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Evaluation of F5 segregating bread wheat (*Triticum aestivum* L.) population for genetic variability, heritability, genetic advance and correlation studies

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Abstract

The primary goals of wheat breeding program are to develop new wheat varieties with increased yields. In order to suggest efficient wheat breeding strategies, researchers need information on genetic variations, heritability, genetic progress, and correlation and path analysis for numerous factors. This research study was executed in Lovely Professional University by Department of Genetics and Plant Breeding, Phagwara, India during rabi season 2022-2023. There were 107 genotypes including 4 checks and 103 F5 segregating populations of three crosses were evaluated in augmented design. Analysis of variance showed significant in all the traits except ear weight, 1000 grain weight and chlorophyll index in test versus check. Analysis of variance for test showed significant for all traits except chlorophyll index. High heritability with genetic advance mean was observed for ear length (93.67% and 42.21%), 1000 grain weight (83.67% and 36.53%), grain yield plant⁻¹ (92.12% and 48.35%), biological yield plant⁻¹ (95.08% and 60.75%), harvest index (98.17% and 71.59%) and chlorophyll index (96.66% and 70.73%). Number of productive tillers, ear length, number of spikelet's ear⁻¹, biological yield plant⁻¹ and harvest index had positive correlation coefficient and path analysis on grain yield plant⁻¹. This suggests that selecting for these features may be beneficial in optimizing grain production.

Keywords: Coefficient of variation, correlation coefficient, path analysis, bread wheat

Introduction

Wheat (*Triticum aestivum* L.) is the second most significant commodity in India. Depending on the severity of winter, Western nations cultivate wheat in the spring and winter, whereas India cultivates it in rabi season. Wheat provides 20% of the daily calories and protein for the human population. Wheat is used to prepare bread, chapatti, biscuits, pasta, and fermented foods (Sahoo *et al.*, 2022) [1]. Wheat production must increase due to population and demand growth. In order to meet the population's rising need for food, wheat breeders are focusing on the potential to enhance the production of bread wheat by creating new varieties with the required genetic make-up (Nizamani *et al.*, 2020) [2]. Therefore, the primary objective of ancient and modern breeding program is still to improve output and productivity. The most effective method for increasing wheat output is genetic modification of plant characteristics (Khokhar *et al.*, 2019) [3]. The majority of economic traits are one of the numerous yield components that go into producing grain yield. Increased grain yield per hectare results from interactions between yield components and their innate physiological processes, crop growth conditions and management practices. Significant variations in the bread wheat genotypes of the yield components were discovered by the researchers (Rind, 2019) [4]. The effectiveness of the breeding program has been attributed to genetic heterogeneity between wheat varieties, which is shown by the variance in yield. Among other things, a variety of genetic variables and environmental changes have a significant impact on food production.

The genetic, physio- morphological, ecological and pathological factors that influence grain yield make it a polygenic trait of extraordinary complexity. Stability and productivity are crucial to a cultivar's or genotype's genetic potential. The extent to which the potential yield is realized is determined by the genetic character and amplitude of relationship between the various yield contributing features (productive tiller, number of grains, 1000 grain weight, etc.) and varying agro climatic conditions. Therefore, it is crucial to gather data on these factors and solve for storage and quantify their relative importance to grain production. Any breeding plan aiming to create varieties with high yield potential and yield stability relies on

the presence of genetic heterogeneity. Understanding the nature of genetic variability for quality components and yield related qualities is important for the genetic modification of both quality and grain yield in cereals. Most wheat quality components are inversely related to wheat yield (Yadav *et al.*, 2022) [5], therefore this is an area that needs significant study. If a characteristic's heritability is high, then it should be simple to enhance that trait, due to heritability's index of transmissibility, which measures the character's genetic correlation in the population. Estimation of genetic progress provide a notion of how the chosen families perform on average compared to the base populations. To investigate the connections between the different yield characteristics, correlation analysis looks to be a useful method. Path coefficient analysis has largely replaced other statistical approaches for estimating the relative importance of individual factors in determining grain yield (Yadav *et al.*, 2022) [5]. The main goal of wheat breeding is to identify and breed high-yielding wheat lines with excellent quality and resilience to biotic and abiotic influences. Researchers can discover relevant traits and generate high-yielding wheat lines if they have a firm grasp of the patterns of current genetic variability and the trends of character association. Identification of genetically superior and acceptable genotypes is crucial for improving the effectiveness of germplasm in order to learn about the genetic basis of variation for economically desirable character. As a result, the goal of this research was to determine the heritability in a broad sense, genetic advance, correlation and path analysis of the bread wheat F₅ population in order to get yield and attributes that are connected to yield.

Materials and Methods

Study area: The research project was conducted by the Department of Genetics and Plant Breeding at Agriculture Research Farm of Lovely Professional University. The experimental region has been meticulously chosen in terms of topography and fertility. Located at an altitude of 243 meters above sea level at the coordinates 31° 19' 32" North, 75° 34' 45" East. A humid subtropical zone characterized by frigid winters (November–February) and sweltering summers (April–June) at (Punjab) Phagwara, India.

