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Genetic association analysis for yield and its attributes in *Bread* wheat (*Triticum aestivum* L.) germplasm

Ravikant Soni, Dr. Animesh Chatterjee, Dr. Vinod Kumar, Deepak Khande and Monika Singh

Abstract
The genetic analysis for crop improvement programme is a prerequisite for the breeding programme. The purpose of this study was to determine the extent and direction of association between yield and yield attributes. An analysis of yield determinants in 50 wheat genotypes under randomized block design was conducted twice at the Powarkheda Research Farm, Zonal Agriculture Research Station, Narmadapuram, Madhya Pradesh during *Rabi* 2019-20 and 2020-21. Studying the association between yield and yield-contributing characteristics at the phenotypic level revealed that grain yield/plot was positively and significantly associated with biological yield, harvest index, and test weight. Path co-efficient and regression analysis revealed that biological yield, harvest index, flag leaf area, number of grains/spike, days to heading and number of tillers/plant proved to be the major direct components of yield.

Keywords: Genetic association, path coefficient, direct and indirect effect, yield, bread wheat

Introduction
Bread Wheat (*Triticum aestivum* L.) is a cereal herb in the *Poaceae* family, genus *Triticum*. Its origin is alleged to be South West Asia near East Region (Smith and Wayne, 1995) [19]. Wheat is known as the 'King of Cereals' in the Middle East. It is believed that it originated in the Fertile Crescent and spread across all continents. It is undeniable that wheat is one of the most widely grown and consumed cereal crops in the world, both in terms of acreage and adaptability to many agroclimatic and crop-growing conditions. In addition to providing energy, wheat grains also provide the body with about 8, 20% of the protein it needs. (Shehzad *et al*., 2014) [18]. There are a variety of climate conditions in which bread wheat is grown from mild, humid to dry, cold and from areas with high rainfall to dry, irrigated areas. This nutri-rich cereal has been under cultivation in 270.8 million hectares during 2021-22, in which wheat is grown in 222.21 million hectares of area and annual production of wheat is estimated at 779.03 million tons (Anonymous, 2022) [3]. The cultivation of wheat in Central India is unique, with the species cultivated there being *Triticum aestivum*, which is grown in a hot tropical climate characteristic of high temperatures at the time of maturity. Many crop improvement programmes also aimed at improving other characteristics along with yield, which are interconnected with yield. As a result, studying the correlation between traits that affect yield can aid in the selection of traits that are linked to yield. A correlation study along with a path analysis gives a better understanding of how different characters interact with grain yield. Breeders should focus on producing productive wheat types by crossing high-yielding lines and selecting transgressive sergeants from the resulting hybrids. Correlation coefficients give insight into the concept of quality activity, which in turn provides insight into whether single plant selection is sufficient. Through the use of appropriate measures for selection, the correlation coefficient and path coefficient analysis may enhance the reproductive effectiveness of the programme. Correlation coefficient analysis evaluates the combination of varieties of plant characters. A genetic selection strategy and further enhanced production strategy are further developed based on the element traits identified. In order to identify performance levels and directions, associations with traits and interactions between traits were identified. The current research was conducted to investigate correlations and path coefficients between yield attribution variables and qualitative traits in bread wheat.

Materials and Methods

The present investigation was carried out in the experimental fields of the Zonal Agriculture Research Station, Powarkheda, Narmadapuram, Madhya Pradesh during *Rabi* season of 2019-20 & 2020-21 with 50 wheat accessions of indigenous and exotic origin (*Triticum aestivum* L. em. Thell) representing a country wide collection from several parts of India. The experiment was laid in completely randomized block design replicated twice. Each genotype was accommodated in a double row plot of 2m length with row to row and plant to plant spacing of 23 and 5 cm, respectively. The sowing was done on 24th December 2019, 26th November 2020 and 24th December 2020 by dibbling the seeds in rows. The experiment was conducted under irrigated and high fertility conditions.

