Plant Archives Vol. 25, Supplement 1, 2025 pp.1451-1459 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-1.199

GENETIC VARIABILITY STUDIES IN WHEAT (*TRITICUM AESTIVUM* L.)

G. Praveenkumar[1]*, S. M. Umate[2], H.V. Kalpande[1], D. K. Zate[1] and Bharat Sharma[1]
[1]Department of Genetics and Plant Breeding, College of Agriculture, VNMKV Parbhani, Maharashtra, India
[2]Wheat and Maize Breeder, VNMKV, Parbhani, Maharashtra, India
*Corresponding author E-mail: Praveenkumar.gundumalla@gmail.com

(Date of Receiving : 15-09-2024; Date of Acceptance : 05-11-2024)

ABSTRACT

The present experiment was conducted by using thirty-six wheat genotypes and four checks at Wheat and Maize Research Unit, College of Agriculture, VNMKV, Parbhani. This investigation was carried out during *Rabi* 2023-2024 in randomized block design with two replications. A set of forty wheat genotypes were used to estimate genetic variability, correlation coefficient and path coefficient for yield and yield attributing characters. A sufficient rang of variation was observed for yield components. GCV and PCV was recorded highest for grain yield per plot. High heritability coupled with high genetic advance for grain yield per plot, harvest index, biological yield per plot, number of productive tillers per plant, spike length, days to 50% heading and spike length. The genetic correlation coefficients were found to be higher in magnitude then that of phenotypic correlation coefficients for most of the traits under experiment, which clearly indicated the presence of inherent association among various characters. The genotypic correlation is the present study observed significant positive association for grain yield contributing characters *viz*., number of productive tillers per plant, number of grains per spike, biological yield per plot and harvest index. Thus, selection for these characters would directly follow the immediate improvement of the grain yield for wheat crop. Number of productive tillers per plant, number of grains per spike, biological yield per plot, 1000 grain weight and harvest index had positive direct effect on grain yield per plot. Henceforward, these traits must be given weightage in selection for improvement of wheat in future breeding programmes.

Keywords **:** Wheat, variability, heritability, genetic advance per mean, correlation and path coefficient.

Introduction

Wheat (*Triticum aestivum*), a self-pollinated crop of the *Graminae* family (sub-family *Poaceae)* and genus *Triticum,* is the world's favourite energy rich cereal crop. It 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. As contrast to rice, wheat is grown in all the continents of the world. Wheat is a C_3 plant grown from temperate, irrigated to dry and high-rain fall areas and from warm, humid to dry cold environment. This broad adaptation has undoubtedly been made possible by the wheat genome's complexity, which gives the crop a tremendous deal of plasticity. Numerous specific end-use quality features and adaptable qualities have been bred into wheat, leading to the establishment of unique cultivars with specialized end uses.

The cultivated wheat's of today constitute an alloploid series, diploids through hexaploids. From the study of morphological similarities between diploid wheat *T. monococcum* L. and tetraploid wheat *T. turgidum* L. It is clear that gene 'A' of the polyploidy wheat came from *T. monococcum.* Archaeological evidences also indicate that diploid wheat that contributed 'A' gene to the tetraploid was a wild form. The source of 'D' gene in hexaploids is *T. tauschi.* As regards 'B' gene there are different opinions and the donor could be *T. speltoides* Sarkar and Stebbins (1956) or *T. longissimum* Feldman (1970) or *T. urartu.* Johnson (1975).

Domestication of wheat and the increase in ploidy (from *diploid* to *tetraploid* to *hexaploid*) had a great effect on its morphology and physiology. Modern wheat has larger leaves, reduced tillering phase, fewer but larger and heavier spikes and reduced to almost nil shattering (Simmons, 1987). Grain filling in modern wheat is more dependent on photosynthates from leaves and stems than from spikes, and grain yield can be largely attributed to the greater distribution of the above ground mass to the grain. Jensen (1978) also observed that a decline in plant height was associated with dwarf Mexican wheat, introduction of which led to the green revolution, truly speaking wheat revolution India.

Wheat grains contains starch (60-68%), protein (6-21%), fat (1.5-2.0%), lipids (1.8%), reducing sugars (2%), cellulose (2.0-2.5%), minerals (1.8%) and vitamins. Its significance comes from the characteristics of wheat gluten, a dense web of resilient endosperm proteins that expand with fermenting dough but coagulate and solidify when heated to create a "risen" loaf of bread. This trait is unique to wheat, with rye and triticale having a lower degree of it. Bread, flour, confections (cakes, cookies, crackers, and pretzels), unleavened bread, semolina, and breakfast cereals are all made using wheat. Because of its many applications, high nutritional value, and storage qualities, wheat is the staple food for more than one-third of the world's population.