Experimental material and design

A total 103 F₅ segregating generation entries of 3 crosses (Table 1) and 4 checks of wheat are sown on 16th November, 2022 with spacing of 22.5 x 5cm under augmented design with 6 blocks. All the necessary agronomic practices for healthy plant development are implemented.

Table 1: List of crosses

Sr. No	Crosses name
1.	HD 2932 X GW 273
2.	HD 2932 X LOK 1
3.	MP 3137 X LOK 1

Data collection

During the rabi season of 2022-2023, at different times throughout the cropping cycle, data on yield and each of its components were collected. The number of days to 50% flowering (DTF) was calculated from the sowing date to the day when half of the flower had completely emerged from the flag leaf. Days to maturity (DTM) were calculated as the number of days between the date of sowing and to the point at which 90% of the crops were ready for harvest. For five randomly selected plants, plant height (PH) was taken in (cm) centimeter from the soil's surface to the top of the spike and number of productive tillers (NPT) are counted per plant. Ear length (EL), was measured in (cm) from its base to its tip and ear weight (EW) is measured in grams (g). The average of five ear from randomly selected plants was used to calculate the number of spikelet's ear⁻¹ (NSE). From five randomly selected plants, the number of grains ear⁻¹ (NGE) were calculated. To determine the 1000-grain weight (GW) for each genotype, 1000 grains were randomly chosen from each plot and weighed on a laboratory precision scale. Grain yield plant⁻¹ (GYP) was calculated by gathering the grain from selected plant and weighing it in grams. Biological yield plant⁻¹ (BYP) was weighed using measuring scale. Harvest index is estimated by dividing grain yield to biological yield in percentage. Last but not least, chlorophyll index (CI) is measured using SPAD meter for three plants.

Statistical analysis

The information that was obtained subsequently put to the following statistical and biometrical analysis: Using the Federer (1956) [6] proposed analysis of variance, to calculate the phenotypic and genotypic coefficients of variation, Burton and De Vane (1952) [7] proposed using the term "coefficient of variation". Al-Jibouri *et al.*, (1958) [8] correlation coefficient analysis was used to determine if there was an important association between the qualities. Using the method described by Dewey and Lu (1959) [9], path coefficient analysis was done to evaluate the direct and indirect effects of the assessed features on grain production. R STUDIO software and Metan were used for the above mentioned statistical analysis.

Result and Discussion

Analysis of Variance (ANOVA)

The mean squares of the 13 characters from the ANOVA are displayed in Table 2. Except for number of productive tillers (NPT) and chlorophyll index (CI), all test characteristics exhibited significant variations. For 107 bread wheat germplasm, all parameters showed significant variation across experiments and checks except ear weight (EW), number of productive tillers (NPT), number spikelet's ear⁻¹ (NSE), 1000-grain weight (GW), and chlorophyll index (CI). This indicates variability that can be utilized in a subsequent breeding program through selection. The close resemblance were disclosed by Kumar *et al.*, (2021) [10] and Singh *et al.*, (2021) [11].

Table 2: ANOVA for all thirteen traits of 107 bread wheat populations

Source of variation	D.F	DTF	DTM	PH	NPT	EL	NSE	EW	NGE	GW	BYP	GYP	HI	CI
Treatment (ignoring Blocks)	106	7.95**	11.67**	48.35**	0.96ns	3.9**	1.84*	0.07ns	43.85	70.44**	62.2**	3.59**	122.29**	19.84ns
Treatment: Check	3	54.39**	71.67**	328.19**	6.25**	6.6**	10.35**	0.23ns	274.88**	92.91**	170.81**	7.77**	18.95**	61.28*
Treatment: Test vs. Check	1	12.46**	151.3**	194.93**	2.45ns	2.76**	2.02ns	0.003ns	130.95*	47.45ns	20.69*	1.84*	361.27**	28.93ns
Treatment: Test	102	6.54**	8.53**	38.68**	0.79ns	3.83**	1.59*	0.07ns	36.2*	70.01**	60.45**	3.48**	122.98**	18.53ns
Block (Eliminating Treatments)	5	0.97ns	0.97ns	0.55ns	0.17ns	0.06ns	0.7ns	0.02ns	2.92 ns	15.48ns	7.8ns	0.51ns	7.06*	25.98ns
Residuals	15	1.06	1.57	0.72	0.57	0.24	0.66	0.03	15.39	11.43	2.97	0.27	2.25	19.51
CV %		1.04	0.96	0.89	10.49	5.53	4.99	9.12	9.43	8.61	6.82	7.18	4.88	12.06

Genetic variability estimation

To evaluate the genetic variation in a population, Singh and Singh (1975) [12] utilized the coefficient of phenotypic, genotypic and environmental changes. The PCV coefficient in the current results was greater than the GCV coefficient (Table 3). Similar findings were discovered in the works of Rajput *et al.* (2018) [13]. Unless the heritability is known, the genotypic coefficient of variation does not provide a clear indication of the amount of genetic gain to be anticipated via selecting features based on phenotypes. The heritability of the characteristic has a significant impact on the population improvement strategy used. The degree to which a characteristic is heritable measures the impact of genetic variation on phenotypic expression. Estimating genetic advancement is so necessary while trying to evaluate plant population development. (Johnson *et al.* 1955) [14] The genetic gain due to natural selection may be better estimated when both heritability and genetic progress are considered simultaneously. If heritability is high, then environmental influences on individual characteristics are relatively less. The term "genetic advancement" is used to describe an improvement in a population's genetic makeup that was not present in the original population. In light of the above data, the current research calculated heritability and genetic advancement to assess the potential for genetic improvement in the existing experimental material.

