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Evaluation and selection in segregating population of bread wheat (*Triticum aestivum* L.)

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Abstract
A study was conducted on 47 wheat genotypes in the Research Farm of the Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Punjab. The study examined yield and yield-attributing traits using the Augmented Design method. The study investigated deeper into analyzing genetic variability, path coefficient analysis and correlation analysis to understand better the underlying factors influencing wheat production. The harvest index showed significant GCV and PCV values. High heritability and high genetic advance observed by traits such as days to maturity indicating improvement for these traits can be made through direct selection, high heritability and low genetic advance noted by spike length, days to 50% heading, canopy temperature and chlorophyll content. Harvest index and no of productive tillers plant^{-1} had a positive (+ve) correlation with grain yield per plant and days to maturity had a negative (-ve) correlation. The path coefficient analysis showed positive (+ve) direct effect on grain yield plant^{-1} by Harvest index, biological yield per plant, days to 50% heading and spike length.

Keywords: ANOVA (Analysis of variance), GCV (Genotypic coefficient of variation), PCV (Phenotypic coefficient of variation), correlation, genetic variability

Introduction
Bread wheat, which belongs to the Poaceae family, is known by its scientific name *Triticum aestivum.* As a segmental allohexaploid plant, bread wheat contains three sets of genomes (AABBDD), adding up to 42 chromosomes arranged into 21 pairs. The place of origin for this crop lies in South West Asia, where it was first domesticated several thousand years ago (Filiz, 2012; Baenziger, 2016) [15, 3]. Wheat is crucial as it's the second-largest crop in area, production, and consumption. It contributes to 20% of human calorie intake and is a significant source of proteins, vitamins, and minerals. It's the second-most dominant crop after rice and vital for human subsistence (Thapa *et al*., 2019) [36]. A nutritious grain is vital for food security, poverty reduction, and sustainable livelihoods.

The enhancement of crops through genetic improvement heavily relies on genetic variability and heritability. Genetic variability refers to the extent to which specific traits differ among individual genotypes in a population, serving as the basis for crop improvement. Heritability also plays a vital role in genetic enhancement by providing essential information (Chimdesa *et al*., 2014) [12]. Genetic advance is a crucial and decisive factor in selecting desirable traits (Boryana and Darina, 2014) [6]. Correlation analysis provides valuable information regarding the associations among various plant features that enhance crop production (Ullah *et al.,* 2018) [38]. Plant breeders can utilize the correlation coefficient as a statistical method to aid in selecting crops with more significant yield potential (Gerema *et al.,* 2020) [17]. The application of path analysis can facilitate understanding how independent variables impact the dependent variable. This approach uses path coefficients to measure the direct effects of one attribute on another, distinguishing between direct and indirect effects. Researchers can use this method to identify critical variables influencing their target variable, leading to better decision-making and goal achievement (Rohith *et al.,* 2022) [29].

Materials and Methods
The present study was carried out during the Rabi season of 2021-2022 at the Experimental Field of Genetics and Plant Breeding of School of Agriculture at Lovely Professional University, Phagwara, India. An augmented experimental design and experiment consisted of 47 genotypes and 5 checks planted at 22.5 cm x 5 cm spacing.

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All recommended plant protection measures and agronomic practices were implemented throughout the experiment. Data were collected for traits such as Days to maturity, Days to 50% heading, Plant height (cm), No of spikelet spike[-1], Spike length (cm), No of productive tillers plant[-1], Spike weight (gm), Biological yield plant[-1] (gm), Test weight (gm), Harvest index (%), Canopy temperature, Chlorophyll content and Grain yield plant[-1] (gm) on an individual basis for each plant. Days to maturity and days to flowering data were recorded on a whole plot basis. Statistical analysis was conducted to evaluate the significance and mean performance of different traits using (Federer 1956) and (Burton 1952) [14, 7] methodologies for the analysis of variance, while GCV and PCV values were computed by applying (Burton and Devane 1953) [8] methodology, respectively. The broad sense heritability and genetic advance were, calculated according to methods given by (Hanson *et al.,* 1956); (Johnson *et al.,* 1955) [18, 20]. Correlation and path coefficient analysis were evaluated by following (Dewey and Lu 1959); (Al-Jibouri *et al.* 1958) [13, 2].

