP	G										1.000	-0.637**	0.233	0.168
	P										1.000	-0.639**	0.229	0.163
HI	G											1.000	-0.380**	0.540**
	P											1.000	-0.377**	0.541**
CI	G												1.000	0.135
	P												1.000	-0.136

5% = \* and 1% = \*\* significant, respectively.

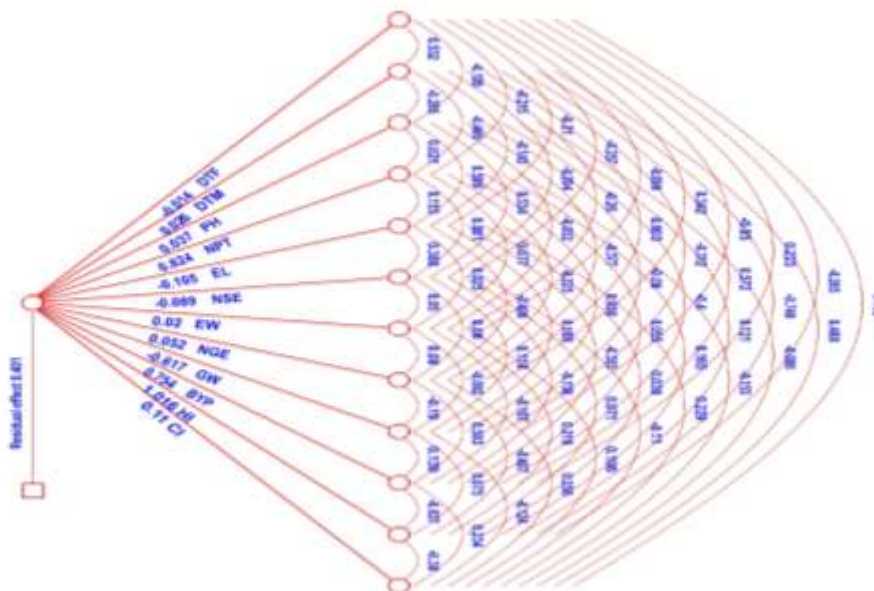
DTF: days to 50% flowering, DTM: days to maturity, PH: plant height, NPT: number of productive tillers, EL: ear length, NSE: number of spikelets ear<sup>-1</sup>, EW: ear weight, NGE: number of grains ear<sup>-1</sup>, GW: 1000 grain weight, BYP: biological yield plant<sup>-1</sup>, HI: harvest index, CI: chlorophyll index, GYP: grain yield plant<sup>-1</sup>.



**Table 5.** Genotypic path coefficient on grain yield per plant in bread wheat.

	DTF	DTM	PH	NPT	EL	NSE	EW	NGE	GW	BYP	HI	CI	GYP
DTF	-0.0141	-0.0075	0.0018	0.0030	0.0030	0.0036	0.0014	-0.0048	0.0007	-0.0031	0.0037	-0.0021	-0.1738
DTM	0.0141	0.0265	-0.0078	-0.0123	-0.0038	-0.0078	-0.0069	0.0160	-0.0083	0.0151	-0.0198	0.0129	-0.3919**
PH	-0.0047	-0.0110	0.0374	0.0008	0.0224	0.0125	-0.0012	-0.0216	-0.0022	-0.0149	0.0045	-0.0032	-0.2249
NPT	-0.1767	-0.3842	0.0177	0.8238	0.1274	0.0666	0.0633	-0.2676	0.7709	0.0450	0.1356	-0.1258	0.3909**
EL	0.0221	0.0150	-0.0629	-0.0162	-0.1050	-0.0407	-0.0027	0.0426	-0.0113	0.0373	-0.0041	-0.0240	-0.2811*
NSE	0.0230	0.0262	-0.0298	-0.0072	-0.0346	-0.0893	-0.0044	-0.0053	-0.0105	0.0141	-0.0063	0.0098	-0.1824
EW	-0.0020	-0.0051	0.0006	0.0015	0.0005	0.0010	0.0197	0.0016	0.0000	-0.0021	0.0043	0.0021	0.2279
NGE	0.0177	0.0312	-0.0299	-0.0168	-0.0210	0.0031	0.0041	0.0517	-0.0098	0.0301	-0.0252	0.0184	-0.0865
GW	0.0305	0.1927	0.0370	-0.5773	-0.0664	-0.0725	0.0015	0.1171	-0.6170	-0.0860	-0.0463	0.0766	0.2801*
BYP	0.1685	0.4313	-0.3014	0.0412	-0.2680	-0.1189	-0.0807	0.4395	0.1051	0.7543	-0.4805	0.1764	0.1684
HI	-0.2689	-0.7606	0.1231	0.1672	0.0394	0.0720	0.2222	-0.4947	0.0762	-0.6471	1.0157	-0.3862	0.5400**
CI	0.0167	0.0536	-0.0094	-0.0168	0.0251	-0.0121	0.0117	0.0391	-0.0136	0.0257	-0.0417	0.1098	-0.1352