Heritability was strong across the board for the qualities included in this study (Table 3). The highest genetic advance, expressed as a percentage of the mean, was found for all variables evaluated in the experiment except NPT, NSE, EW and NGE which expressed a low and moderate genetic advance, respectively. Research by Fellahi *et al.*, (2013) [15] is in agreement with these findings. The relevance of additive gene action in the transmission of characteristics is shown by their high heritability and genetic advancement. The traits which showed high heritability with high genetic advance percent of mean (GAM) were EL, GW, BYP, GYP, HI and CI were considered to selection for further grain yield improvement breeding program.

Days to 50% flowering (DTF)

DTF indicates low genotypic coefficient of variance (GCV) 2.37%, low phenotypic coefficient of variance (PCV) 2.59% and low environmental coefficient of variance (ECV) 1.04% with very high heritability (83.85%) and low GAM (4.47%) (Graph 1). Osekita *et al.*, (2022) [16] disclosed the similar result that high heritability, low GCV and PCV for DTF.

Days to maturity (DTM)

DTM showed low GCV (2.02%), PCV (2.24%) and GCV (0.96%) with very high heritability (81.64%) and low GAM

(3.77%) (Graph 2). The similar result had been reported by Osekita *et al.* (2022) [16] for DTM, which showed high heritability, low GAM, PCV and GCV.

Plant height (PH)

PH had low GCV (6.45%), PCV (6.51%) and ECV (0.89%) with very high heritability (98.13%) and moderate GAM (13.17%) (Graph 3). Since additive genes are the main determinants of plant height according to research with greater heritability estimates and substantial genetic advancement, direct selection may be successful in isolated generations.

Number of productive tillers (NPT)

NPT showed low GCV (7.88%), moderate PCV (14.86%) and moderate ECV (12.61%) with low heritability (28.11%) and GAM (8.62%) (Graph 4).

Ear length (EL)

EL had high GCV (21.14%), PCV (21.85%) and low ECV (5.5%) with very high heritability (93.67%) and high GAM (42.21%) (Graph 5). The close resemblance was reported by Srivastava *et al.*, (2020) [17] for EL with high heritability and GAM, low GCV and PCV.

Number of spikelet's ear⁻¹ (NSE)

NSE showed low GCV (5.97%), PCV (7.79%) and ECV (5.01%) with moderate heritability (58.66%) and low GAM (9.43%) (Graph 6). Srivastava *et al.*, (2020) [17] also showed moderate heritability and low genetic advance with low GCV and PCV.

Ear weight (EW)

EW had moderate GCV (11.19%), PCV (14.43%) and low ECV (9.11%) moderate heritability (60.14%) and GAM (17.91%) (Graph 7).

Number of grains ear⁻¹ (NGE)

NGE showed moderate GCV (10.86%), PCV (14.33%) and low ECV (9.34%) with moderate heritability (57.49%) and GAM (17.91%) (Graph 8). Moulali *et al.*, (2022) [18] reported close result for NGE which showed moderate heritability and GAM.

1000 grain weight (GW)

GW had moderate GCV (19.36%), high PCV (21.16%) and low ECV (8.55%) with very high heritability (83.67%) and high GAM (36.53%) (Graph 9). These results are similar to research done by Moulali *et al.*, (2022) [18] for GW which showed high heritability and GAM.

Biological yield plant⁻¹ (BYP)

BYP showed high GCV (30.2%) PCV (30.97%) and low ECV (6.87%) with very high heritability (95.08%) and high GAM (60.75%) (Graph 10). High heritability and genetic gain were also noted by Sohail *et al.*, (2018) [19] among genotypes.

Grain yield plant⁻¹ (GYP)

