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Radhika Rajesh Khandekar
P.G. Scholar, Department of
Genetics and Plant Breeding,
GHRU, Saikheda, Madhya
Pradesh, India

Deepak Sapkal
Associate Professor,
Department of Genetics and
Plant Breeding, GHRU,
Saikheda, Madhya Pradesh,
India

Corresponding Author:
Radhika Rajesh Khandekar
P.G. Scholar, Department of
Genetics and Plant Breeding,
GHRU, Saikheda, Madhya
Pradesh, India

Genetic variability and trait association in diverse genotypes of bread wheat (*Triticum aestivum* L.) under field conditions

Radhika Rajesh Khandekar and Deepak Sapkal

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Abstract

The present investigation was conducted to assess genetic variability and trait association among 17 bread wheat (*Triticum aestivum* L.) genotypes under field conditions during the rabi season of 2025–26 at G. H. Raisoni University, Saikheda, Madhya Pradesh. The experiment was laid out in a Randomized Block Design with three replications, and eleven quantitative traits related to yield and its components were evaluated. Significant genotypic differences were observed for all the traits, indicating substantial genetic variability among the genotypes. High heritability along with high genetic advance as percentage of mean was recorded for biological yield per plant and grain yield per plant, suggesting the predominance of additive gene action and good scope for selection. Grain yield showed a strong positive association with biological yield at both genotypic (0.8121) and phenotypic (0.7513) levels. Path analysis identified 1000-seed weight and biological yield per plant as important direct contributors to grain yield. Overall, biological yield, 1000-seed weight and harvest index were identified as important selection criteria for improving grain yield in bread wheat under the agro-climatic conditions of the Satpura Plateau region of Madhya Pradesh.

Keywords: Genetic Variability, Heritability, Genetic Advance, GCV, PCV, Correlation Coefficient, Path Coefficient Analysis

Introduction

Wheat (*Triticum aestivum* L.) stands as the undisputed "King of Cereals" owing to the vast acreage devoted to its cultivation, its high nutritive value, and its central role in the food and economic systems of the world. It is cultivated across a broader range of environments than any other cereal crop, spanning tropical lowlands to temperate highlands, and from sea level to elevations as high as 3,300 meters above mean sea level. Wheat provides sustenance to approximately 40 per cent of the global population, contributing nearly 20 per cent of the total dietary caloric intake worldwide Bhutto *et al.*, 2016 ^[1]. The crop is grown as a staple food in more than 40 countries and is cultivated on approximately 222.21 million hectares globally, yielding an all-time record production of 779.03 million tonnes during 2021-22, reflecting the enormous significance of this crop in ensuring global food and nutritional security Anonymous, 2022 ^[2]. Botanically, wheat belongs to the genus *Triticum* of the family Poaceae, with its centre of origin traced to the Middle East region of Asia Lupton, 1987 ^[3]. Bread wheat (*Triticum aestivum* L.), an allohexaploid ($2n = 6x = 42$, genome AABBDD), is the most widely cultivated species and belongs to the tribe *Triticeae* within the family Poaceae. Genomic and cytogenetic investigations have established that hexaploid bread wheat originated through natural hybridization between *Triticum turgidum* L. (tetraploid; AABB) and the wild diploid grass *Triticum tauschii*, followed by spontaneous chromosome doubling Bayisha *et al.*, 2020 ^[4]. In India, three commercial wheat species are recognized: *Triticum aestivum* (bread wheat, hexaploid, $2n = 42$), *Triticum durum* (macaroni wheat, tetraploid, $2n = 28$), and *Triticum dicoccum* (emmer wheat, tetraploid, $2n = 28$), of which bread wheat occupies the major share of the cultivated area across all wheat-growing regions of the country Das, 2008 ^[5]. Wheat is essentially a rabi (winter season) crop in India, requiring cool and moist conditions during the vegetative and reproductive phases, followed by dry and warm weather for proper grain ripening.

The optimum temperature for seed germination ranges between 20–25°C, although germination can occur within a broader range of 3.5 to 35°C Das, 2008 ^[5]. High atmospheric temperatures exceeding 25°C during the critical grain-filling stage are particularly detrimental to grain weight and overall productivity, as excessive transpiration reduces residual energy available for grain formation. The crop is equally sensitive to terminal heat stress during heading and anthesis. On the other hand, cloudy weather with high humidity and low temperatures tends to favour the incidence and spread of rusts and other foliar diseases, thereby undermining yield stability.