Result and Discussion
An investigation is conducted on 47 different genotypes utilizing an augmented design method. ANOVA indicated notable differences among the various genotypes regarding their traits. Such as days to 50% heading, days to maturity, plant height, no of productive tillers plant[-1], spike length, spike weight, no of grains spike[-1], biological yield plant[-1] and harvest index (as seen in Table 1), are highly significant that all examined characteristics exhibited substantial genetic variation. In light of these findings, specific genotypes were recommended as optimal for future use. Similar findings are reported in (Sood *et al.,* 2021), (Sharma *et al.,* 2023), (Chaudhary *et al et.,* 2022), (Hassani *et al et.,* 2022) [35, 31, 10, 19].

The current study thoroughly analyses various additional variables namely GCV, PCV, genetic advance, heritability and genetic advance mean. The outcomes of this are available in Table 2 and Figure 1. The PCV values ranged between 4.42 and 32.47, whereas the GCV values varied from 3.7 to 29.52. Amongst all the characteristics evaluated, it is observed that the harvest index (29.52) and no of productive tillers plant[-1] (21.66) had the highest GCV values, respectively. The PCV value for harvest index (42.11) was higher than other traits like grain yield plant[-1] (32.47), no of productive tillers plant[-1] (29.37), biological yield plant[-1] (29.9), spike weight (18.84), and no of grains spike[-1] (14.04). The observations mentioned in Table 2 are congruent with the outcomes reported by (Tolwain and Shukla 2022) [37], (Khinchi *et al.,* 2022), (Singh and Sharma 2021), (Gerema *et al.,* 2020) [23, 33, 17]. From this observation, we can conclude that apart from genotypic effects, environmental influences also play a significant role in variation within genotypes concerning trait expression.

The investigation analyzed the heritability of characteristics to anticipate their manifestation in future generations. The findings demonstrated that heritability varied across the studied traits, fluctuating between 1.3% for grain yield plant[-1] and 99.06% for days to maturity. Traits with a significant high heritability included spike length (73.27%), days to 50% heading (73.02%), canopy temperature (71.27%), and chlorophyll content (70.15%). Traits with a moderate degree of heritability involved no of productive tillers plant[-1] (54.37%), no of grains spike[-1] (52.6%), harvest index

(49.16%), and no of spikelets spike[-1] (38.69%). The traits such as spike weight (26.79%), plant height (22.14%), test weight (18.48%), and biological yield plant[-1] (15.69%) displayed low levels of heritability. These observations are consistent with prior studies, which suggest that genes with an additive effect account for outcomes associated with high heritability. In contrast, non-additive gene action contributes to results linked to low heritability.

The percentage of genetic advance with relation to the mean was highest for days to maturity (27.06%), moderate for harvest index (15.76%), and low for chlorophyll content (7.17%), no of grains spike[-1] (6.19%), days to 50% heading (6.17%), plant height (4.03%), canopy temperature (2.67%), biological yield plant[-1] (2.51%), test weight (2.11%), no of productive tillers[-1] (1.98%), spike length (1.64 %), no of spikelets spike[-1] (1,23%), spike weight (0.2%) and grain yield plant[-1] (0.08%). Similar finding was reported by Shah *et al.,* (2023), Singh and Sharma (2021) and Regmi *et al.,* (2021) [31, 33, 28]. Suggesting that additive genes largely control traits with high genetic advance while non-additive genes mainly influence those with low genetic advance; therefore, selecting additive gene-controlled traits is more beneficial than selecting non-additive gene-controlled ones. Traits like days to maturity have high heritability. They can be directly improved through selection, whereas traits including chlorophyll content, canopy temperature, spike length and days to 50% heading have high heritability but poor genetic advance, indicating that environmental factors play a greater role than genetics. Traits such as the no of productive tillers plant[-1], harvest index, no of grains per spike and the no of spikelets spike[-1] exhibit moderate heritability but low genetic advance, which suggests that they too, are mainly influenced by non-additive gene action, as shown in studies done by (Ahamad *et al.,* 2022), Khinchi *et al.,* (2022), Tolwani and Shukla (2022) and Kumar *et al.,* (2019) [1, 23, 37, 36].