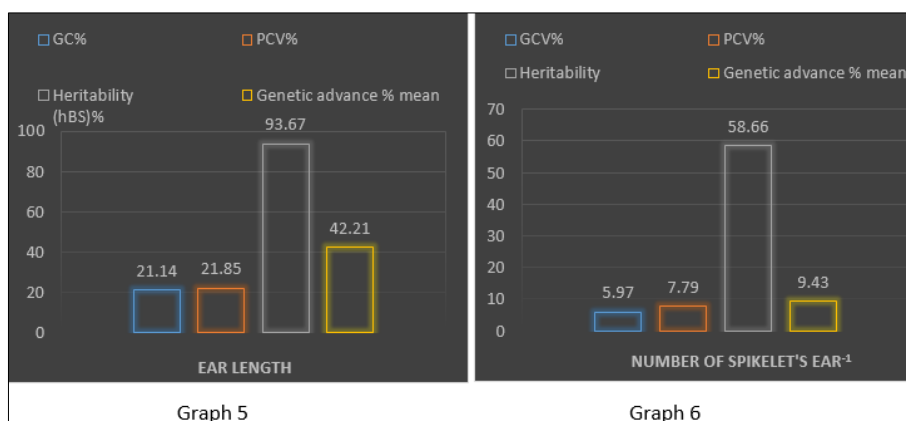
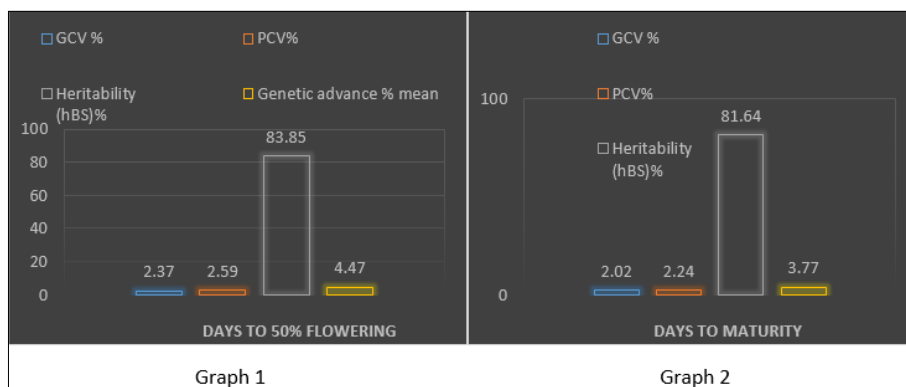
GYP had high GCV (24.42%), PCV (25.44%) and low ECV (7.14%) with very high heritability (92.12%) and GAM (48.35%) (Graph 11). Shah *et al.*, (2019) [20] reported the similar result that stated higher heritability and genetic advancement for grain yield may be advantageous when selecting cross combinations with high yield.

Harvest index (HI)

HI showed high GCV (35.02%), PCV (35.35%) and low ECV (4.78%) with very high heritability (98.17%) and GAM (71.59%) (Graph 12). Additionally, significant heritability and genetic advancement are shown by Sohail *et al.*, (2018) [19].

Chlorophyll index (CI)

CI had high GCV (33.23%), moderate PCV (11.82%) and ECV (12.13%) with very high heritability (96.66%) and GAM (70.73%) (Graph 13). Mohapatra *et al.* (2019) [21] resulted close result in case of CI, which showed high heritability and GAM.