Material and Methods

The experimental material constituted forty wheat genotypes acquired from Wheat and Maize Research Unit, College of Agriculture, VNMKV, Parbhani, Maharashtra, India (Table 1). The sowing was done with 20 × 10 cm inter and intra row spacing and with a plot size of 6 m × 0.40 m. The seed were sown on 8th November, 2023-2024 these genotypes were sown in Randomized Block Design with two replications. Five competitive plants per genotype in each replication were selected randomly and observations are recorded as per the DUS guidelines.

Statistical Analysis

The mean values of each genotype were employed for statistical analysis. The phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) was estimated as per the formula suggested by Burton (1952).

Heritability percent in broad sense, genetic advance and genetic advance as per cent Mean was estimated by the formula given by Johnson *et al.* (1955).

Genotypic and phenotypic correlation coefficient between characters were computed utilized respective components of variances and co-variances, by following formula suggested by Johnson *et al.* (1955).

The proportion of direct and indirect contribution of various characteristics to total correlation coefficient with grain yield per plot was established through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

Results and Discussion

Analysis of Variance

Analysis of variance revealed that all the forty genotypes differed significantly high for all the ten characters *viz.,* days to 50 % heading, days to maturity, number of productive tillers per plant, length of main spike, number of grains per spike, biological yield per plot, 1000 seed weight, grain yield per plot, plant height and harvest index (Table 2)

Estimation of Genetic Parameters

The genetic characteristics for the characters under study, including mean, range, PCV and GCV, heritability estimation and genetic advance as a percentage of mean are shown in Table 3 and Fig. 1. In the present investigation large differences in mean values for all the traits were observed. The trait days to 50 % heading ranged from 42.50 to 78 days, days to maturity 102.50 to 125 days, number of productive tillers per plant 4.10 to 18.20, length of main spike 6.51 cm to 11.93 cm, number of grains per spike 35.00 to 71.50, biological yield per plot 0.36 kg to 1.29 kg, 1000 seed weight 32.88 g to 54.04 g, grain yield per plot 0.18 kg to 0.96 kg, plant height 72.90 cm to 107.96 cm and harvest index 22.45% to 95.40%. The experimental material had wide range of variability favourable mean performance for the most of the traits studied.

Estimation of Genotypic and Phenotypic Variance

Variability plays and important role in crop breeding. The development of an effective breeding programme depends on genetic variability. The total variation present in a population arises due to genotypic and environmental effect. Presence of genetic variability in the breeding material is essential for a successful plant breeding programme. The efficiency of selection largely depends on the magnitude of genetic variability present in plant population variability was measured by estimation of mean value, coefficient of variation (genotypic and phenotypic), heritability, genetic advance and genetic gain.

Estimation of PCV (σ^2p) and GCV (σ^2g) were obtained for different characters (Table 3, Fig. 1). A wide range of variance is documented for all the traits. The estimates of PCV were higher than their respective GCV for all the traits. A proximity between GCV and PCV values for almost all the characters revealed less influence of the environment on expression of the characters. Phenotypic variance was higher than genotypic variance for all the yield and yield contributing characters indicating that these characters are not much influenced by the environment. PCV and GCV was recorded high by grain yield per plot (kg) followed by harvest index (%), biological yield per plot (kg) and number of productive tillers per plot. Naik *et al.* (2015), Dutamo *et al.* (2015), Ali *et al.* (2008) and Fellahi *et al.* (2013) also reported similar results for high heritability estimates. Whilst moderate PCV and GCV were recorded for the traits number of grains per spike, days to 50% heading, spike length (cm) and 1000 grain weight. The presence findings are in confirmation with results of Fellahi *et al.* (2013), Arya *et al.* (2017), Kumar *et al.* (2013), and Ali *et al.* (2008). Whereas low PCV and GCV were found for plant height (cm) and days to maturity Dabi *et al.* (2019) has also been reported earlier similar finding. This indicates the environmental factors had more influence on the expression of these characters than the genetic factors, suggesting the limited scope for improvement of these traits through direct selection for better-performing genotypes.