Table 3 presents the Genotypic correlation of coefficient analysis for 14 traits under investigation. The results estimate highlighted that the harvest index (0.6382) and the no of productive tillers plant[-1] (0.5948) were positive (+ve) and highly significant association with grain yield plant[-1]. Spike length (0.3263) and days to 50% heading (0.2991) positive (+ve) and significant association grain yield plant[-1]. Days to maturity (-0.4324) indicated a negative (-ve), significantly associated with grain yield plant[-1]. These findings are consistent with previous studies conducted by Upadhyay (2020), Baye *et al.* (2020), Kaur *et al.,* (2019), and Ozukum *et al.,* (2019) [39, 5, 21, 26]. The days to 50% heading exhibited positive (+ve) and significantly associated through the number of grains spike[-1] (0.5018), spike length (0.3502), spike weight (0.3342), canopy temperature (0.3556) and grain yield plant[-1] (0.2991). However, it is significantly negatively (-ve) associated with test weight (-0.3556). Similarly, the days to maturity had a significantly positive (+ve) associated with no of grains spike[-1] (0.4766) and biological yield plant[-1] (0.5395), exhibited negative (-ve) and significantly associated with the plant height(-0.4263), no of productive tillers plant[-1] (-0.4130), spike length (-0.5331), harvest index (-0.7191), grain yield plant[-1] (-0.4324) and no of spikelets spike[-1] (-0.3204). Plant height was positive (+ve) and significantly associated through the no of productive tillers plant[-1] (0.3845) and harvest index (0.4185) exhibited negative (-ve) and significant association with no of grains spike[-1] (-0.5202) and biological yield plant[-1] (-0.4309). No of

productive tillers[-1] had a positive (+ve) and significantly associated with grain yield plant[-1] (0.5948), harvest index (0.3618) and test weight (0.3124). Still, it displayed a significant negative (-ve) association with the no of grains spike[-1] (-0.3381). Moreover, spike length showed a positive (+ve) and significantly associated with the no of spikelets spike[-1] (0.6929), spike weight (0.4431), harvest index (0.4696), canopy temperature (0.3524) and Grain yield per plant (0.3263) while indicating a negative (-ve) significantly associated with biological yield plant[-1] (-0.2995). No of spikelets spike[-1] showed a significantly positive (+ve) association responded with canopy temperature (0.4044) and spike weight (0.3078) but a negative (-ve) significant association represented with biological yield plant[-1] (-0.3221). A positive (+ve) significant correlation was responded between the spike weight and harvest index (0.3558). No of grains spike[-1] had a significant positive relationship with the biological yield plant[-1] (0.4857), but a negative (-ve) association with the harvest index (-0.3735). A significant negative (-ve) association is observed between the biological yield plant[-1] and harvest index (-0.6323). Conversely, the harvest index has a positive (+ve) and significantly associated with grain yield plant[-1] (0.6382). Chlorophyll content has positive (+ve) and significantly associated with canopy temperature (0.3143).