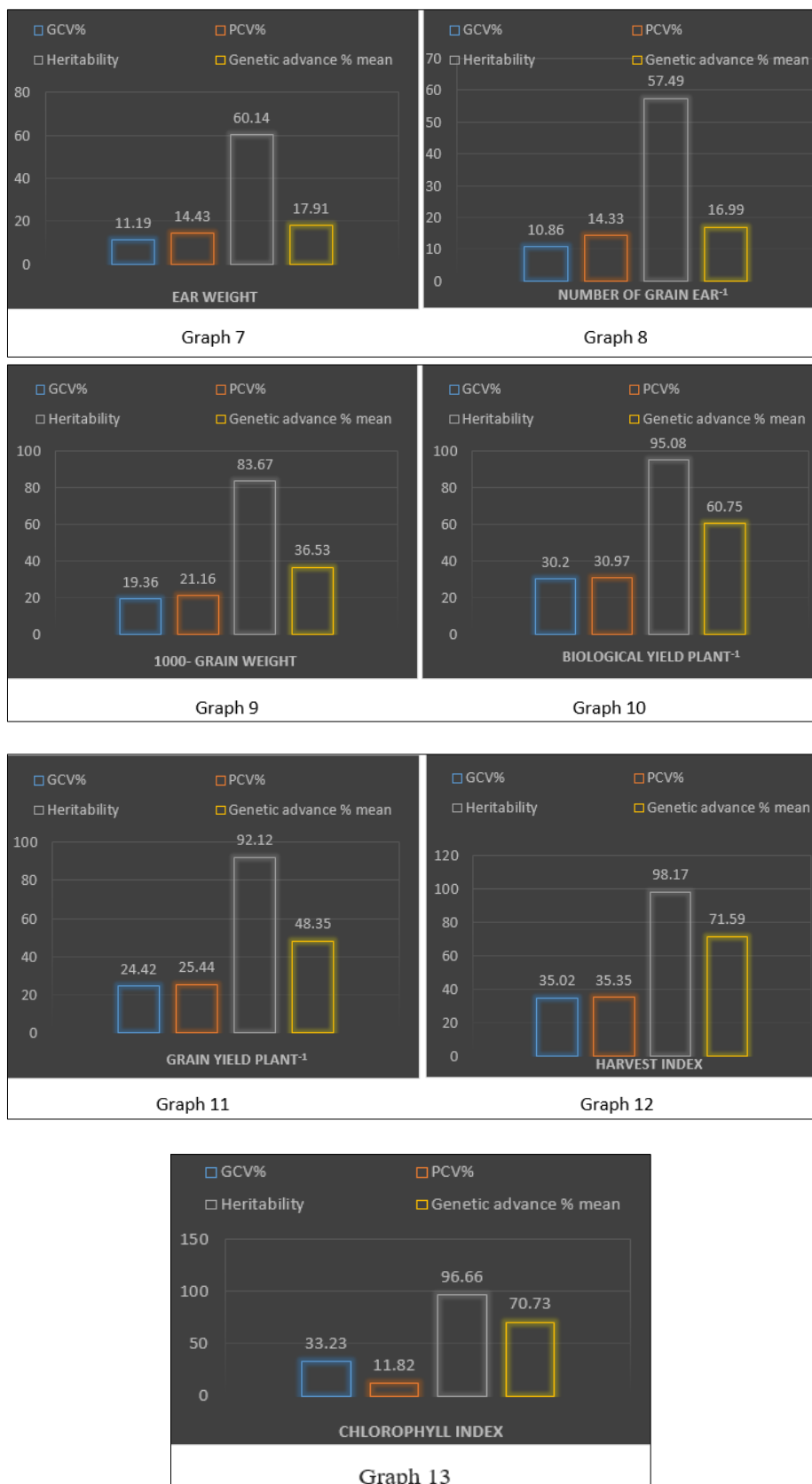


Fig 1: Graphs on genetic variability for different traits

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

Traits	Range		Mean	GCV (%)	PCV (%)	ECV (%)	Heritability (hBS)%	Genetic advance	Genetic advance % mean
	Minimum	Maximum							
Days to 50% flowering	91.58	104.58	98.85	2.37	2.59	1.04	83.85	4.42	4.47
Days to maturity	123.08	138.33	130.51	2.02	2.24	0.96	81.64	4.92	3.77
Plant height	80.58	109.45	95.58	6.45	6.51	0.89	98.13	12.59	13.17
Number of productive tillers	4.36	8.71	5.97	7.88	14.86	12.61	28.11	0.51	8.62
Ear length	6.35	27.08	8.96	21.14	21.85	5.5	93.67	3.78	42.21
Number of spikelet's ear ⁻¹	12.88	18.78	16.17	5.97	7.79	5.01	58.66	1.52	9.43
Ear weight	1.3	2.61	1.83	11.19	14.43	9.11	60.14	0.33	17.91
Number of grains ear ⁻¹	29.59	56.44	42	10.86	14.33	9.34	57.49	7.14	16.99
1000 grain weight	14.63	64.72	39.54	19.36	21.16	8.55	83.67	14.44	36.53
Biological yield plant ¹	11.84	46.61	25.11	30.2	30.97	6.87	95.08	15.25	60.75
Grain yield plant ⁻¹	4.07	12.26	7.34	24.42	25.44	7.14	92.12	3.55	48.35
Harvest index	16.3	71.54	31.37	35.02	35.35	4.78	98.17	22.46	71.59
Chlorophyll index	25.26	46.14	36.42	33.23	11.82	12.13	96.66	20.43	70.73

Genotypic correlation coefficient on yield related characters

The result of this study on genotypic correlation coefficient of grain yield revealed that NGE, BYP were highly significant and NPT, EL, NSE, HI were significant. The similar report were disclosed by Kumar *et al.*, (2022) [22] for DTF, PH, NPT, EL, NSE, BYP and HI which were highly positive significant correlated with yield. These reports are consistent with the findings of the current study, which suggests that selection based on NGE (0.1947), BYP (0.2221), NPT (0.3432), EL (0.3067), NSE (0.2853) and HI (0.5311) may be more effective in enhancing wheat grain yield. At the genotypic level, there was a non-significant positive correlation between grain yield and PH, EW, GW and CI suggesting that these factors will not significantly affect grain yield. Yadav *et al.*, (2022) [5] disclosed significant correlation for BYP. Sohail *et al.*, (2018) [19] showed significant correlation of grain yield with BYP and HI. Mecha *et al.*, (2017) [23] divulged positive significant correlation with EL, NPT, NSE, NGE, BYP and HI.

Genotypic correlation among yield related characters

DTF is significantly correlated with DTM (0.9258). This implies that increase in DTF will leads to increase in DTM. Mecha *et al.*, (2017) [23] also revealed that DTF is significantly correlated with DTM. DTF also showed

significant and highly significant negative correlation with PH (-0.2669*) and CI (-0.2354) and negative non-significant correlation among all yield related traits except HI. Devesh *et al.*, (2021) [24] showed negative significant correlation with GW, PH, and BYP. DTM had negative highly significant and significant correlation with GW (-0.1950), CI (-0.2469) and PH (-0.2546). DTM correlation among other yield related traits were non-significant. PH showed highly significant correlation associated with CI (0.2052). NPT had positive significant correlation associated with GW (0.2818) and BYP (0.3003). This implies that increase in NPT will increase in GW and BYP. Haleem *et al.*, (2022) [25] disclosed that NPT had positive significant correlation with PH, NSE, EL, GW and BYP. Din *et al.*, (2018) [26] revealed that NPT had positive significant correlation with BYP. EW showed significant correlation with NSE (0.3326) and NGE (0.4509) which indicates that increase in EW leads to increase in NSE and NGE. NSE showed positive significant correlation with NGE (0.6785), BYP (0.1998), and CI (0.1923). Non-significant positive correlation were present among other yield related traits except HI. NGE had positive highly significant correlation with BYP (0.1998) and CI (0.1923). BYP showed negative correlation association with HI (-0.6521) at genotypic level. The similar result were revealed by Devesh *et al.*, (2021) [24] for BYP which is negatively correlated with HI.

