

Phenotypic variability among parental lines and progenies of bread wheat

Abstract

Wheat is the second most important cereal staple food crop consumed nearly 35% of world population and provides 20% food calories. It's a self-pollinating annual plant in the true grass family Gramineae (Poaceae) and genus *Triticum*, is the world's most famous energy rich cereal crop. The wheat is a hexaploid (allohexaploid) species ($2n = 6x = 42$) having AABBDD with A, B and D genome. The present research investigates fifty-six genotypes of bread wheat consisting of 33 F1s obtained by crossing eleven lines with three varieties in a line x tester mating design along with their parents and two well-known checks. The experiment was laid out in a randomized block design with three replications. Results revealed considerable genetic variability among the genotypes. Traits like grain yield per plant and number of tillers per plant exhibited higher values of PCV with moderate GCV. High heritability with moderate values of genetic advance were recorded for grain weight per spike (17.688%) followed by number of grains per spike (17.4 %), biological yield per plant (14.7 %), 1000 grain weight (11.9 %) indicating involvement of additive gene action in the inheritance of these traits and hence selection along with progeny testing can be employed for improvement of these characters. Correlation studies revealed that number of tillers per plant, harvest index, biological yield per plant have significant positive correlation with the trait grain yield per plant. Therefore, selection for these traits will ultimately aid increase in overall productivity of the genotypes. It was also observed that days to maturity had a negative association with the yield; hence, early maturing cultivars should be preferred while breeding for the higher yield.

Keywords: Bread wheat, correlation coefficient, genetic advance, genetic divergence, heritability and PCV

Introduction

Common bread wheat (*Triticum aestivum*) is one of the most important grain crops serving as staple food for around 40% of the population throughout the globe (Arya et al., 2017). India holds second position in terms of overall wheat production after China having highest coverage in terms of area with a record production of 101.20 million tonnes in 2018-19 with an average productivity of 3424 kg/ha (MoA& FW, 2019). With the ongoing expansion of population in the nation, there will be requirement of more than 140 million tons of wheat grain to be produced by 2050, which is about 40% increase from our present production scenario (Singh et al., 2019). To achieve this goal there is an urgent need to improve the yield per unit area as the crop acreage cannot be expanded beyond a ceiling. Hence, it is important to increase the genetic potential of the varieties to increase the overall productivity of the crop. Crop yield being a

complex genetic trait is significantly influenced by various interrelated component traits associated with it and considerably varies according to the prevailing environmental fluctuations. Therefore, direct selection for yield without taking component characters into consideration may produce misleading results with commissioning of a faulty breeding programme. Hence, to increase overall yield our objective must be directed towards increasing the effects of the components with favourable action and minimizing the effects of the undesirable factors. Hence, correlation analysis could be an important tool to decipher the inter relationships between yield and the component traits. Genetic variability and correlation analysis helps us to identify the genetic associations of different plant traits and their association with the overall productivity levels (Haydar et al., 2020). Genetic variability is the prerequisite for undertaking any successful breeding programme. Therefore, it is very important to have fine knowledge of different variability parameters and their relative significance to improve the overall production level. Information on genetic variability parameters along with heritability and genetic advance provides guidance in predicting response of a genotype in a breeding programme and leads to the formulation of an efficient breeding programme. Parents with higher genetic distance will be able to produce higher extent of heterosis in the progeny (Joshi and Dhawan, 1966). Therefore, the present investigation was undertaken to study the diversity and character association analysis in wheat (*T. aestivum*L.) during Rabi season 2021-2022.