The observations were recorded on five randomly selected plants of each genotype under each replication and per plant data were obtained by averaging the values.

A. **Pre-harvest observations:** days to heading, days to maturity, flag leaf length, flag leaf width, flag leaf area, canopy temperature at vegetative stage, canopy temperature at flowering stage, chlorophyll content (SPAD).
B. **Post-harvest observations:** awns length (cm), spike length (cm), peduncle length, biological yield, grain yield/plot (g), harvest index, number of spikelets/spike, number of grains/spike, test weight (cm), tillers/plant, paniculated leaf distance (cm), plant height (cm).

Statistical analysis

The estimated correlation coefficients were compared with the table values (Fisher and Yates, 1957) [12] at n-2 degrees of freedom at 5% and 1% levels of significance, with in being the sample size on which the correlation is based. Path analysis was conducted in accordance with Dewy and Lu (1959) [9] and Ramanujam and Rai (1963) [17] to assess direct and indirect influences on grain yield/plot. The regression analysis was carried out as per the procedures described by Gomez and Gomez (1984) [13] for assessing the effect of independent variables on the dependent variable.

Table 1: Analysis of variance of 18 bread wheat genotypes of yield and its attributes traits in bread wheat

Trait	DF	X_1	X_2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X14	X15	X16	X17	X18	X19	X20	X13
Rep.	1	0.48	1.08	0.35	0.01	0.54	25.34	0.29	188.07	8.43	24.54	40.49	2160.08	1.58	1.61	138.72	2.61	0.08	2.39	0.37	71.05
Geno.	49	74.94	2203.52	5.81	13.55	88.41**	56.05**	0.84**	290.12**	6.02**	7.72**	76.99**	93454.79**	39.33**	27.52**	245.42**	105.43**	4.40**	65.15**	780.88**	15510.36**
Error	245	1.70	1.74	0.39	0.09	1.24	1.93	0.03	12.17	0.47	1.73	8.05	4784.98	6.13	4.15	9.05	3.08	0.28	1.46	8.07	928.33

X_1-Days to heading, X_2-Days to maturity, X_3-Awns length (cm), X_4-Spike length, X_5-Peduncle length (cm), X_6-Flag leaf length, X_7-Flag leaf width, X_8-Flag leaf area, X_9-Canopy temperature at vegetative stage (°C), X_{10}-Canopy temperature at flowering stage (°C), X_{11}-Chlorophyll content (SPAD), X_{12}-Biological yield (g), X_{13}-Grain yield/plot (g), X_{14}-Harvest index, X_{15}-Number of spikelets/spike, X_{16}-Number of grains/spike, X_{17}-Test weight (g), X_{18}-Tillers/plant, X_{19}-Peniculated leaf distance (cm), X_{20}-Plant height (cm).

Table 2: Genotypic and phenotypic co-efficient of correlations for yield and its attributing traits in bread wheat