Heritability (Broad Sense) and Genetic Advance as Percent of Mean

The estimates of heritability measure the degree of inheritance of any particular traits. Although, high heritability suggests high component of heritable portion of variation that can be exploited by breeders in the selection of superior genotypes. Heritability predicts the transmission of characters from parents to offspring while genetic advance clarifies the involvement of the type of gene action in the expression of any trait. High heritability coupled with higher genetic advance in an indication of the involvement of additive gene action in the transmission as well in the expression of any trait and the selection may be effective in such a case.

The estimate of broad sense heritability varied from 74.63% to 99.23% (Table 3). In the present study high heritability accompanied with higher genetic advance was documented for days to 50% heading, harvest index, biological yield per plot, grain yield per plot, number of productive tillers per plant, 1000 grain weight, spike length and number of grains per spike. However, high heritability coupled with moderate genetic advance was recorded for plant height indicating the lesser influenced by the environment and are governed by both additive as well as non-additive gene action. While days to maturity showed low genetic advance. These findings are in confirmation with the outcome of the research work conducted by Arya *et al.* (2017), Dutamo *et al.* (2015), Ali *et al.* (2008), Naik *et al.* (2015), Kumar *et al.* (2013), Fellahi *et al.* (2013) and Dabi *et al.* (2019).

Estimates of Phenotypic and Genotypic Correlation Coefficients

Estimation of genetic and phenotypic correlation coefficients were calculated among all characters under investigation (Table 4). Phenotypic correlation is the observable correlation between two variables, including both genotypic and environmental effect and genotypic correlation is the inherent heritable association between two variables, hence genotypic correlation is of greater importance to the plant breeder as compared to phenotypic correlation for the genetic improvement of any one character by selecting the other character which is genetically correlated with the selected trait. In the present investigation, genotypic correlation coefficients were found to be higher in magnitude then that of phenotypic correlation coefficient for most of the traits under study, which clearly indicated the presence of inherent association among various characters. Many earlier research findings also reported lesser magnitude of phenotypic correlation coefficients than the genotypic correlation coefficients that revolved the presence of inherent genetic relationships among various characters and the phenotypic expression of these traits were less influenced by the environment.

In the present study the analysis of genotypic and phenotypic correlation disclosed a significant positive correlation of grain yield per plot with number of productive tillers per plant, number of grains per spike, biological yield per plot and harvest index. While days to 50% heading displayed positive correlation with plant height and days to maturity. Whereas, days to maturity had a significant positive correlation with days to 50% heading, number of grains per spike. Number of productive tillers per plant exhibited significant positive correlation with grain yield per plot and biological yield per plot. Number of grains per spike disclosed significant correlation with grain yield per plot and days to maturity. Number of grains per spike presented significant positive correlation with grains yield per plot and days to maturity. Biological yield per plot disclosed significant positive correlation with grain yield per plot and number of productive tillers per plant. However, plant height exhibited positive correlation with days to 50% heading. Harvest index is significant positively correlated with grain yield per plot. The interrelationship among yield components would help in increasing the yield levels and therefore, more emphasis should be given to these components while selecting better types of wheat. Likewise, the association of grain yield with either one or more than one trait has also been reported by Dashora *et al.* (2022), Azimi *et al.* (2017), Mecha *et al.* (2017), Meles *et al.* (2017), Kumar *et al.* (2013), Ali *et al.* (2008), Kaddem *et al.* (2014), Kalimullah *et al.* (2012) and Fellahi *et al.* (2013).

Path Analysis

This was first used for plant selection. The path coefficient analysis is the simply a standardized partial regression coefficient which split the correlation into measure of direct and indirect effect. According to Sigh *et al.* (2012) and Gelalcha and Hanchinal (2013), path analysis not measure the direct effect of one variable, but also partition both direct and indirect effects and also measure the residual effect of all those passively independent variables which are not taken into consideration during the study, this assist plant breeder to identify traits that are useful as selection criteria to improve yield.

Analysis of genotypic path coefficient is present in Table 5. It is disclosed that the positive direct effect on grain yield was recorded for number of productive tillers per plant, number of grains per spike, biological yield per plot, 1000 grain weight and harvest index. The similar findings were also addressed by Ali *et al.* (2008), Kumar *et al.* (2013), Meles *et al.* (2017), Hakimi *et al.* (2017), Ayer *et al.* (2017), Dutamo *et al.* (2015) and Mecha *et al.* (2017).