Materials and Methods

The experiment was conducted to study the diversity and character association analysis in wheat (*T. aestivum* L.) during Rabi season 2021-2022. The experiment was evaluated at the Research Farm, Department of Genetics & Plant Breeding, C. C. S. University, Meerut during rabi 2021-2022. The experimental materials consist of fifty-six genotype of spring wheat were grown in randomized block design with two replications. Each genotype was assigned to one row per replication of 2 m length with inter row spacing of 25 cm. The recommended agronomical package and crop protection practice were adopted to raise a good crop. The collected data were subjected to analysis of variance (ANOVA) by SPSS software. Error variance for the two locations was not homogeneous as it was checked by F-test method. Since F-test was applied as there are two error variances rather than Bartlett's test which is used when there are more than two error variances (Gomez & Gomez, 1984). So due to this case, the analysis were done separately for the individual location. Phenotypic and genotypic correlations were estimated using the standard procedure suggested by Miller et al. (1958) and Kashiani and Saleh (2010) from the corresponding variance and covariance components with SPSS. Path coefficient analysis was performed for traits that had significant correlations with grain yield both at genotypic and phenotypic levels in order to know the direct and indirect effect of yield component traits on grain yield using the general formula of Dewey and Lu (1959) by considering grain yield per hectare as dependent variable

3. Results and discussion

3.1. Analysis of variance

Mean squares of characters under study from ANOVA among heat genotype are presented in Tables 1. The result revealed that there were highly significant differences ($p \leq 0.01$) among the genotypes for days to 50% heading, days to maturity, grain-filling period, plant height, Chlorophyll content, , biological weight, thousand grain weight, and harvest index, thereby indicating the presence of sufficient variability among the tested genotypes and provides a good opportunity for further bread wheat improvement programs, while number of seed per spike, spike length, biomass yield, grain yield, showed significant difference among the tested genotypes. These might be due to erratic rainfall during the growing period (Table 2). Similar results were reported by Kotal et al. (2010), Tsegaye et al. (2012), Fikre et al. (2015), and Arya et al. (2017) in their previous studies on bread wheat.

The minimum and maximum value were 3.67 and 108.87, observed in (CT) and (PH) respectively. The minimum and maximum mean value were 14.88 and 105.30, also observed in (NSPS) and (DOM) respectively. The minimum and maximum standard Error (SE) value was observed in 0.10 and 1.51 observed in (DOM) and (Biomass yield) respectively. The minimum and maximum variance observed in 0.48 and 127.87 in (NSPS) and (Biomass yield) respectively. The values of coefficient of variation (C.V. %) are from 0.1 to 0.81. plant height showed a high value of broad sense heritability (0.87) (Tazeen et al 2009) followed by yield (0.74) and Chlorophyll content (0.72).

Path Coefficient Analysis

The table highlights several variables that have significant positive correlations with economic yield. These include the number of spikelets per Spike (NSPS) with a correlation of 0.11924, plant height (PH) at 0.05384, canopy humidity at heading time (CHC) at 0.05156, tillers number (TN) at 0.05597, and biomass weight (BW) at 0.04481. These variables, marked in yellow in the table, indicate their notable positive impact on economic yield. Additionally, the residual effect is recorded as 0.7733. Similar findings have been reported in various studies, such as the research on agronomic traits affecting rice yield in Anhui, China, which also identified significant positive correlations between yield components and economic yield (Ren et al, 2024). Another study on rice yield traits in Pakistan found that the number of productive tillers per plant and flag leaf area had significant positive correlations with grain yield (wang et al, 2021).

Pearson's correlations

The study identifies significant positive correlations between several variables and economic yield, including the NSPS with a coefficient of 0.12, PH at 0.05384, CHC at 0.05156, TN at 0.05597, and BW

at 0.04481. These findings suggest that these traits positively influence economic yield, as highlighted in yellow in the table. Similar studies have corroborated these findings, such as research on agronomic traits affecting rice yield in Anhui, China, which also identified significant positive correlations between yield components and economic yield (Ren et al, 2024). Another study on rice yield traits in Pakistan found that the number of productive tillers per plant and flag leaf area had significant positive correlations with grain yield (Wang et al, 2021).