Traits	(X_1)	(X_2)	(X_3)	(X_4)	(X_5)	(X_6)	(X_7)	(X_8)	(X_9)	(X_{10})	(X_{11})	(X_{12})	(X_{14})	(X_{15})	(X_{16})	(X_{17})	(X_{18})	(X_{19})	(X_{20})	(X_{13})
(X1)	1.000	-0.041	0.043	0.034	-0.236**	0.175*	0.108	0.190**	0.298**	0.085	-0.027	0.116*	0.027	-0.010	0.304**	0.003	-0.122*	-0.011	-0.289	0.123*
(X2)		1.000	-0.061	0.358**	0.208**	-0.023	0.136*	0.087	-0.138*	-0.176*	0.121*	-0.321**	-0.128*	0.045	0.019	-0.132*	-0.018	0.102	0.352**	-0.359**
(X3)			1.000	-0.094	-0.322**	-0.116*	0.044	-0.013	0.098	-0.001	-0.069	0.207**	-0.083	-0.152*	0.061	0.061	0.140*	0.186*	0.170*	0.131*
(X4)				1.000	0.266**	0.222**	0.525**	0.527**	0.067	-0.064	-0.133*	-0.203**	-0.023	0.062	-0.092	0.050	-0.088	0.036	-0.005	-0.189*
(X5)					1.000	0.009	0.129*	0.074	-0.215**	-0.082	0.029	-0.097	0.046	0.094	-0.051	-0.011	0.002	-0.060	0.187*	-0.052
(X6)						1.000	0.240**	0.660**	0.268**	0.053	0.074	-0.023	0.037	0.158*	0.265**	0.027	0.019	0.119*	-0.078	-0.001
(X7)							1.000	0.880**	0.232**	0.022	-0.125*	-0.017	0.051	-0.040	0.099	0.057	-0.156*	-0.094	-0.170*	0.013
(X8)								1.000	0.323**	0.051	-0.075	-0.023	0.056	0.040	0.193**	0.052	-0.113	0.002	-0.169*	0.010
(X9)									1.000	0.115*	0.125*	0.045	0.145*	-0.007	0.202**	0.032	-0.155*	-0.135*	-0.273**	0.114*
(X10)										1.000	-0.224**	0.153*	0.038	0.025	-0.152*	-0.056	0.026	-0.050	-0.060	0.155*
(X11)											1.000	-0.215**	0.090	-0.031	0.206**	-0.060	-0.080	-0.022	0.095	-0.144*
(X12)												1.000	0.006	0.030	0.084	0.216**	0.040	0.083	0.056	0.866**
(X14)													1.000	0.141*	0.013	0.269**	-0.053	-0.171*	-0.244**	0.496**
(X15)														1.000	0.116*	0.094	-0.224**	0.044	0.080	0.089
(X16)															1.000	0.014	-0.315**	-0.036	-0.060	0.088
(X17)																1.000	0.165*	0.086	-0.113	0.311**
(X18)																	1.000	0.377**	0.120*	0.009
(X19)																		1.000	0.481**	-0.019
(X20)																			1.000	-0.087

*Significant of 5% level of significance. **Significant of 1% level of significance.

X_1-Days to heading, X_2-Days to maturity, X_3-Awns length (cm), X_4-Spike length, X_5-Peduncle length (cm), X_6-Flag leaf length, X_7-Flag leaf width, X_8-Flag leaf area, X_9-Canopy temperature at vegetative stage (°C), X_{10}-Canopy temperature at flowering stage (°C), X_{11}-Chlorophyll content (SPAD), X_{12}-Biological yield (g), X_{13}-Grain yield/plot (g), X_{14}-Harvest index, X_{15}-Number of spikelets/spike, X_{16}-Number of grains/spike, X_{17}-Test weight (g), X_{18}-Tillers/plant, X_{19}-Peniculated leaf distance (cm), X_{20}-Plant height (cm).

Results and Discussion

Analysis of variance and performance of genotypes

All characters showed highly significant differences between genotypes based on mean sum squares. The co-efficient of variation (CV) ranged from 1.4 (days to maturity) to 12.9% (number of spikelets/spike) in Table No. 1.

Correlation analysis

The present investigation of association among grain yield and yield contributing characters at phenotypic level revealed that grain yield/plot was positively and significantly associated with biological yield, harvest index and test weight, while days to maturity showed significant negative association giving a possibility to select early maturity genotypes with high grain yield/plot. Most of the characters showed similar relationships among themselves at the genotypic level also Table-2. In the present investigation, positive correlation coefficient between any two traits suggested that they can be improved simultaneously and improvement in one will automatically improve the other. However, such simultaneous improvement is not possible for those correlated traits, which exhibited significant association in negative direction. Therefore, such traits could be improved using indirect selection methods such as independent culling levels, etc. Kumar *et al.* (2022) and Singh M. (2022) [20] for biological yield and harvest index. Thus, based on association analysis this investigation could only suggest that the yield in bread wheat could conceivably be improved by increasing awn length, canopy temperature at vegetative stage, canopy temperature at flowering stage and test weight.