Positive indirect effect of various characters was recorded *via*. other traits on grain yield which are prominent for days 50% heading showed a positive indirect effect on grain yield *via* spike length. Days to maturity exhibited positive indirect effect on grain yield *via* spike length, 1000 grain weight and harvest index. Number of productive tillers per plant exhibited positive indirect effect on grain yield *via* days to 50% heading, days to maturity, spike length, biological yield per plot, plant height and harvest index. Spike length revealed a positive indirect effect on grain yield *via* days to 50% heading, days to maturity, number of grains per spike, 1000 grain weight and harvest index. Number of grains per spike had a positive indirect effect on grain yield *via* days to 50% heading, days to maturity, biological yield per plot, plant height and harvest index. Biological yield per plot exposed positive indirect effect on grain yield *via* days to 50% heading, days to maturity, number of productive tillers per plant, spike length, number of grains per spike and plant height. 1000 grain weight had a positive indirect effect on grain yield *via* plant height and harvest index. Harvest index showed positive indirect effect on grain yield *via* days to 50% heading, days to maturity, number of grains per spike, 1000 grain weight and plant height. The residual path effect value found to be 0.2297 indicated that contribution of characters included in this study explained almost all the variation for grain yield as shown in Table 5. These findings are in conformation with the outcome of the research work done by Ali *et al.* (2008), Kumar *et al.* (2013), Meles *et al.* (2017), Hakimi *et al.* (2017), Ayer *et al.* (2017), Dutamo *et al.* (2015) and Mecha *et al.* (2017).

Analysis of phenotypic path coefficient for various traits under study on grain yield disclosed as the highest positive direct effect on grain yield was recorded for harvest index, biological yield per plot, number of grains per spike and number of productive tillers per plant whereas it was recorded lowest for 1000 grain weight.

Positive indirect effect on grain yield was recorded for days to 50% heading *via* spike length and 1000 grain weight. Days to maturity had positive indirect effect on grain yield *via* spike length, 1000 grain weight and harvest index. Number of productive tillers per plant displayed a positive indirect effect on grain yield *via* days to 50% heading, days to maturity, spike length, biological yield per plot, plant height and harvest index. Spike length exhibited indirect positive effect on grain yield *via* days to 50% heading, days to maturity, number of grains per spike, 1000 grain weight and harvest index. Number of grains per spike had positive indirect effect on grain yield *via* days to 50% heading, days to maturity, biological yield per plot, plant height and harvest index. Biological yield per plot showed positive indirect effect on grain yield *via* days to 50% heading, days to maturity, number of productive tillers per plant, spike length, number of grains per spike and plant height. 1000 grain weight had positive indirect effect on grain yield *via* harvest index. Plant height disclosed positive indirect effect on grain yield *via* 1000 grain weight. Harvest index showed positive indirect effect on grain yield *via* days to 50% heading, number of productive tillers per plant, number of grains per spike, 1000 grain weight and plant height. The residual path effect value found to be 0.2367 which indicated that contribution of characters included in this study explained almost all the variation for grain yield as shown in Table 5. These results are in conformation with the outcome of the research work done by Sharma *et al.* (2023), Meles *et al.* (2017), Hakimi *et al.* (2017).

Conclusion

Significant variability was observed in forty wheat genotypes for all the traits studied including the need for effective selection. High heritability coupled with higher genetic advance was recorded for days to 50% heading, harvest index, biological yield per plot, grain yield per plot, number of productive tillers per plant, 1000 grain weight, spike length and number of grains per spike indicating that these characters are governed by additive gene action and hence direct selection for this trait will give more effective results for increasing the grain yield through genetic improvement in wheat. Significant positive correlation was reported for grain yield per plot with number of productive tillers per plant, number of grains per spike, biological yield per plot and harvest index. Hence selection for these characters may be followed for the improvement of grain yield in wheat. Outcome of path analysis revealed higher positive and direct effects of number of productive tillers per plant, number of grains per spike, biological yield per plot, 1000 grain weight and harvest index over grain yield. Hence, these traits must be given weightage in selection for the improvement of wheat in future breeding programmes.