Chlorophyll content (0.67) is highly positive significant with biological weight. Grain yield show (0.52) highly positively significant with Chlorophyll content and (0.36) positively significant with biological weight. Biomass shows (0.48) highly positive significant with (0.40) biological weight and positive significant effect with chlorophyll content followed by (0.33) plant height. TGW show (0.48) highly significant positive correlation with Chlorophyll content positive significant effect with (0.40) biological weight and (0.36) biomass.

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

Option 2:

Author(s) hereby declare that generative AI technologies such as Large Language Models, etc. have been used during the writing or editing of manuscripts. This explanation will include the name, version, model, and source of the generative AI technology and as well as all input prompts provided to the generative AI technology

Details of the AI usage are given below:

- 1.
- 2.
- 3.

References

- Kour A, Kumar B, Singh B. Genetic evaluation of yield and yield attributing traits in rice (*Oryza sativa* L.) using line x tester analysis. *Electronic Journal of Plant Breeding* 2019;10(1):39-46.
- MoA and FW 2020. https://eands.dacnet.nic.in/Advance_Estimate/3rd_Adv_Estimates. 2019-20_Eng.pdf [Accessed: 2020-09-14].
- Ramadas S, Kumar TMK, Singh GP. Wheat production in india: Trends and prospects. In: Shah F, Khan Z, Iqbal A, Turan M, Olgun M, edited. *Recent Advances in Grain Crops Research*. London: Intech Open Limited. 2019, 1- 16. doi: 10.5772/intechopen.86341
- Haydar FMA, Ahamed MS, Siddique AB, Uddin GM, Biswas KL, Alam MF. Estimation of genetic variability, heritability and correlation for some quantitative traits in wheat (*Triticum aestivum* L.). *Journal of Bio-Science* 2020;28:81-86
- Joshi AB, Dhawan NL. Genetic improvement in yield with special reference to self-fertilizing crops. In *Indian Journal of Genetics and Plant Breeding Indian Agriculture Res Inst, New Delhi Delhi-110012, India: Indian Soc Genet Plant Breed* 1966, 101.
- Ren, Yi, Ending Xu, Peijiang Zhang, Xinchun Zhan, Qingyuan He, and Yu Zou. 2024. "Impact of Key Agronomic Traits on Economic Yield Traits in Anhui Rice (*Oryza sativa* L. spp. *japonica*)" *Agronomy* 14, no. 6: 1101.
- Wang, D., Jenkins, K., Forstenhäusler, N., Lei, T., Price, J., Warren, R., ... & Guan, D. (2021). Economic impacts of climate-induced crop yield changes: evidence from agri-food industries in six countries. *Climatic Change*, 166(3), 30.

(Table 1) Mean squares of the 12 characters from analysis of variance (ANOVA)

Traits	DOH	DOM	NSPS	PH	ChC	CT	TN	SL	Biomass	Yield	BW	TGW
Mean	7.06	1.7366	1.4	167.39	101.24	2.68	9.4	230.		89.	2386.1	58.85
Sq	2*	***	41	***	***	**	92	14	383.6	72	***	***

(Table 2) Descriptive Statistics

Traits	min	max	range	Sum	median	mean	SE. mean	Variance	std.dev	coef.var	Heritability
DOH	71.67	80.67	9.00	4295.33	76.84	76.70	0.20	2.35	1.53	0.02	0.33
DOM	104.00	107.67	3.67	5897.01	105.00	105.30	0.10	0.58	0.76	0.01	0.51
NSPS	12.93	16.47	3.54	833.54	14.90	14.88	0.09	0.48	0.69	0.05	0.02
PH	71.60	108.87	37.27	4576.98	80.20	81.73	1.00	55.80	7.47	0.09	0.87