Figure 2 and Table 3 present the phenotypic correlation of coefficient analysis for 14 traits, where harvest index (0.7186), no of productive tillers plant[-1] (0.5897), spike length (0.3259), and plant height (0.3056) were found to have significant and positive (+ve) association with grain yield plant[-1], indicating these traits as crucial contributors for enhancing grain yield in genotypes by emphasizing on their component characters. Moreover, it was reported that days to maturity (-0.4841) had a significant and negative(-ve) association with grain yield plant[-1]; these findings are consistent with previous studies conducted by Upadhyay (2020), Baye et al., (2020), Kaur et al., (2019), and Ozukum et al., (2019) [39, 5, 24, 26]. The days to 50% heading presented significant and positive (+ve) correlation with the spike weight (0.3692), canopy temperature (0.4067), no of grains spike[-1] (0.5637), and spike length (0.3359). Conversely, its negative (-ve) association with test weight (-0.3822). Similarly, days to maturity showed significant and positive (+ve) association with biological yield plant[-1] (0.4145) and the number of grains spike[-1] (0.5175). However, it exhibited a negative (-ve) association through grain yield plant[-1] (-0.484), harvest index (-0.6967), plant height (-0.414), and spike length (-0.4297). Plant height is significantly and positive (+ve) correlated with grain yield plant[-1] (0.3056), canopy temperature (3419%), harvest index (0.4688), and the number of productive tillers plants[-1] (0.4128). In contrast, it shows negative (-ve) association with biological yield plant[-1] (-0.3096) and no of grains spike[-1] (-03873%). No of productive tillers plant[-1] showed a significant and positive (+ve) associated with grain yield plant[-1] (0.5897%), canopy temperature (0.3701), test weight (0.2971) as well as harvest index (0.3207%). However, it has a significant negative (-ve) association with chlorophyll content (-0.3016). The spike length has a significant positive (+ve) association with the no of spikelets spike[-1] (0.6571), harvest index (0.3873), spike weight (0.3789), as well as grain yield plant[-1] (0.3259). Similarly, the no of spikelets spike[-1] has a significant and positive (+ve) association with no of grains spike[-1] (0.4417),

spike weight (0.3641) and canopy temperature (0.3184). Conversely, a negative (-ve) significant association was observed between the spike weight and test weight (-0.3157). The no of grains spike[-1] with biological yield plant[-1] (0.3809) resulted in the identification of a positive (+ve) significant correlation, but negative (-ve) and significant association were found for harvest index (-0.3662) and test weight (-0.3082). Furthermore, biological yield plant[-1] displayed a negative (-ve) significant association with harvest index (- 5239), while harvest index displayed significant positive (+ve) association with grain yield plant[-1] (0.7186).

Path coefficient analysis offers a practical approach to evaluating the direct and indirect impacts of different traits and their correlations. As per the details presented in Table 4 and Figure 3. The direct positive (+ve) effect on grain yield plant[-1] they are harvest index (1.1302), continued by biological yield plant[-1] (0.9206), days to 50% heading (0.0815), and spike length (0.0544). Conversely, the negative (-ve) direct effect on grain yield plant[-1] they are days to maturity (-0.1391), no of grains spike[-1] (-0.0623), canopy temperature (-0.0534), no of productive tillers plant[-1] (-0.0512), spike weight (-0.0457), plant height (-0.0448), no of spikelets spike[-1] (-0.0349), test weight (-0.0303) and chlorophyll content (-0.0244). These findings are reliable with previous studies showed by Soni et al., (2023), Rohith et al., (2022), Chauhan et al., (2022), Chaudhary et al., (2020), Barman et al., (2020,) Ozukum et al., (2019) and Pooja et al., (2018) [34, 30, 11, 26, 27] have also confirmed these findings.

Furthermore, based on path coefficient analysis, it was observed that days to 50% heading had a positive (+ve) indirect effect on several characteristics, such as the no of grains spike[-1] (0.0409), canopy temperature (0.0290), spike length (0.0285), spike weight (0.0272), no of spikelets spike[-1] (0.0213), chlorophyll content (0.0209), harvest index (0.0144), biological yield plant[-1] (0.0058) and days to maturity (0.0022). In addition, days to maturity exhibited positive (+ve) indirect effects through the harvest index (0.1001), spike length (0.0742), plant height (0.0575), no of productive tillers plant[-1] (0.0575), no of spikelet spike[-1] (0.0446), canopy temperature (0.0393), spike weight (0.0318), chlorophyll content (0.086) and test weight (0.041).

