International Journal of Research in Agronomy 2025; 8(9): 1066-1070

International Journal
of
Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
© Agronomy
NAAS Rating (2025): 5.20
www.agronomyjournals.com
2025; 8(9): 1066-1070
Received: 05-06-2025
Accepted: 08-07-2025

Association analysis studies in bread wheat (*Triticum aestivum* L.) genotypes under timely sown irrigated condition

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DOI: https://www.doi.org/10.33545/2618060X.2025.v8.i9o.3896

Abstract
The present investigation was conducted on twenty-six wheat genotypes during the rabi season of 2024 at BTC College of Agriculture and Research Station, Bilaspur (Chhattisgarh), to assess genetic variability, correlation, and path coefficient analysis. Analysis of variance revealed significant differences among genotypes for most of the studied traits, including days to maturity, plant height (cm), effective tillers per plant, spike length (cm), spike weight (g), total spikelet's per spike, peduncle length (cm), biological yield per plot (kg), grain yield per plot (kg), harvest index (%), and 1000-grain weight (g). Genetic parameters indicated low to moderate GCV and PCV values for grain yield, biological yield, and spike length, reflecting environmental influence on these traits. However, high heritability coupled with high genetic advance as a percentage of mean for biological yield and grain yield suggested predominance of additive gene action and minimal environmental effects, making these traits suitable for selection. Correlation analysis revealed a strong, positive, and significant association of grain yield with days to heading, effective tillers per plant, spike length, total spikelet's per spike, biological yield, harvest index, and 1000-grain weight. Path analysis further highlighted that biological yield, harvest index, plant height, and spike weight exerted positive direct effects on grain yield, supported by indirect contributions through other characters. Based on mean performance, genotypes HI8853(d), MACS4146(d), and HI8854(d) outperformed the checks HI8713(d), GW322, HI8737(d), and MACS6768 in grain yield and associated traits. These superior genotypes should be advanced for further screening trials.

Keywords: Wheat (*Triticum aestivum* L.), genetic variability, heritability, correlation coefficient and path analysis.

Introduction

Wheat (*Triticum aestivum* L.) is a hexaploid (2n = 6x = 42; AABBDD genomes), annual, self-pollinated, cool-season rabi cereal belonging to the tribe *Triticeae* of the family *Poaceae*. The earliest cultivated forms included diploid einkorn (AA) and tetraploid emmer (AABB) wheat, which originated in the south-eastern region of Turkey, as revealed by genetic relationships. In India, wheat production during 2023-24 was estimated at 110.55 million metric tons, contributing nearly 14% of global production (Anonymous, 2024). Globally, wheat ranks second after rice and provides approximately 21% of total food calories and 20% of dietary protein to more than 4.5 billion people across 94 developing countries (Braun *et al*., 2010) [4]. Due to its extensive cultivation, high productivity, and crucial role in international food grain trade, wheat is often referred to as the "king of cereals." When consumed as whole grain, it is also a valuable source of minerals, dietary fibre, and micronutrients such as iron, zinc, and copper (Shewry & Hey, 2015) [14].

Nutritionally, wheat is rich in gluten protein, which governs dough strength and determines its suitability for a wide range of products. Hard wheat, with higher gluten content, is used for chapatti, roti, naan, and maida, while soft wheat is better suited for biscuits and bakery products. Given its global importance, understanding genetic variability, heritability, correlation, and path analysis in wheat genotypes is essential. Such studies provide insights into yield-attributing traits, identify promising lines for direct selection, and assist in choosing suitable parents for hybridization, thereby accelerating breeding programs aimed at developing improved cultivars.

2. Materials and Methods

The present investigation was carried out during *rabi* season of 2024, at BTC college of Agriculture and Research Station, Bilaspur, Chhattisgarh. Twenty-six wheat genotypes with four checks *viz*, GW322 (C), HI8737(d) (C), HI8713(d) (C) and MACS6768 (C) were used. Experimental material were planted in randomized block design (RBD) with four replications. Each genotype was grown in a plot size of 8 m^2 for each entry in each replication. The observations were recorded on five randomly selected plants from each plot in all the four replications of all the twelve characters *viz*, days to heading, days to maturity, plant height (cm), number of effective tillers/plant, spike length (cm), spike weight (g), total number of spikelet's/spike, peduncle length (cm), biological yield/plot (kg), grain yield/plot (kg), harvest index (%) and 1000 grains weight (g)

Table 1: List of 26 wheat genotypes used in the present study along with place of origin:

S. No.	Name of Genotypes	Place of Origin
1.	MACS4146(d)	ARI, Pune
2.	MACS4135(d)	ARI, Pune
3.	MACS6837	ARI, Pune
4.	HI8858(d)	IARI, Indore
5.	HI8849(d)	IARI, Indore
6.	HI88853(d)	IARI, Indore
7.	HI8854(d)	IARI, Indore
8.	HI1683	IARI, Indore
9.	HI8855(d)	IARI, Indore
10.	HI8850(d)	IARI, Indore
11.	GW561	SDAU, Vijaypur
12.	GW1369(d)	SDAU, Vijaypur
13.	GW554	JAU, Junagarh
14.	GW555	JAU, Junagarh
15.	MP3570	JNKVV, Powarkheda
16.	MPO1395(d)	JNKVV, Powarkheda
17.	MP1401	JNKVV, Jabalpur
18.	UAS485(d)	UAS, Dharwad
19.	AKDW5520(d)	PDKV, Akola
20.	WHD969(d)	HAU, Hisar
21.	DBW457	IIWBR, Karnal
22.	DBW509B	IIWBR, Karnal
23.	GW322 (Check)	RARS, Vijapur
24.	MACS6768 (Check)	ARI, Pune
25.	HI8737(d) (Check)	IARI RS, Indore
26.	HI8713(d) (Check)	IARI RS, Indore

3. Results and Discussion

3.1 Analysis of variance

The analysis of variance showed the presence of significant difference among the genotypes for the characters studied *viz.* days to maturity, plant height (cm), number of effective tillers/plant, spike length (cm), spike weight (g), total number of spikelet's/spike, peduncle length (cm), biological yield/plot (kg), grain yield/plot (kg), harvest index (%) and 1000 grains weight (g). The results indicated a significant level of variability among the genotypes. This offers wheat breeders the potential to enhance these traits through selection and hybridization in order to improve the desired characteristics.

Similar results were observed by Hassani *et al.*, (2022) [6], Sohail *et al.* (2018) [15], Sharma *et al.*, (2018) [13] and Chawla *et al.*, (2018) [5].

3.2 Genetic Parameters

From the study of variability parameters, moderate estimates of GCV and PCV were observed for grain yield/plot (kg) followed by biological yield/plot (kg), spike length (cm), low to moderate estimates of PCV and GCV were observed for number of effective tillers/plant and spike weight (g), low estimates of GCV and PCV were observed for 1000 grains weight (g), peduncle length (cm), total number of spikelet's/spike, days to heading, days to maturity and plant height (cm). The moderate magnitude of genotypic coefficient of variation revealed the presence of high amount of genetic variability for the characters studied in the population and thus offers scope for genetic improvement through selection for these traits. High heritability coupled with high genetic advance as% of mean was observed for biological yield/plot (kg) and grain yield/plot (kg) indicates that there in presence of additive gene action and less influenced by environmental effect suggesting that selection of these traits accumulate more additive genes leading to further improvement in their performance. Similar results were observed by Bayisa and Letta., (2020) [3], Yadav *et al.*, (2020) [16], Malbhage *et al.*, (2020) [10], Kaur *et al.*, (2019) [7] and Kumar *et al.*, (2019) [9].

3.3 Correlation coefficient analysis

The correlation study revealed that grain yield/plot (kg) has positive association with days to heading, number of effective tillers/plant, spike length (cm), total number of spikelet's/spike, biological yield/plot (kg), harvest index (%) and 1000 grains weight. The study suggested that wheat grain yield can be enhanced by selecting genotypes that exhibit superior performance in the mentioned traits under timely sown irrigated conditions. Similar result were observed by Devesh *et al.*, (2021), Kumar *et al.*, (2022) [8] and Phougat *et al.*, (2017) observed grain yield/plot (kg) showed a significant positive correlation with the biological yield/plot (kg), plant height (cm), harvest index (%) and 1000 grains weight (g).

3.4 Path coefficient analysis

The path coefficient analysis between grain yield/plot (kg) and its related traits revealed biological yield/plot (kg), harvest index (%), plant height (c), and spike weight (g) showed positive direct effect. From the correlation and path coefficient analysis it is investigated that biological yield/plot (kg), number of effective tillers/plant, spike length (cm), days to heading, 1000 grains weight (g), total number of spikelet's/spike were most important traits which should be given proper emphasis during selection programmes for the improvement of grain yield in wheat genotypes under timely sown irrigated conditions. Similar results were observed by Kumar *et al.*, (2022) [8], Milkessa (2022) [11], Sahu *et al.*, (2021) [12] and Abdulhamed *et al.*, (2021) [1].