ChC	9.97	42.43	32.46	1399.04	25.84	24.98	0.78	33.76	5.81	0.23	0.72
CT	3.67	13.20	9.53	324.19	5.60	5.79	0.24	3.16	1.78	0.31	0.41
TN	29.13	34.17	5.04	1784.16	31.69	31.86	0.13	0.89	0.95	0.03	0.11
SL	8.17	55.77	47.60	605.40	9.00	10.81	1.17	76.72	8.76	0.81	0.00
Biomass	32.33	103.67	71.34	3000.33	51.66	53.58	1.51	127.87	11.31	0.21	0.00
Yield	10.00	46.67	36.67	977.00	16.50	17.45	0.73	29.91	5.47	0.31	0.74
BW	28.67	154.33	125.66	5590.69	98.33	99.83	3.77	795.33	28.20	0.28	0.76
TGW	18.67	38.33	19.66	1566.34	27.66	27.97	0.59	19.61	4.43	0.16	0.30

(Table 3) Phenotypic path coefficient.

Phenotypic path coefficient											
	DOH	DOM	NSPS	PH	ChC	CT	TN	SL	Biomass	BW	TGW
DOH	- 0.07579	0.00242	0.00002	- 0.00191	0.00514	0.00197	- 0.00311	- 0.00669	- 0.07741	0.00013	- 0.00654
DOM	- 0.00449	0.04087	0.00004	- 0.00153	0.00711	0.00117	- 0.00461	- 0.00573	- 0.00341	-0.0073	- 0.01008
NSPS	- 0.00518	0.00623	0.00028	- 0.00217	0.00675	0.00757	- -0.0014	0.00127	- 0.02345	- 0.00341	- 0.00625
PH	0.00856	0.0037	- 0.00004	0.01695	- 0.00551	- 0.00231	- -0.0051	0.00213	0.0518	0.00576	0.00856
ChC	- 0.00327	0.00244	0.00002	- 0.00078	0.11924	0.00961	0.00117	0.00146	0.05902	0.01663	0.03866
CT	0.00255	- 0.00082	0.00004	0.00067	- 0.01963	0.05838	- 0.00207	- 0.00003	0.01857	- 0.00671	0.00531
TN	- 0.00458	0.00366	0.00001	0.00168	- 0.00271	- 0.00234	0.05156	0.00253	0.02997	0.00392	- 0.00828
SL	0.00888	-0.0041	0.00001	0.00063	0.00305	0.00004	- 0.00228	0.05597	- 0.00143	0.00325	0.00948

Biomass	0.01602	-	-	0.0024	0.01921	-	-	-	0.30588	0.00801	0.02649
BW	-	-	-	0.00218	0.04426	0.00874	0.00451	0.00414	0.06547	0.04481	0.023
TGW	0.00417	-	-	0.00122	0.03874	-0.0026	0.00359	0.00456	0.08155	0.00866	0.11899

Dependent variable = Economic yield

Residual effect = 0.7733

(Table 4) Genotypic path coefficient.