Table 1: Details of genotypes pedigree name and their source

Sr. No.	Genotypes	Pedigree name	Source
1	EC 10970	SPRING WHEAT*GABO*LERMA, 11-3046-2H-3H-4H-2T/-	United States of America
2	EC 11129	GOVERNOR EGYPT NA 101, CI 12100/-	United States of America
3	EC 178071-279	-NA-	-NA-
4	EC 178071-647	-NA-	-NA-
5	EC 178071-691	-NA-	-NA-
6	EC 190899	Cultivar NO.-37/-	Mexico
7	EC 277051	-NA-	Mexico
8	EC 299197	-NA-	Syrian Arab republic
9	EC 313755	-NA-	-Na-
10	EC 425303	-NA-	Nepal
11	EC 444951	-/DS10863	Mexico
12	EC 445054	-/DS14059	Mexico
13	EC 445265	-/DS18601	Mexico
14	EC 445278	-/DS18643	Mexico
15	EC 445427	-/DS51270	Mexico
16	EC 498424	SERI.1B/KAUZ/HEVO/3/AMAD/-	Mexico
17	EC 574735	-NA-	-NA-
18	EC 575376	-NA-	-NA-
19	EC 664229	-NA-	-NA-
20	IC 111840	-NA-	-NA-
21	IC 111922	-NA-	-NA-
22	IC 122726	-NA-	-NA-
23	IC 128669	-NA-	Punjab
24	IC 145341	-NA-	-NA-
25	IC 252414	-NA-	-NA-
26	IC 252814	-NA-	-NA-
27	IC 252960	-NA-	-NA-
28	IC 290215	-NA-	-NA-
29	IC 290255	-NA-	Himachal Pradesh
30	IC 335589	-NA-	-NA-
31	IC 335703	-NA-	-NA-

32	IC 335776	-NA-	-NA-
33	IC 35715	-NA-	-NA-
34	IC 416098	-NA-	Punjab
35	IC 532890	-NA-	-NA-
36	IC 539250	-NA-	Haryana
Checks			
1	NIAW 1994	NIAW 34/ PBW 435	-NA-
2	MACS 6222	MACS 6222	Pune
3	GW 322	GW-322	Gujarat
4	HD 2932	KAUZ/ STAR/ HD2645	New Delhi

Table 2: Analysis of variance for yield and yield contributing characters in forty genotypes of wheat

S. No	Characters	Mean sum of squares		
		Replications (df=1)	Treatments (df=39)	Error (39)
1	Days to 50% heading	0.000	278.409**	1.077
2	days to maturity	0.000	51.046**	1.077
3	number of productive tillers per plant	0.073	17.317**	0.401
4	spike length	0.411	5.201**	0.215
5	number of grains per spike	94.612	154.248**	22.407
6	biological yield per plot	0.001	0.097**	0.001
7	1000 grain wheat	3.164	61.075**	1.501
8	plant height	5.020	163.822**	7.525
9	harvest index	0.927	894.869**	4.233
10	grain yield per plot	0.0002	0.045**	0.0004

*, ** Significant at P = 0.05 and P = 0.01 levels of probability, respectively

Table 3: Estimates of variability parameters for ten characters for yield and yield contributing characters in forty genotypes of wheat

S. No	Characters	Mean	Range		Phenotypic Variance	Genotypic Variance	PCV (%)	GCV (%)	Heritability in broad sense (H^2) (%)	Genetic Advance as % of mean
			Min	Max						
1	Days to 50 % heading	62.775	42.5	78	139.7429	138.666	18.83	18.76	99.23	38.49
2	Days to maturity	108.2	102.5	125	26.0615	24.9846	4.72	4.62	95.87	9.32
3	Number of productive tillers/ plant	10.26	4.1	18.2	8.8589	8.4577	29.01	28.35	95.47	57.05
4	Spike length	8.7968	6.51	11.93	2.7077	2.4932	18.71	17.95	92.08	35.48
5	Number of grains/spike	49.188	35	71.5	88.3279	65.9205	19.11	16.51	74.63	29.38
6	Biological yield/plot	0.7113	0.36	1.29	0.0487	0.0481	31.03	30.83	98.77	63.13
7	1000 grain weight	42.761	32.88	54.04	31.2883	29.7869	13.08	12.76	95.2	25.65
8	Plant height	90.803	72.9	108	85.6753	78.1433	10.19	9.74	91.21	19.15
9	Harvest index	65.441	22.45	95.4	449.5504	445.3188	32.4	32.25	99.06	66.12
10	Grain yield/plot	0.442	0.166	0.969	0.0227	0.0223	34.09	33.79	98.24	68.99

GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation

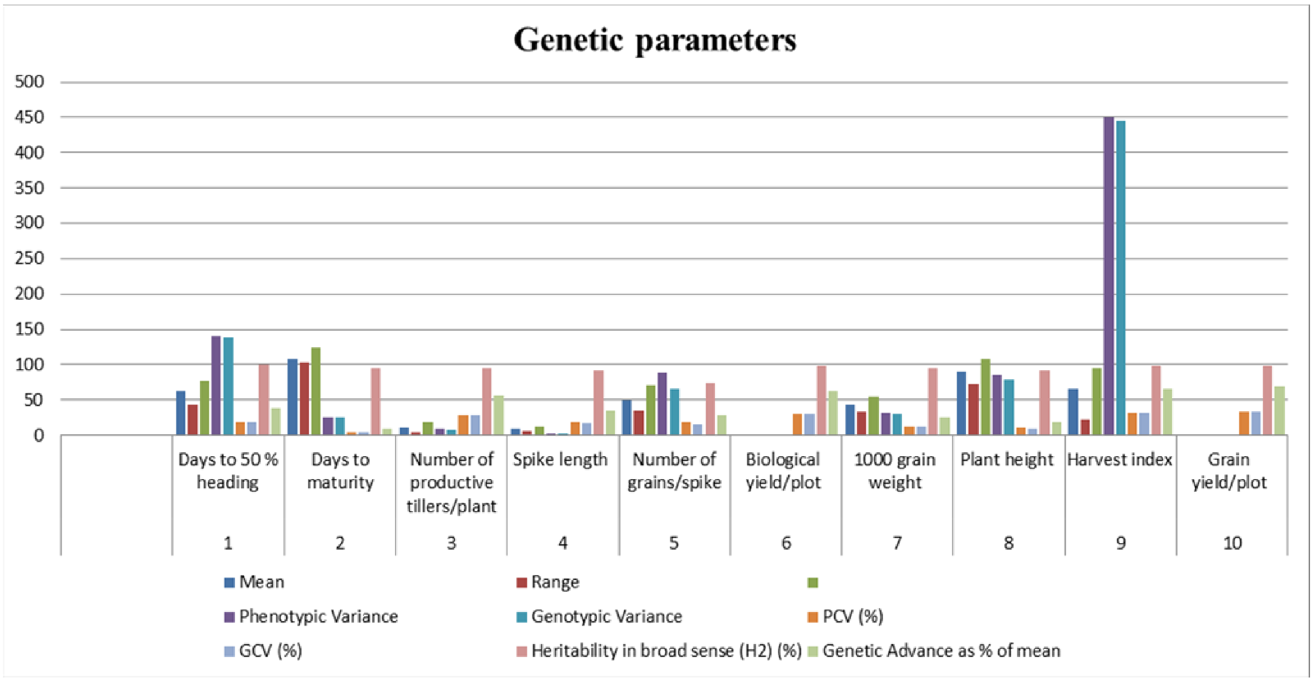

Fig. 1: Components of variance and genetic parameters present among various traits of wheat genotypes

Table 4: Genotypic correlation (Above diagonal) and phenotypic (below diagonal) correlation coefficients of wheat genotypes

	DH	Dm	TL/Pl	SPL	Gs/sp	Bi/Pl	TW	PH	HI	Gr/Plo
DH	1**	0.4495**	0.1816	-0.3709*	0.2964	0.1006	-0.0133	0.4823**	0.2237	0.2855
Dm	0.4417**	1**	0.1595	-0.0125	0.4015*	0.0736	-0.2458	0.2978	-0.0068	-0.0216
TL/Pl	0.1816	0.1563	1**	0.1106	-0.0642	0.3545*	-0.1390	0.0685	0.1921	0.5290**
SPL	-0.3616**	-0.0110	0.0995	1**	-0.2409	0.1644	-0.2744	0.0230	-0.4907**	-0.3897*
Gs/sp	0.2768*	0.3735**	-0.0675	-0.2081	1**	0.2428	-0.2785	0.1016	0.2162	0.4545**
Bi/Pl	0.1018	0.0713	0.3584**	0.1538	0.2196	1**	-0.0222	0.0348	-0.5202**	0.3652**
TW	-0.0140	-0.2373*	-0.1385	-0.2652*	-0.2595*	-0.0204	1**	0.0060	0.0464	0.0810
PH	0.4731**	0.2771*	0.0617	0.0334	0.0751	0.0320	-0.0021	1**	0.0177	0.0006
HI	0.2230*	-0.0071	0.1912	-0.4792**	0.1961	-0.5167**	0.0459	0.0157	1**	0.5713**
Gr/Plo	0.2853*	-0.0219	0.5306**	-0.3844**	0.4130**	0.3679**	0.0802	-0.0023	0.5719**	1**