Table 4: Genotypic correlation coefficient on grain yield plant⁻¹ of all traits

Traits	Y1	Y2	Y3	Y4	Y5	Y6	Y7	Y8	Y9	Y10	Y11	Y12	Y13
Y1	1	0.9258**	-0.266**	-0.0851	-0.0632	-0.0007	-0.0905	-0.1318	-0.1420	-0.0809	0.0822	-0.235*	-0.0305
Y2		1	-0.254*	-0.0927	-0.0669	-0.051	-0.0828	-0.0821	-0.195*	-0.1547	0.1627	-0.246*	-0.0132
Y3			1	0.0179	0.1407	0.1525	0.0768	0.0727	0.0082	0.1056	0.0082	0.2052*	0.1482
Y4				1	-0.0152	0.1305	0.1808	0.0567	0.2818**	0.3003**	-0.0038	0.0215	0.3432**
Y5					1	0.1658	0.1706	0.1013	-0.0928	0.1346	0.0685	0.1241	0.3067**
Y6						1	0.3326**	0.4509**	0.0702	0.1073	-0.1099	0.1199	0.0366
Y7							1	0.6785*	0.0777	0.1921*	-0.0126	0.2060*	0.2853**
Y8								1	0.0360	0.1998*	-0.0436	0.1923*	0.1947*
Y9									1	0.0665	0.0032	-0.1372	0.0840
Y10										1	-0.652**	0.0569	0.2221*
Y11											1	-0.0756	0.5311**
Y12												1	0.0566

5%=* and 1% = **significant respectively

Y1- days to 50% flowering, Y2- days to maturity, Y3- plant height, Y4- number of productive tillers⁻¹, Y5- ear length, Y6- ear weight, Y7- number of spikelet's ear⁻¹, Y8- number of grains ear⁻¹, Y9- 1000- grain weight plant⁻¹, Y10- biological yield plant⁻¹, Y11- harvest index, Y12- chlorophyll index, Y13- grain yield plant⁻¹