Path coefficient and regression analysis

In the present study, path coefficient analysis is conducted at genotypic and phenotypic levels with grain yield/plot as dependent variable. In general, genotypic, direct and indirect effects were slightly higher in magnitude as compared to phenotypic effects and it have been presented in table-3. Most of the characters had shown similar relationships among themselves at the phenotypic level also Table-3 & 4.

Path coefficient analysis revealed that the maximum amount of positive direct effect on grain yield/plot (dependable variable) was used by flag leaf area, biological yield, harvest index, number of grains/spike, days to heading and number of tillers/plant, whereas, number of spikelets/spike followed by flag leaf width, awns length, flag leaf length, days to maturity and test weight exhibited direct effect in a negative direction. These results agreed with the findings of Phougat *et al.* (2017) [16] for days to heading, harvest index, biological yield and number of tillers/plant and Ali *et al.* (2016) [1] for biological yield and Kumar and Payasi (2016) for days to heading, number of grains/spike, tillers/plant and test weight and Kumar *et al.* (2022) for biological yield, harvest index, number of grains/spike, days to maturity and test weight.

Present investigation revealed that grain yield was positively correlated with biological yield, harvest index and test weight. However, path analysis strongly pointed out the role of biological yield and harvest index in the determination of grain yield/plot. Hence, more weightage should be given to these traits while working out selection. Thus, results of path analysis suggested that while aiming at the improvement in grain yield, more weightage should be given to biological yield, harvest index, flag leaf area, number of grains/spike, days to heading and number of tillers/plant during selection for developing high-yielding genotypes in bread wheat. Based on correlation and path studies it was observed that biological yield, harvest index and test weight could be used as significant selection traits in order of merit to expand crop efficiency.

Table 3: Direct and indirect effects of yield contributing characters on grain yield/plot at genotypic level in *bread* wheat