Various characteristics exhibited positive (+ve) indirect effects on grain yield plant[-1] through plant height is no of grains spike[-1] (0.0233), biological yield plant[-1] (0.0193), days to maturity (0.0191) chlorophyll content (0.0078) and days to 50% heading (0.0055). No of productive tillers plant[-1] showed a positive(+ve) indirect effects via days to maturity(0.0211), no of grains spike[-1] (0.0173), chlorophyll content (0.0118), spike weight (0.0045), and no of spikelets spike[-1] (0.0022), days to 50% heading (0.0014). Spike length also had positive (+ve) indirect effects seen through the no of spikelets spike[-1] (0.0377), harvest index (0.0256), spike weight (0.0241), canopy temperature (0.0192), days to 50% heading (0.0191), chlorophyll content (0.0051) plant height (0.0146), no of productive tillers plant[-1](0.0073) and no of grains spike[-1] (0.0031). No of spikelet spike[-1] positive (+ve) indirect effects impact biological yield plant[-1] (0112), days to maturity (0.0112), and test weight (0046) and no of productive tillers plant[-1](0.0015). The spike weight exhibited positive (+ve) indirect effects via days to maturity (0.0105), test weight (0.0120), biological yield plant[-1] (0.0080), chlorophyll content (0.0052) and no of productive tillers plant[-1](0.0040). Similarly, the no of grains spike[-1] positive (+ve) indirect

effects via plant height (0.0324), harvest index (0.0233), no of productive tillers plant⁻¹ (0.0211) and test weight (0.0132). Additionally, test weight demonstrated a positive (+ve) indirect effect through days to 50% heading (0.0108), spike weight (0.0080), no of grains spike⁻¹ (0.0064), no of spikelets spike⁻¹ (0.0040), canopy temperature (0.0035) and harvest index (0.0028), spike length (0.0021) and days to maturity (0.0009). Furthermore, biological yield plant⁻¹ had a positive (+ve) indirect effect through days to maturity (0.4966), no of grains spike⁻¹ (0.4471), no of productive tillers plant⁻¹ (0.1747), test weight (0.1740), days to 50% heading (0.0656) and chlorophyll content (0.0247). The harvest index exhibited