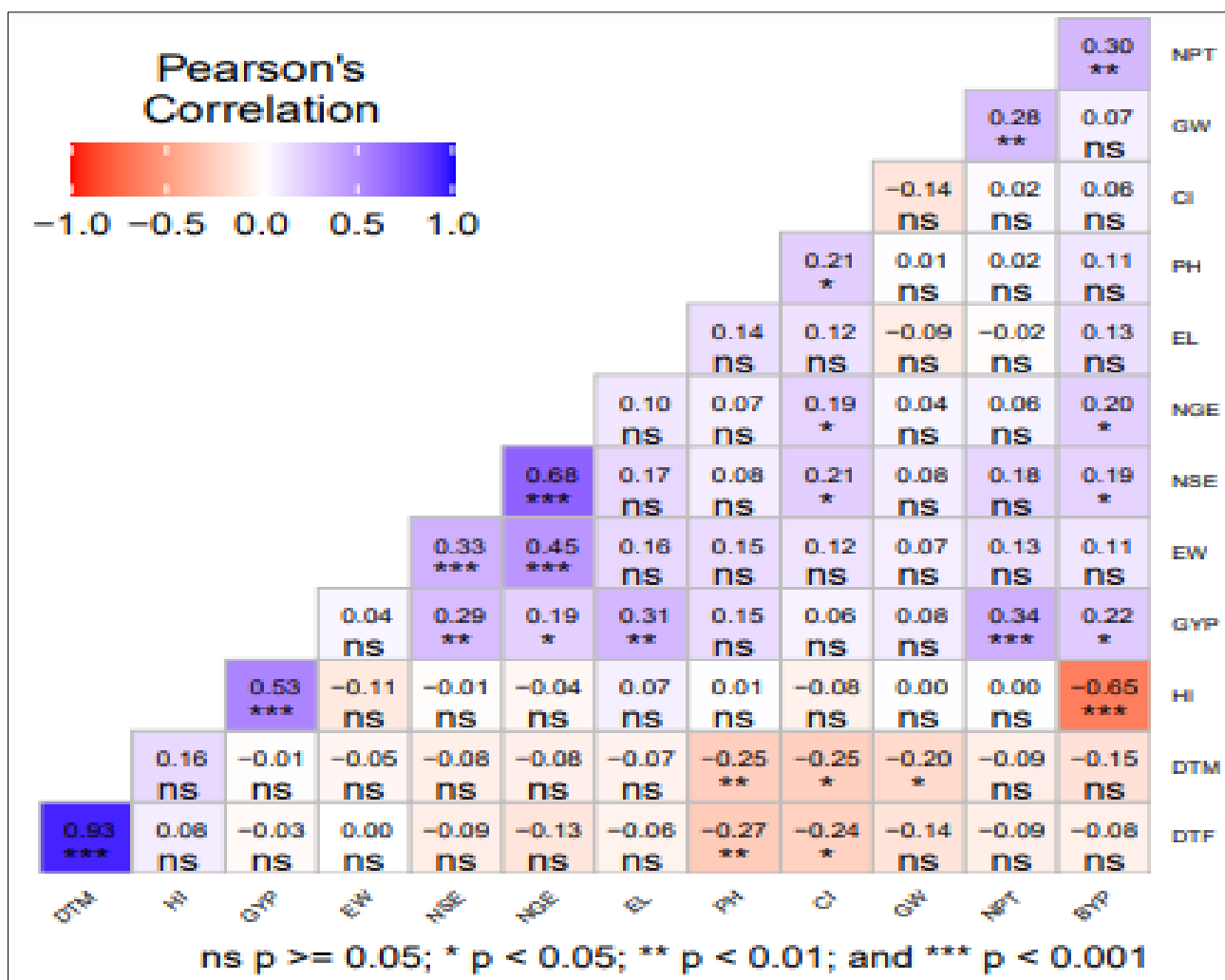


Fig 2: Genotypic correlation coefficient on grain yield plant⁻¹

Genotypic path analysis

HI, BYP, NSE, EL, CI, NPT, EW, PH and DTF shown direct effect (Figure 3). The negative direct effect is shown in NGE and DTM on dependent trait (Table 5). Similar to the current research, Sabit *et al.*, (2017)^[27] found that factors such as PH, DTF, EL, BYP and HI had a positive direct influence on grain yield at the genotypic level in bread wheat. In a similar vein, the study by Mecha *et al.*, (2017)^[23] revealed that DTF, EL, NSE, NGE, GW, BYP all had a favorable direct influence on grain production. The highest positive direct impact on dependent trait GYP is HI (1.1281) followed by BYP (0.9093), NSE (0.1132), EL (0.0819), CI (0.0570), NPT (0.0500), EW (0.0166), PH (0.0053) and DTF (0.0053) shown direct effect on dependent trait GYP. Additionally, Dutamo *et al.*, (2015)^[28] findings indicated that HI and BYP had the most beneficial direct effects on grain yield. The findings of this research were also supported by Baye *et al.*, (2020)^[29] and Abinasa *et al.*, (2011)^[30] who showed that HI exhibited the most positive direct influence on GYP, followed by BYP. This suggests that selecting individuals based on these qualities may increase the grain production of bread wheat. Correlation coefficient between a causative factor and the effect is almost equivalent to its direct impact, the correlation describes the underlying link and direct selection based on

these features is successful. NGE (-0.0463) and DTM (-0.0274) showed negative direct effect on grain yield. The similar results has been disclosed by Baye *et al.*, (2020)^[29] for DTM and NGE.

Moderate positive indirect impact compelled by BYP through NPT (0.2730) on dependent trait i.e., GYP. Low positive indirect impact was compelled by BYP through EL (0.1224), NSE (0.1746) and NGE (0.1816) on dependent trait GYP. Low positive indirect effect was compelled by HI through DTM (0.1836) on grain yield. High negative impact was compelled by BYP through HI (-0.5929) and low negative indirect effect compelled by BYP through DTM (-0.1406) on grain yield. High negative effect was imposed by HI through BYP (-0.7356) and low negative indirect effect imposed by HI through EW (-0.1239) on dependent trait i.e., GYP. The Residual effect of genotypic path correlation coefficient is 0.3576 which is negligible.

Most of the indirect effects of independent characters on other traits were negligible. Few characteristics exhibited high to moderate positive indirect impacts. BYP via HI, NPT and HI via BYP had a positive indirect effect. Therefore, while making selection to increase yield, these indirect impacts should also be taken into consideration.