Beyond its caloric contribution, wheat is a nutritionally complex cereal offering an impressive array of proteins, minerals, dietary fibre, and vitamins. The protein content of wheat, particularly its gluten-forming proteins — gliadin and glutenin — imparts unique viscoelastic properties to dough, enabling the production of leavened bread, a characteristic absent in other major cereals. The amino acid yield per acre from wheat surpasses that of many animal protein sources for several essential amino acids. Whole grain wheat flour is particularly rich in B-vitamins, iron, zinc, and dietary fibre. These properties make wheat the preferred raw material for a wide range of human food products including chapattis, bread, biscuits, pasta, cakes, and breakfast cereals, positioning it as an irreplaceable crop in global food systems Kaur *et al.*, 2019 ^[6].

India occupies the second position among the leading wheat-producing nations of the world, next only to China, reflecting its remarkable agricultural capacity and diverse agro-ecological suitability for wheat cultivation Sharma and Sendhil, 2016 ^[7]. The major wheat-growing states of India include Uttar Pradesh, Punjab, Madhya Pradesh, Haryana, Rajasthan, Bihar, Maharashtra, Gujarat, Karnataka, and West Bengal. During 2021-22, wheat was cultivated on 30.54 million hectares with a total production of 106.84 million tonnes and a productivity of 3,484 kg/ha Anonymous, 2022 ^[2]. In the 2024-25 crop year, national wheat production reached 117.94 million tonnes, and this has been surpassed further in 2025-26, with the Ministry of Agriculture and Farmers Welfare estimating an all-time record production of 120.65 million tonnes — approximately 2.71 million tonnes higher than the previous year — from a sown area of 33.4 million hectares Ministry of Agriculture and Farmers Welfare [MoAFW], 2026 ^[8]. This remarkable achievement was attributed to an increase in cultivated area by 0.6 million hectares, timely sowing practices, and accelerated adoption of high-yielding and climate-resilient varieties through an enhanced varietal replacement rate MoAFW, 2026 ^[8]. India's target of producing 140 million tonnes of wheat by 2050 to meet the nutritional demands of its expanding population underlines the urgency of sustained yield improvement through genetic and agronomic means Anonymous, 2015 ^[9].

Madhya Pradesh, the second largest state in India by geographical area, is endowed with 11 diverse agro-ecological zones that support a wide range of cropping systems. The state occupies the second position in national food grain production, contributing approximately 12 per cent of the country's total food grain output Government of Madhya Pradesh, 2023 ^[10]. Wheat is one of the principal rabi crops of the state, cultivated predominantly in the Satpura Plateau, Bundelkhand, Gird, Vindhya Plateau, and Central Narmada Valley agro-climatic zones, where a

wheat-jowar or rice-wheat cropping pattern is commonly followed. The Satpura Plateau zone, which administratively encompasses districts such as Betul, Chhindwara, and Pandhurna, represents an important wheat-growing belt where improving varietal performance under field conditions has significant implications for regional food security Government of Madhya Pradesh, 2023 ^[10]. Notably, during 2025-26, Madhya Pradesh revised its wheat procurement target upward from 78 lakh tonnes to 100 lakh tonnes in recognition of its above-average production, reflecting the state's growing contribution to national wheat production MoAFW, 2026 ^[8]. The present investigation was conducted at G. H. Rasoni University, Dhoda Borgaon, Village-Saikheda, Tahsil Sausar, District Pandhurna (M.P.), which falls within this agro-climatically diverse Satpura Plateau zone. The field conditions and subtropical climate of this region, characterized by distinct rabi seasons with adequate winter chilling, make it an ideal location for evaluating the genetic potential of diverse bread wheat genotypes under actual field environments.