a positive (+ve) indirect impact through spike length (0.5308), plant height (0.4725), no of productive tillers plant⁻¹ (0.4089), spike weight (0.4021), canopy temperature (0.2933), no of spikelets spike⁻¹ (0.2878) and days to 50% heading (0.2001). Chlorophyll content had a positive (+ve) indirect effect through no of productive tillers plant⁻¹ (0.0056), plant height (0.0042), spike weight (0.0028), days to maturity (0.0015) and harvest index (0.0002). Canopy temperature had a positive (+ve) indirect effect through days to maturity (0.0151), biological yield plant⁻¹ (0.0136) and test weight (0.0063).
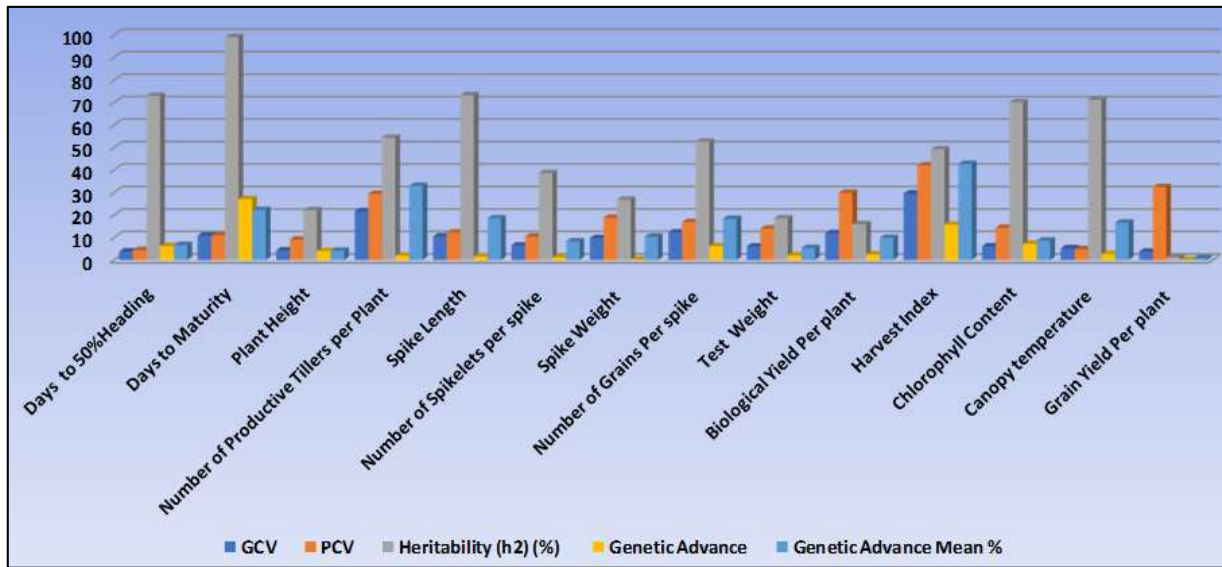
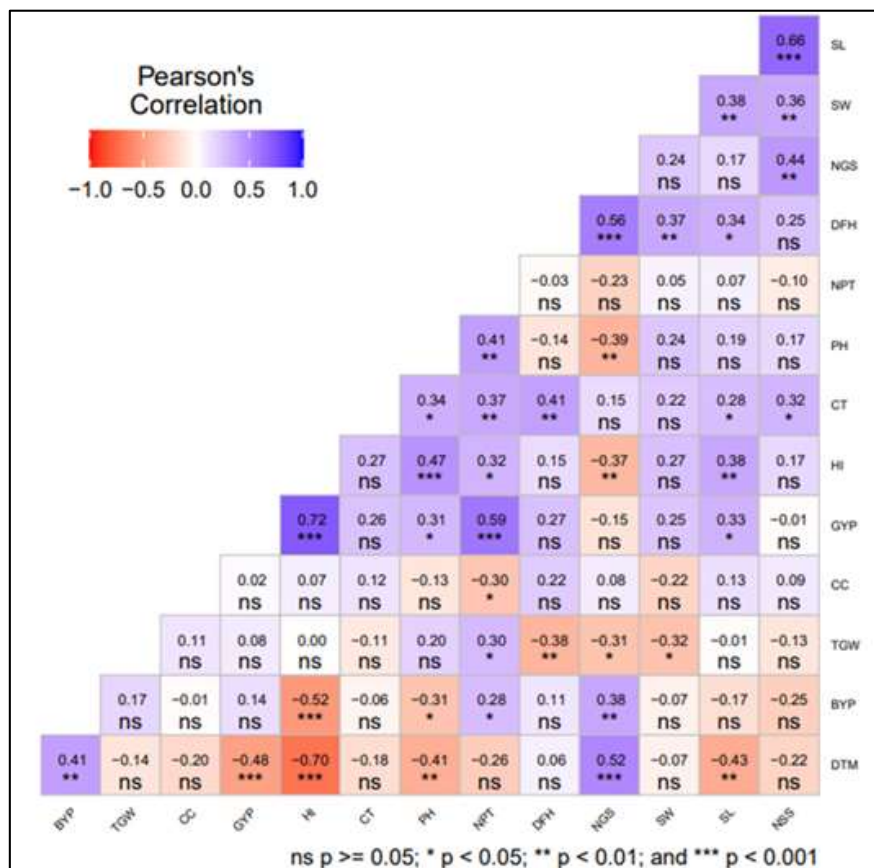