Traits	(X_1)	(X_2)	(X_3)	(X_4)	(X_5)	(X_6)	(X_7)	(X_8)	(X_9)	(X_{10})	(X_{11})	(X_{12})	(X_{14})	(X_{15})	(X_{16})	(X_{17})	(X_{18})	(X_{19})	(X_{20})	(X_{13})
(X1)	0.011	0.002	0.000	0.000	-0.004	0.002	0.002	-0.005	-0.001	0.000	0.001	0.129	0.010	0.000	0.006	0.000	-0.002	0.000	0.002	0.154*
(X2)	-0.001	-0.027	0.001	0.002	0.003	0.000	0.002	-0.002	0.000	-0.001	-0.001	-0.323	-0.075	-0.001	0.000	0.002	0.000	0.000	-0.003	-0.423**
(X3)	0.001	0.002	-0.007	-0.001	-0.006	-0.001	0.001	0.000	0.000	0.000	0.001	0.259	-0.056	0.002	0.001	-0.001	0.002	0.000	-0.002	0.195**
(X4)	0.000	-0.010	0.001	0.006	0.004	0.002	0.008	-0.013	0.000	0.000	0.002	-0.208	-0.014	-0.001	-0.002	-0.001	-0.001	0.000	0.000	-0.226**
(X5)	-0.003	-0.006	0.003	0.002	0.014	0.000	0.002	-0.002	0.001	0.000	0.000	-0.095	0.024	-0.001	-0.001	0.000	0.000	0.000	-0.001	-0.065
(X6)	0.002	0.001	0.001	0.001	0.000	0.009	0.003	-0.015	-0.001	0.000	-0.001	0.012	0.003	-0.002	0.005	0.000	0.000	0.000	0.001	0.020
(X7)	0.001	-0.004	0.000	0.004	0.002	0.002	0.014	-0.019	-0.001	0.000	0.002	-0.024	0.034	0.000	0.002	-0.001	-0.002	0.000	0.001	0.011
(X8)	0.003	-0.003	0.000	0.004	0.001	0.006	0.012	-0.022	-0.001	0.000	0.001	-0.010	0.023	-0.001	0.004	-0.001	-0.001	0.000	0.001	0.017
(X9)	0.005	0.004	-0.001	0.000	-0.004	0.003	0.004	-0.009	-0.002	0.000	-0.002	0.034	0.084	0.000	0.003	0.000	-0.002	0.000	0.002	0.122*
(X10)	0.002	0.008	-0.001	-0.001	-0.002	0.001	0.001	-0.002	0.000	0.002	0.005	0.291	0.013	-0.001	-0.005	0.001	0.001	0.000	0.001	0.315**
(X11)	-0.001	-0.004	0.001	-0.001	0.000	0.001	-0.002	0.002	0.000	-0.001	-0.009	-0.288	0.064	0.001	0.004	0.002	-0.001	0.000	-0.001	-0.235**
(X12)	0.002	0.010	-0.002	-0.001	-0.002	0.000	0.000	0.000	0.000	0.001	0.003	0.874	0.037	-0.001	0.002	-0.004	0.000	0.000	0.000	0.918**
(X14)	0.000	0.005	0.001	0.000	0.001	0.000	0.001	-0.001	-0.001	0.000	-0.001	0.082	0.397	-0.002	0.000	-0.007	0.000	0.001	0.003	0.478**
(X15)	0.000	-0.002	0.002	0.001	0.002	0.002	-0.001	-0.002	0.000	0.000	0.001	0.081	0.074	-0.009	0.003	-0.002	-0.002	0.000	-0.001	0.147*
(X16)	0.004	-0.001	-0.001	-0.001	-0.001	0.003	0.002	-0.006	-0.001	-0.001	-0.003	0.105	-0.007	-0.002	0.016	0.000	-0.004	0.000	0.000	0.106
(X17)	0.000	0.004	0.000	0.000	0.000	0.000	0.001	-0.001	0.000	0.000	0.001	0.236	0.171	-0.001	0.000	-0.015	0.002	0.000	0.001	0.397**
(X18)	-0.002	0.001	-0.001	-0.001	0.000	0.000	-0.003	0.003	0.000	0.000	0.001	0.047	-0.011	0.003	-0.007	-0.003	0.009	-0.001	-0.001	0.035
(X19)	0.000	-0.003	-0.002	0.000	-0.001	0.001	-0.001	0.000	0.000	0.000	0.000	0.089	-0.103	-0.001	-0.001	-0.001	0.004	-0.002	-0.004	-0.023
(X20)	-0.004	-0.010	-0.002	0.000	0.003	-0.001	-0.003	0.004	0.001	0.000	-0.001	0.035	-0.149	-0.001	-0.001	0.002	0.001	-0.001	-0.007	-0.132*

Residual Effect = 0.01.

Table 4: Direct and indirect effects of yield contributing characters on grain yield/plot at phenotypic level in bread wheat