Table 2: Values of mean sum of squares of analysis of variance for yield and yield attributing traits in wheat genotypes.

S. No.	Traits	Mean sum of square (MSS)		
		Replication	**Genotype**	**Error**
	Degree of freedom (df)	**3**	**25**	**75**
1	Days to heading	3.369	9.2	6.249
2	Days to maturity	1.949	153.605**	8.622
3	Plant height (cm)	102.064	38.826**	10.651
4	Number of effective tillers/plant	0.308	1.525**	0.448
5	Spike length (cm)	1.682	2.966**	0.326
6	Spike weight (g)	0.139	0.256**	0.019
7	Total number of spikelet's/spike	2.885	1.995**	0.751
8	Peduncle length (cm)	73.599	13.243**	4.933
9	Biological yield/plot (kg)	0.186	5.907**	0.281
10	Grain yield/plot (kg)	0.049	1.104**	0.069
11	Harvest index (%)	4.247	52.943**	8.989
12	1000 grains weight (g)	1.551	69.854**	0.218

**Significant at 1% Probability level, *Significant at 5% Probability level
F table value - Replication (3, 75) = 4.05 at 1% and 2.72 at 5%
Genotype (3,75) = 2.03 at 1% and 1.65 at 5%

Table 3: Genetic parameters of variation for grain yield and its component in wheat genotypes.

S. No.	Characters	Mean	Range		CD at 5%	CV%	Coefficient of variance		h^2 (bs)	GA	GA as% of mean
			Min	Max			PCV	GCV			
1	Days to Heading	67.45	59.5	78	3.52	3.70	7.73	6.79	77.05	8.28	12.28
2	Days to Maturity	108.11	95.5	119.5	4.12	2.7	6.19	5.56	80.78	11.14	10.31
3	Plant height (cm)	70.55	60.5	75.75	4.60	4.62	5.96	3.76	39.80	3.45	4.88
4	No. of Effective Tillers/Plant	5.88	4.75	7.25	0.94	11.37	14.38	8.81	37.55	0.65	11.13
5	Spike Length (cm)	7.55	6.5	9.62	0.80	7.55	13.14	10.75	66.93	1.36	18.12
6	Spike Weight (g)	2.57	2.20	3.26	0.19	5.37	10.87	9.45	75.57	0.43	16.93
7	Total no. of spikelet's/spike	13.17	11.75	14.5	1.22	6.58	7.82	4.23	29.27	0.62	4.71
8	Peduncle Length (cm)	33.35	30.75	38	3.13	6.65	7.93	4.32	29.63	1.61	4.84
9	Biological yield/plot (kg)	6.98	5.37	9.82	0.74	7.58	18.60	16.98	83.36	2.23	31.94
10	Grain yield/plot (kg)	2.97	2.2	4.42	0.37	8.86	19.27	17.10	78.82	0.93	31.29
11	Harvest index (%)	42.77	36.51	51.18	4.23	7.00	10.45	7.75	55.00	5.06	11.84
12	1000 grains weight (g)	45.78	37.75	53.75	0.70	1.08	9.169	9.11	98.76	8.54	18.65

Table 4: Genotypic and phenotypic correlation matrix. (Above diagonal Phenotypic and below diagonal Genotypic)

Characters	DH	DM	PH	ETPP	SL	SW	SPS	PL	BYPP	HI	TW	GYPP
DH	1	0.669^{**}	0.182	0.157	0.163	0.192	0.026	-0.071	0.311**	-0.07	0.313^{**}	0.237*
DM	0.757^{**}	1	0.021	0.156	0.023	0.349^{**}	-0.178	0.045	0.174	-0.149	0.183	0.062
PH	0.208^{*}	0.152	1	0.158	0.116	0.063	0.309^{**}	0.327^{**}	0.154	-0.104	0.098	0.084
ETPP	0.387^{**}	0.259^{**}	0.4^{*}	1	0.516^{**}	0.139	0.011	0.041	0.594^{**}	0.287^{**}	0.18	0.739^{**}
SL	0.188	-0.006	0.038	0.598^{**}	1	0.273^{**}	0.1	0.039	0.704^{**}	0.12	0.235^{*}	0.766^{**}
SW	0.242^{*}	0.480^{**}	0.031	0.229^{*}	0.318^{**}	1	-0.045	0.028	0.106	0.044	-0.036	0.138
SPS	-0.203^{*}	-0.398^{**}	0.574^{**}	0.222^{*}	0.216^{*}	0.014	1	0.210^{*}	0.112	-0.008	-0.048	0.106
PL	0.025	0.238^{*}	0.470^{**}	0.125	0.033	0.122	0.444^{**}	1	0.112	-0.225^{*}	-0.073	-0.003
BYPP	0.345^{**}	0.187	0.128	0.831^{**}	0.765^{**}	0.102	0.089	0.132	1	-0.260^{**}	0.272^{**}	0.855^{**}
HI	-0.044	-0.235^{*}	0.007	0.056	-0.001	0.081	0.222^{*}	-0.281^{**}	-0.284^{**}	1	0.019	0.269^{**}
TW	0.355^{**}	0.200^{*}	0.171	0.294^{**}	0.285^{**}	-0.05	-0.069	-0.137	0.301^{**}	0.025	1	0.245*
GYPP	0.291^{**}	0.048	0.127	0.872^{**}	0.797^{**}	0.154	0.195^{*}	0.025	0.901^{**}	0.155	0.278^{**}	1