Fig 1: Genetic Variability Parameters
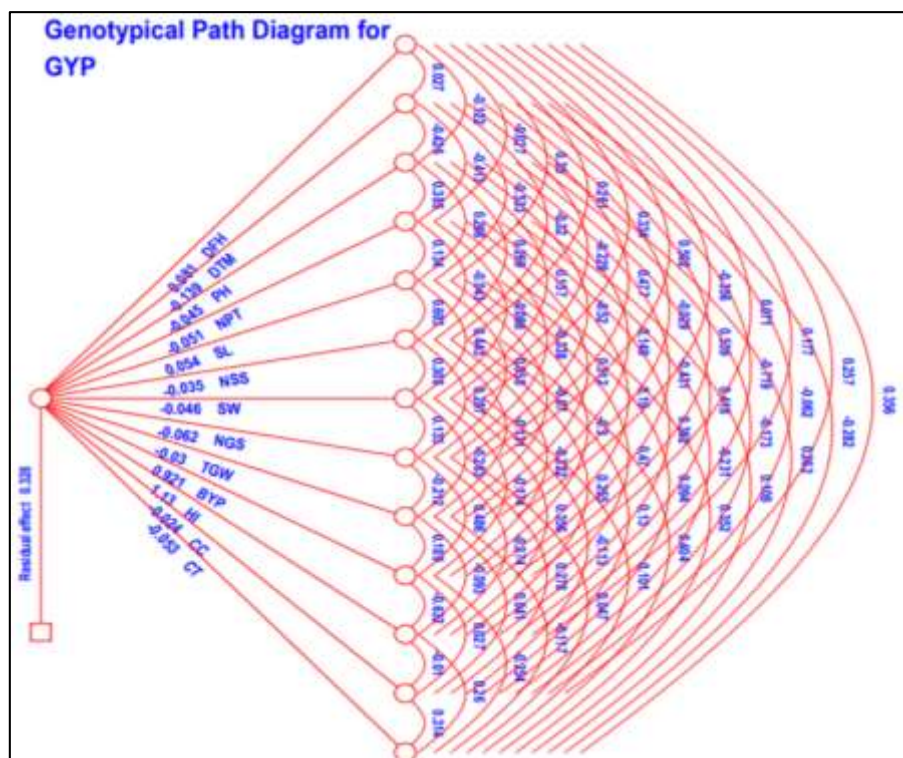

Fig 2: Phenotypic Correlation heat map

Fig 3: Genotypic path diagram for grain yield per plant

Table 1: Analysis of variance for yield and yield attributing traits in bread wheat

Source	Df	DFH	DTM	PH	NPT	SL	NSS	SW	NGS	TW	BYP	HI	CC	CT	GYP
Treatment (ignoring Blocks)	51	44.72**	224.3**	124.0ns	3.87*	1.12**	2.27ns	0.12ns	46.08**	39.14ns	83.93ns	243.19ns	30.29ns	2.31ns	7.88ns
Treatment: Check	4	41.2**	22.7**	508.44**	8.16**	0.26ns	0.77ns	0.07ns	8.83ns	109.19*	60.93ns	36.79ns	69.56ns	1.5ns	4.09ns
Treatment: Test vs. Check	1	1344.47**	3284.74**	710.11**	21.13**	1.84*	2.76ns	0.02ns	819.65**	146.14*	1358.17**	1147.74**	3.92ns	3.81ns	9.8ns
Treatment: Test	46	16.77**	175.3**	77.93ns	3.12*	1.18**	2.39ns	0.13ns	32.51ns	30.72ns	58.23ns	241.48ns	27.45ns	2.35ns	8.16ns
Block (Eliminating Treatments)	4	1.2ns	7.7*	155.73ns	1.13ns	1.32*	1.24ns	0.49**	210.43**	16.25ns	266.51**	41.59ns	40.54ns	6.15ns	9.87ns
Error	16	4.53	1.65	60.67	1.43	0.32	1.46	0.1	15.41	25.04	48.94	122.76	36.12	3.09	8.06
CV		2.24	1.03	7.93	18.96	6.29	8.09	15.96	10.82	12.91	24.58	32.09	16.44	5.43	31.12

ns *p*>0.05; * *p*<= 0.05; ** *p*<= 0.01

X1: Days to flowering, X2: Days to maturity, X3: Plant height, X4: Number of productive tillers per plant, X5: Spike length X6: Number of spikelets per spike, X7: Spike weight, X8: Number of grains per spike, X9: Test weight, X10: Biological yield per plant, X11: Harvest index, X12: Chlorophyll content, X13: Canopy temperature, X14 Grain yield per plant.

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