Traits	(X_1)	(X_2)	(X_3)	(X_4)	(X_5)	(X_6)	(X_7)	(X_8)	(X_9)	(X_{10})	(X_{11})	(X_{12})	(X_{14})	(X_{15})	(X_{16})	(X_{17})	(X_{18})	(X_{19})	(X_{20})	(X_{13})
(X1)	0.008	0.001	0.000	0.000	-0.004	0.000	0.001	-0.002	0.000	0.000	0.000	0.100	0.013	0.000	0.004	0.000	-0.001	0.000	0.002	0.123*
(X2)	0.000	-0.024	0.000	0.002	0.003	0.000	0.001	-0.001	0.000	0.000	0.000	-0.276	-0.062	0.000	0.000	0.001	0.000	0.000	-0.003	-0.359**
(X3)	0.000	0.001	-0.004	0.000	-0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.178	-0.041	0.000	0.001	-0.001	0.001	0.000	-0.001	0.131*
(X4)	0.000	-0.008	0.000	0.005	0.004	0.000	0.005	-0.006	0.000	0.000	0.000	-0.175	-0.011	0.000	-0.001	-0.001	-0.001	0.000	0.000	-0.189*
(X5)	-0.002	-0.005	0.001	0.001	0.016	0.000	0.001	-0.001	0.000	0.000	0.000	-0.083	0.023	0.000	-0.001	0.000	0.000	0.000	-0.002	-0.052
(X6)	0.001	0.001	0.000	0.001	0.000	-0.002	0.002	-0.007	0.000	0.000	0.000	-0.020	0.018	0.000	0.004	0.000	0.000	0.000	0.001	-0.001
(X7)	0.001	-0.003	0.000	0.002	0.002	0.000	0.010	-0.010	0.000	0.000	0.000	-0.015	0.025	0.000	0.001	-0.001	-0.001	0.000	0.001	0.013
(X8)	0.002	-0.002	0.000	0.002	0.001	-0.001	0.009	-0.011	0.000	0.000	0.000	-0.020	0.027	0.000	0.003	-0.001	-0.001	0.000	0.001	0.010
(X9)	0.003	0.003	0.000	0.000	-0.003	-0.001	0.002	-0.004	0.001	0.000	0.000	0.038	0.071	0.000	0.003	0.000	-0.001	0.000	0.002	0.114*
(X10)	0.001	0.004	0.000	0.000	-0.001	0.000	0.000	-0.001	0.000	0.003	0.000	0.131	0.019	0.000	-0.002	0.001	0.000	0.000	0.001	0.155*
(X11)	0.000	-0.003	0.000	-0.001	0.000	0.000	-0.001	0.001	0.000	-0.001	-0.001	-0.185	0.044	0.000	0.003	0.001	-0.001	0.000	-0.001	-0.144*
(X12)	0.001	0.008	-0.001	-0.001	-0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.859	0.003	0.000	0.001	-0.002	0.000	0.000	0.000	0.866**
(X14)	0.000	0.003	0.000	0.000	0.001	0.000	0.001	-0.001	0.000	0.000	0.000	0.005	0.488	0.000	0.000	-0.003	0.000	0.000	0.002	0.496**

(X15)	0.000	-0.001	0.001	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.069	-0.003	0.002	-0.001	-0.002	0.000	-0.001	0.089
(X16)	0.003	0.000	0.000	0.000	-0.001	-0.001	0.001	-0.002	0.000	0.000	0.000	0.072	0.006	0.000	0.013	0.000	-0.003	0.000	0.001	0.088
(X17)	0.000	0.003	0.000	0.000	0.000	0.000	0.001	-0.001	0.000	0.000	0.000	0.186	0.131	0.000	0.000	-0.011	0.001	0.000	0.001	0.311**
(X18)	-0.001	0.000	-0.001	0.000	0.000	0.000	-0.002	0.001	0.000	0.000	0.000	0.034	-0.026	0.001	-0.004	-0.002	0.008	0.000	-0.001	0.009
(X19)	0.000	-0.002	-0.001	0.000	-0.001	0.000	-0.001	0.000	0.000	0.000	0.000	0.071	-0.084	0.000	0.000	-0.001	0.003	0.001	-0.004	-0.019
(X20)	-0.002	-0.008	-0.001	0.000	0.003	0.000	-0.002	0.002	0.000	0.000	0.000	0.048	-0.119	0.000	-0.001	0.001	0.001	0.001	-0.009	-0.087

Residual Effect = 0.088.

The study on association analysis suggested that the yield in bread wheat could possibly be improved by increasing biological yield, harvest index and test weight. Path coefficient analysis revealed that the maximum amount of positive direct effect on grain yield per plot (dependable variable) was exerted by biological yield, harvest index, flag leaf area, number of grains/spike, days to heading and number of tillers/plant. Biological yield, harvest index and test weight should be used as the selection parameters to enhance grain yield in bread wheat as they possessed a high association with grain yield/plot. These traits can be directly and easily selected in a breeding program and appears to be valuable of further consideration as a selection criterion by bread wheat breeders.

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