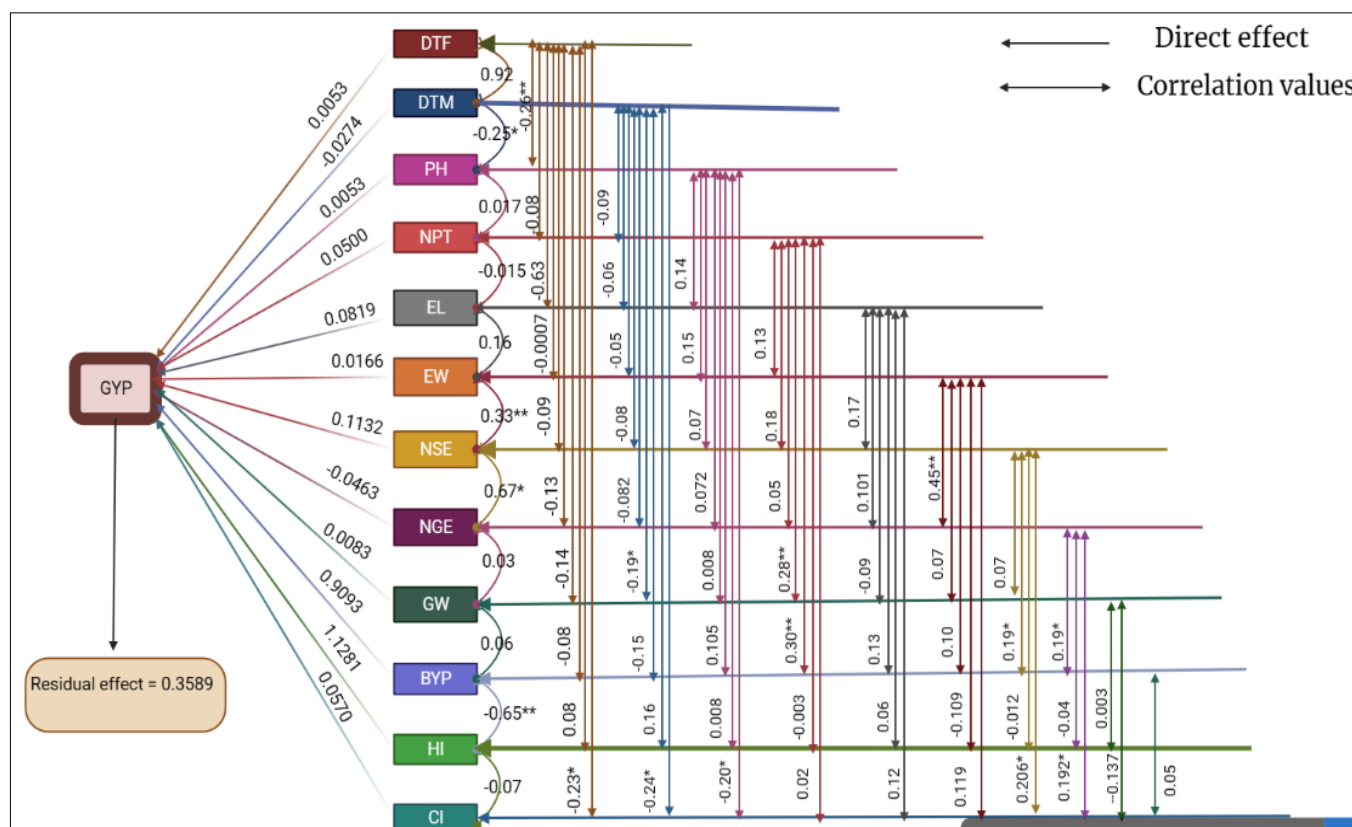


Fig 3: Genotypic path analysis on different traits

Table 5: Genotypic correlation coefficient on grain yield plant⁻¹

Traits	Y1	Y2	Y3	Y4	Y5	Y6	Y7	Y8	Y9	Y10	Y11	Y12	Y13
Y1	0.0053	0.0049	-0.0014	-0.0004	-0.0003	0.0000	-0.0005	-0.0007	-0.0007	-0.0004	0.0004	-0.0012	-0.0305
Y2	-0.0254	-0.0274	0.0070	0.0025	0.0018	0.0014	0.0023	0.0022	0.0053	0.0042	-0.0045	0.0068	-0.0132
Y3	-0.0014	-0.0013	0.0053	0.0001	0.0007	0.0008	0.0004	0.0004	0.0000	0.0006	0.0000	0.0011	0.1482
Y4	-0.0043	-0.0046	0.0009	0.0500	-0.0008	0.0065	0.0090	0.0028	0.0141	0.0150	-0.0002	0.0011	0.3432*
Y5	-0.0052	-0.0055	0.0115	-0.0012	0.0819	0.0136	0.0140	0.0083	-0.0076	0.0110	0.0056	0.0102	0.3067*
Y6	0.0000	-0.0008	0.0025	0.0022	0.0027	0.0166	0.0055	0.0075	0.0012	0.0018	-0.0018	0.0020	0.0366
Y7	-0.0102	-0.0094	0.0087	0.0205	0.0193	0.0377	0.1132	0.0768	0.0088	0.0217	-0.0014	0.0233	0.2853*
Y8	0.0061	0.0038	-0.0034	-0.0026	-0.0047	-0.0209	-0.0314	-0.0463	-0.0017	-0.0093	0.0020	-0.0089	0.1947**
Y9	-0.0012	-0.0016	0.0001	0.0023	-0.0008	0.0006	0.0006	0.0003	0.0083	0.0005	0.0000	-0.0011	0.0840
Y10	-0.0735	-0.1406	0.0961	0.2730	0.1224	0.0975	0.1746	0.1816	0.0605	0.9093	-0.5929	0.0517	0.2221**
Y11	0.0927	0.1836	0.0093	-0.0043	0.0773	-0.1239	-0.0142	-0.0492	0.0036	-0.7356	1.1281	-0.0852	0.5311*
Y12	-0.0134	-0.0141	0.0117	0.0012	0.0071	0.0068	0.0117	0.0110	-0.0078	0.0032	-0.0043	0.0570	0.0566

Residual effect= 0.3589. Y1- days to 50% flowering, Y2- days to maturity, Y3- plant height, Y4- number of productive tillers⁻¹, Y5- ear length, Y6- ear weight, Y7- number of spikelet's ear⁻¹, Y8- number of grains ear⁻¹, Y9- 1000- grain weight plant⁻¹, Y10- biological yield plant⁻¹, Y11- harvest index, Y12- chlorophyll index, Y13- grain yield plant⁻¹

Conclusion

The present study suggests that the genotypes analyzed might be a potential source of material for future breeding program. As a result, understanding genetic features such as coefficient of variation, heritability, genetic advance, genetic correlation coefficient and path analysis may help breeders quickly evolve ideal cultivars. The above-mentioned findings suggest that number of productive tillers, ear length, number of spikelet's ear⁻¹, biological yield plant⁻¹ and harvest index are promising characteristics to use as selection criteria in breeding for higher-yielding, higher-quality bread wheat.

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