*Significant at 5% probability level, ** Significant at 1% probability level

Note: DH = Days to heading, DM = Days to maturity, PH = Plant height (cm), ETPP = Numbers of effective tillers/plant, SL = Spike length (cm), SW = Spike weight (g), TNSPS = Total number of spikelet's/spike, PL = Peduncle length (cm), BYPP = Biological yield/plot (kg), GYPP = Grain yield /plot (kg), HI = Harvest index (%), TW = Test weight (%)

Table 5: Genotypic path coefficient analysis showing direct effect (bold and diagonal values) and indirect effect (non-bold and off diagonal values).

	DH	DM	PH	ETPP	SL	SW	TNSPS	PL	BYPP	HI	TW	GYPP
DH	-0.065	-0.117	0.094	-0.303	-0.044	0.054	0.052	0.000	0.675	-0.033	-0.023	0.291^{**}
DM	-0.049	-0.154	0.069	-0.202	0.001	0.108	0.102	-0.003	0.366	-0.176	-0.013	0.048
PH	-0.014	-0.023	0.451	-0.377	-0.009	0.007	-0.147	-0.007	0.251	0.006	-0.011	0.127
ETPP	-0.025	-0.040	0.218	-0.781	-0.139	0.051	-0.057	-0.002	1.624	0.042	-0.019	0.872^{**}
SL	-0.012	0.001	0.017	-0.467	-0.233	0.071	-0.055	0.000	1.496	-0.001	-0.019	0.797^{**}
SW	-0.016	-0.074	0.014	-0.179	-0.074	0.224	-0.004	-0.002	0.200	0.061	0.003	0.154
TNSPS	0.013	0.061	0.259	-0.174	-0.050	0.003	-0.256	-0.006	0.174	0.166	0.005	0.195^{*}
PL	-0.002	-0.037	0.212	-0.097	-0.008	0.027	-0.114	-0.014	0.258	-0.210	0.009	0.025
BYPP	-0.022	-0.029	0.058	-0.649	-0.178	0.023	-0.023	-0.002	1.955	-0.212	-0.020	0.901^{**}
HI	0.003	0.036	0.003	-0.044	0.000	0.018	-0.057	0.004	-0.555	0.748	-0.002	0.155
TW	-0.023	-0.031	0.077	-0.230	-0.066	-0.011	0.018	0.002	0.589	0.019	-0.066	0.278^{**}

*Significant at 5% probability level, ** Significant at 1% probability level
Residual effect: 0.006

Note: DH = Days to heading, DM = Days to maturity, PH = Plant height (cm), ETPP = Numbers of effective tillers/plant, SL = Spike length (cm), SW = Spike weight (g), TNSPS = Total number of spikelet's/spike, PL= Peduncle length (cm), BYPP = Biological yield/plot (kg), GYPP = Grain yield /plot (kg), HI = Harvest index (%), TW = Test weight (%)

Table 6: Phenotypic path coefficient analysis showing direct effect (bold and diagonal values) and indirect effect (non-bold and off diagonal values)