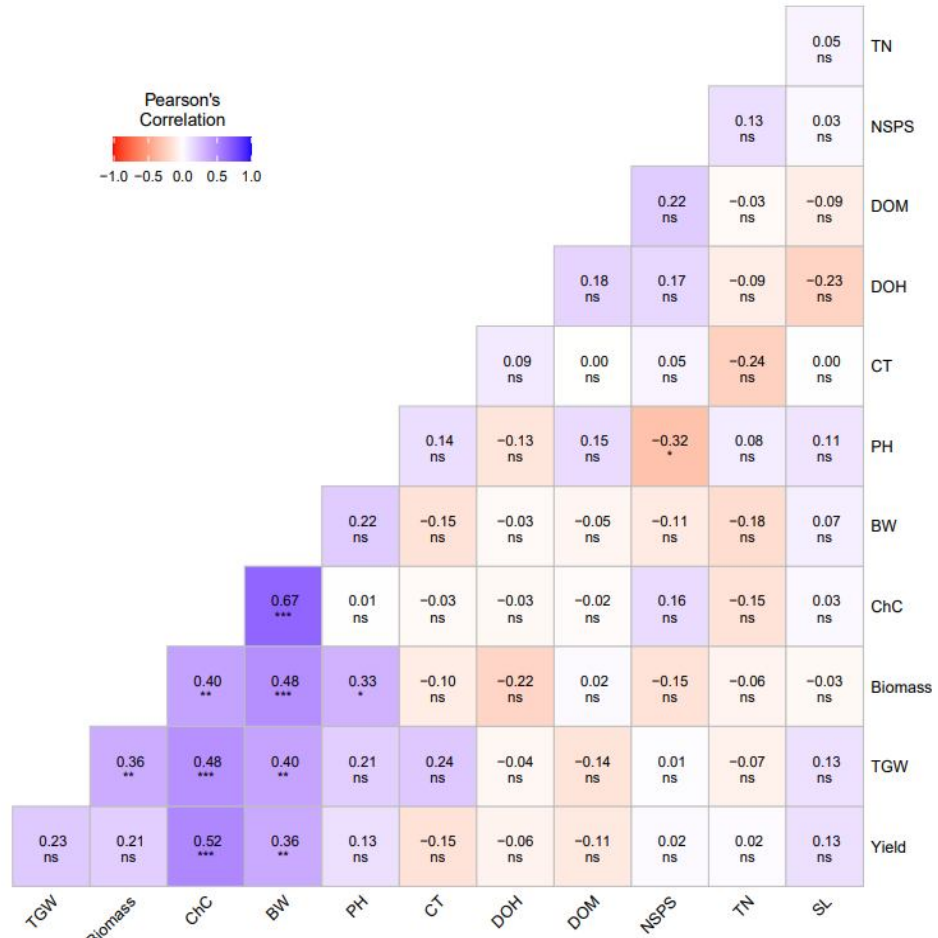
Genotypic path coefficient											
	DOH	DOM	NSPS	PH	ChC	CT	TN	SL	Biomass	BW	TGW
DOH	0.25909	-	0.204	-0.1792	0.35431	0.15522	0.07996	0.76229	0.02246	0.10218	0.03356
DOM	0.13408	0.56341	0.14717	0.22324	-0.2653	0.02616	0.12264	0.04066	0.05673	0.09367	0.06463
NSPS	0.56832	0.89154	0.093	-	2.96049	3.05509	0.27893	0.19816	0.17689	0.72906	-0.3505
PH	-0.0471	0.12759	0.27932	0.98573	0.09718	0.08879	0.10246	0.34812	0.3122	-0.2136	0.07624
ChC	-0.0479	0.078	0.14827	0.04999	1.91633	0.08174	0.02235	0.03747	0.40371	0.45768	0.30419
CT	0.06605	0.0242	0.04261	0.14376	0.25727	0.60884	0.51236	0.29035	0.23252	0.04254	0.0104
TN	0.07857	0.26205	0.0699	0.38307	0.16245	1.18312	0.26366	0.53384	0.77808	0.72963	0.22226
SL	-	0.05301	0.03807	0.79406	0.16615	0.40907	-	0.43215	-	-	-

	0.45703						0.32571		0.21315	0.58132	0.30319
Biomass	0.01077	-0.05915	-0.12548	0.56951	1.43171	-0.26199	-0.37965	0.17046	-0.54037	-0.45004	-0.02059
BW	-0.03387	0.06751	0.08588	0.26933	1.12191	0.03313	0.24608	-0.32135	0.31108	-0.78175	-0.11042
TGW	-0.02064	0.08642	0.07736	0.17835	1.38345	-0.01503	-0.13908	-0.31096	0.0264	-0.20487	-0.42135

Dependent variable = Economic yield

Residual effect = -1.3308

Fig 1- Pearson's correlations among different quantitative characters in wheat.



ns $p \geq 0.05$; * $p < 0.05$; ** $p < 0.01$; and *** $p < 0.001$

UNDER P