Residual effect= 0.4008, DTF: days to 50% flowering, DTM: days to maturity, PH: plant height, NPT: number of productive tillers, EL: ear length, NSE: number of spikelets ear<sup>-1</sup>, EW: ear weight, NGE: number of grains ear<sup>-1</sup>, GW: 1000 grain weight, BYP: biological yield plant<sup>-1</sup>, HI: harvest index, CI: chlorophyll index, GYP: grain yield plant<sup>-1</sup>.

**Figure 4.** Genotypic path coefficient analysis diagram.

EW (0.0197) on the dependent trait, GYP. Results from Anwar *et al.* (2009) for HI, Bhushan *et al.* (2013) for EW, Sabit *et al.* (2017) for EL, and Ali *et al.* (2008) for PH and BYP exhibited a positive direct impact on GYP. Singh *et al.* (2019) have shown the direct effect of BYP, HI, NSE, DTM, and PH on GYP. Barman *et al.* (2020) reported similar results for PH and NPT showing positive direct effect on GYP. The highest negative direct impact had applications from GW (-0.6170), EL (-0.1050), NSE (-0.0893), and DTF (-0.0141). The close resemblance was in reports by Fellahi *et al.* (2013) for GW, followed by EL, having a negative direct effect. The GW imposed a low and positive indirect outcome via DTM (0.1927) and NGE (0.1171) on the dependent trait, GYP, with the less indirect positive effect imposed by BYP via DTF (0.1685) and GW (0.1051). Similarly, HI through PH (0.1231) and NPT (0.1672) inflicted a low indirect positive effect on the dependent trait, GYP. Kumar *et al.* (2019) disclosed a low indirect positive impact of HI through PH. The moderate indirect positive effect had HI imposing via EW (0.2222) on the dependent trait. In contrast, BYP via DTM (0.4313) and NGE (0.4395) forced a high indirect positive effect on GYP, with a high indirect negative influence on NPT via DTM (-0.3842) on the dependent trait. A high indirect negative result had BYP imposed through PH (-0.3014) on GYP, a dependent feature. Likewise, HI via DTM (-0.7606), BYP (-0.6471), and NGE (-0.4947) imposed an excessive indirect negative effect on dependent trait GYP. Singh *et al.* (2012) revealed similar results for the negative indirect impact imposed by HI through DTF, BYP, and NGE. Neglecting the residual effect (0.4008) on GYP, most yield-related components were taken in the study (Figure 4).

## CONCLUSIONS

Genetic variation for the required maturity and yield attributes in segregating populations is necessary for developing superior germplasm to generate suitable agricultural cultivars. For the examined maturity and yield

characteristics, the F<sub>4</sub> populations showed significant variations. As a result, days to maturity, ear weight, the number of grains ear<sup>-1</sup>, biological yield plant<sup>-1</sup>, grain yield plant<sup>-1</sup>, and harvest index had the highest genetic progress and heritability. The correlation coefficient between the productive tillers (NPT), days to 50% flowering (DTF), days to maturity (DTM), plant height (PH), ear length (EL), grains ear<sup>-1</sup> (NGE), and harvest index (HI) is exceptionally positive and significant. Harvest index (HI), productive tillers (NPT), biological yield plant<sup>-1</sup> (BYP), grains ear<sup>-1</sup> (NGE), plant height (PH), days to maturity (DTM), chlorophyll index (CI), and ear weight (EW) all have a significantly beneficial direct impact on grain yield plant<sup>-1</sup> (GYP). Harvest index (HI) and productive tillers (NPT) showed a positive correlation and absolute influence on grain yield plant<sup>-1</sup> (GYP); therefore, it can be beneficial for improving harvest. These characteristics have demonstrated value when choosing wheat cultivars for higher production and need focus for further in-depth study in primary and secondary breeding in regional and global wheat breeding programs.

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