	DH	DM	PH	ETPP	SL	SW	SPS	PL	BYPP	HI	TW	rxy
DH	-0.012	-0.020	-0.002	0.000	0.000	0.004	0.000	0.000	0.313	-0.037	-0.009	0.237^{*}
DM	-0.008	-0.030	0.000	0.000	0.000	0.007	0.001	0.000	0.176	-0.078	-0.005	0.062
PH	-0.002	-0.001	-0.012	0.000	0.000	0.001	-0.002	0.002	0.155	-0.054	-0.003	0.084
ETPP	-0.002	-0.005	-0.002	0.001	0.000	0.003	0.000	0.000	0.598	0.151	-0.005	0.739^{**}
SL	-0.002	-0.001	-0.001	0.000	0.000	0.005	-0.001	0.000	0.709	0.063	-0.007	0.766^{**}
SW	-0.002	-0.010	-0.001	0.000	0.000	0.019	0.000	0.000	0.107	0.023	0.001	0.138
SPS	0.000	0.005	-0.004	0.000	0.000	-0.001	-0.006	0.001	0.113	-0.004	0.001	0.106
PL	0.001	-0.001	-0.004	0.000	0.000	0.001	-0.001	0.005	0.113	-0.118	0.002	-0.003
BYPP	-0.004	-0.005	-0.002	0.000	0.000	0.002	-0.001	0.001	1.008	-0.137	-0.008	0.855^{**}
HI	0.001	0.004	0.001	0.000	0.000	0.001	0.000	-0.001	-0.262	0.526	-0.001	0.269^{**}
TW	-0.004	-0.005	-0.001	0.000	0.000	-0.001	0.000	0.000	0.274	0.010	-0.028	0.245^{*}

*Significant at 5% probability level, ** Significant at 1% probability level Residual effect: 0.007

NOTE - DH = Days to heading, DM = Days to maturity, PH = Plant height (cm), ETPP = Numbers of effective tillers/plant, SL = Spike length (cm), SW = Spike weight (g), TNSPS = Total number of spikelet's/spike, PL= Peduncle length (cm), BYPP = Biological yield/plot (kg), GYPP = Grain yield /plot (kg), HI = Harvest index (%), TW = Test weight (%)

4. Conclusions

The analysis of variance revealed highly significant differences among the genotypes for all studied traits, indicating the presence of substantial variability at the 1% level. This suggests ample scope for selecting promising genotypes for further yield improvement. Moderate estimates of GCV and PCV were recorded for grain yield, highlighting considerable genetic variability within the population and providing opportunities for genetic enhancement through selection. High heritability coupled with high genetic advance as a percentage of mean was observed for biological yield per plot (kg) and grain yield per plot (kg), suggesting predominance of additive gene action with minimal environmental influence. This indicates that selection for these traits would facilitate the accumulation of favorable alleles, leading to significant genetic improvement. Correlation analysis showed that grain yield per plot (kg) was positively associated with days to heading, number of effective tillers per plant, spike length (cm), total spikelet's per spike, biological yield per plot (kg), harvest index (%), and 1000-grain weight. This suggests that selection for these traits could enhance grain yield under timely sown irrigated conditions. Path coefficient analysis further confirmed that biological yield per plot (kg), harvest index (%), plant height (cm), and spike weight (g) exerted positive direct effects on grain yield, supported by favorable indirect contributions through other yield components. Based on mean performance for grain yield and related traits, the genotypes HI8853(d), MACS4146(d), and HI8854(d) were found significantly superior to the checks HI8713(d), GW322, HI8737(d), and MACS6768. These promising genotypes should therefore be advanced for subsequent screening trials to evaluate their potential in breeding programs.

5. Acknowledgement

The authors are sincerely grateful to the Department of Genetics and Plant Breeding, BTC College of Agriculture and Research Station, Indira Gandhi Krishi Vishwavidyalaya, Bilaspur (C.G.), for providing the necessary facilities and support to carry out this research work. The first author extends heartfelt thanks to her major advisor and co-advisors for their valuable guidance, encouragement, and constructive suggestions throughout the study. Special gratitude is also expressed to the technical and field staff of the experimental farm for their assistance during field trials. The cooperation and support of fellow researchers and colleagues are also deeply acknowledged.

6. Future Scope

1. Validation of the identified superior genotypes under multilocational trials to assess their stability and adaptability across diverse environments.
2. Incorporation of promising genotypes into hybridization programs to develop high-yielding, climate-resilient cultivars.
3. Integration of molecular tools such as marker-assisted selection (MAS) to further dissect genetic variability and trait associations.
4. Exploration of genotype × environment interactions to

identify wheat lines suited for specific agro-climatic zones under timely sown irrigated conditions.

5. Extension of association analysis to include physiological and biochemical traits for a holistic approach to wheat improvement.

7. Conflict of Study

The authors declare no conflict of interest regarding the publication of this research work.

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