**** - Significant at p = 0 .01 * - Significant at p = 0. 05**

DH- Days to 50 % heading, **Dm-** Days to maturity, **TL/Pl-** Number of productive tillers per plant, **SPL-** Spike length, **Gs/sp-** Number of grains per spike, **Bi/Pl-** Biological yield per plot, **TW-** 1000 grain weight, **PH-** Plant height, **HI-** Harvest index, **Gr/Plo-** Grain yield per plot.

Table 5: Genotypic path and phenotypic path coefficient matrix of direct and indirect effects of different traits on grain yield in wheat genotypes

		DH	Dm	TL/Pl	SPL	Gs/sp	Bi/Pl	TW	PH	HI	Gr/Plo
DH	G	**-0.0018**	-0.0008	-0.0003	0.0007	-0.0005	-0.0002	-0.001	-0.0009	-0.0004	0.2855
DH	P	**-0.0072**	-0.0032	-0.0013	0.0026	-0.002	-0.0007	0.0001	-0.0034	-0.0016	0.2853*
Dm	G	-0.0586	**-0.1303**	-0.0208	0.0016	-0.0523	-0.0096	0.032	-0.0388	0.0009	-0.0216
Dm	P	-0.0491	**-0.1112**	-0.0174	0.0012	-0.0415	-0.0079	0.0264	-0.0308	0.0008	-0.0219
TL/Pl	G	0.026	0.0229	**0.1433**	0.0158	-0.0092	0.0508	-0.0199	0.0098	0.0275	0.529**
TL/Pl	P	0.021	0.0181	**0.1159**	0.0115	-0.0078	0.0415	-0.0161	0.0072	0.0222	0.5306**
SPL	G	0.0152	0.0005	-0.0045	**-0.0409**	0.0099	-0.0067	0.0112	-0.0009	0.0201	-0.3897*

SPL	P	0.0148	0.0004	-0.0041	**-0.0408**	0.0085	-0.0063	0.0108	-0.0014	0.0196	-0.3844**
Gs/sp	G	0.0473	0.0641	-0.0103	-0.0385	**0.1597**	0.0388	-0.0445	0.0162	0.0345	0.4545**
Gs/sp	P	0.034	0.0459	-0.0083	-0.0256	**0.1229**	0.027	-0.0319	0.0092	0.0241	0.413**
Bi/Pl	G	0.0755	0.0552	0.266	0.1233	0.1822	**0.7503**	-0.0166	0.0261	-0.3903	0.3652**
Bi/Pl	P	0.0801	0.0561	0.282	0.121	0.1728	**0.7869**	-0.0161	0.0252	-0.4066	0.3679**
TW	G	-0.001	-0.0192	-0.0109	-0.0215	-0.0218	-0.0017	**0.0783**	0.0005	0.0036	0.081
TW	P	-0.0009	-0.0154	-0.009	-0.0172	-0.0169	-0.0013	**0.065**	-0.0001	0.003	0.0802
PH	G	-0.013	-0.008	-0.0018	-0.0006	-0.0027	-0.0009	-0.0002	**-0.0269**	-0.0005	0.0006
PH	P	-0.0106	-0.0062	-0.0014	-0.0008	-0.0017	-0.0007	0.0005	**-0.0225**	-0.0004	-0.0023
HI	G	0.1959	-0.006	0.1683	-0.4297	0.1893	-0.4556	0.0407	0.0155	**0.8758**	0.5713**
HI	P	0.2031	-0.0064	0.1741	-0.4365	0.1786	-0.4706	0.0418	0.0143	**0.9108**	0.5719**

**** - Significant at p = 0 .01 * - Significant at p = 0. 05**

DH- Days to 50 % heading, **Dm-** Days to maturity, **TL/Pl-** Number of productive tillers per plant, **SPL-** Spike length, **Gs/sp-** Number of grains per spike, **Bi/Pl-** Biological yield per plot, **TW-** 1000 grain weight, **PH-** Plant height, **HI-** Harvest index, **Gr/Plo-** Grain yield per plot.

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