Genetic improvement of crop yield is an intricate and continuous process that fundamentally depends on the nature and extent of genetic variability present in the breeding material. The success of any plant breeding programme is contingent upon the identification of superior genotypes possessing desirable levels of variability and transmissibility for economically important traits. Variability studies that estimate genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (h^2), and genetic advance as per cent of mean (GAM) provide a comprehensive understanding of the existing genetic architecture within a population and serve as indispensable guides for formulating effective selection strategies Mary and Gopalan, 2006 ^[11]. High heritability coupled with high genetic advance is particularly indicative of additive gene action, thereby favouring directional selection. Grain yield in wheat is a highly complex polygenic trait that is influenced by numerous component characters, each contributing directly or indirectly to the final yield. Understanding the nature and magnitude of associations between yield and its component traits through genotypic and phenotypic correlation analysis is indispensable for the effective indirect selection for yield improvement. Correlation analysis, however, does not distinguish between direct and indirect influences of component traits on yield. Path coefficient analysis, as developed by Wright (1921) and subsequently refined and applied in plant breeding, partitions the correlation coefficient into direct and indirect effects, thereby providing a more realistic and mechanistic understanding of the cause-and-effect relationships between yield and its determinants. This information guides breeders in identifying characters that exert genuine direct effects on yield and, therefore, merit priority in selection programmes Khan *et al.*, 2003 ^[12]. Selection index analysis, a technique originally formulated as a discriminant function by Smith (1936) and later elaborated for crop breeding contexts, enables the simultaneous improvement of multiple traits by integrating the information from all correlated characters associated with economic yield. By assigning appropriate weights to component traits based on their heritabilities and genetic correlations with yield, selection indices increase the efficiency of selection beyond what is achievable through selection on yield alone. This approach is particularly

advantageous for wheat breeding, where grain yield is the primary target but is mediated through several measurable secondary traits such as number of productive tillers per plant, spike length, number of spikelets per spike, number of grains per spike, and 1000-grain weight.

In view of the strategic importance of wheat in ensuring food and nutritional security at national, state, and regional levels — and considering the imperative need for developing high-yielding, locally adapted varieties for the Satpura Plateau agro-climatic zone of Madhya Pradesh—the present investigation entitled "Genetic variability and trait association in diverse genotypes of bread wheat (*Triticum aestivum* L.)

Materials and Methods

Experimental site and plant material

The present investigation was carried out during the rabi season of 2025-26 at the Research Farm, School of Agricultural Sciences, G. H. Rasoni University, Saikheda, Madhya Pradesh, India, situated at 21.514862° N latitude and 78.76364° E longitude. The experimental material for the present investigation comprised of 17 genotypes of wheat, namely Zincol, HPAN 111, Ankur, HPAN 127, PBW Zn 1, CRD Genhun 1, WB 02, PBW 677, HPAN 101, HD 2967, Lok-1, Phule Anupam (NIAW 3624), Sonalika, HI-1621, HI-1628, HD-3237, DBW-233.

Experimental design and crop management

The 17 genotypes were tested in a Randomised Block Design (RBD) replicated three times, resulting in 51 single row plots. The experimental area was laid out in plots, the dimensions of which were 2.0 m × 0.225 m (row length 2.0 m; row-to-row spacing 22.5 cm; plant-to-plant spacing 10 cm; 20 plants per row), leaving 22.95m² excluding borders and paths. The crop was fertilised with the recommended dose of 120:60:40 kg N:P₂O₅:K₂O ha⁻¹, and the standard agronomic package of practices recommended for the rabi sorghum region was adhered to across all plots.

The meteorological observations recorded on weekly basis during crop growing period (Standard Meteorological Weeks 46 of 2025 to 13 of 2026) revealed that rainfall ranged from 0.0 to 5.0 mm, with the maximum temperature ranged from 24.8 to 35.0 °C and minimum temperature ranged from 11.2 to 21.2 °C, and relative humidity ranged from 30 to 52%, signifying that the crop was produced under typical dry, cool to warm weather conditions of the rabi season with no significant weather aberration.

Observations recorded

Observations were recorded on five randomly selected and tagged plants in each plot of every replication for eleven quantitative, yield-attributing traits, viz., days to 50 per cent flowering (DF50), days to maturity (DM), plant height (PH,

cm), Effective Tillers per Plant (ET/plant), Spike Length(cm), Spikelets per Spike(PS), Grains per Spike (GPS), 1000-Seed Weight (g), Grain Yield per Plant (g/pl), Biological Yield per Plant (g/pl) and harvest index (HI, %), following standard agronomic and biometrical procedures. Days to 50 per cent flowering and days to maturity were recorded on a plot basis, while the remaining nine traits were recorded on the five tagged plants and averaged to obtain the plot mean.

Statistical analysis

All of the data for the 11 quantitative traits were collected and statistically analyzed by R software (Version 4.5.1). Analysis of variance for the Randomised Block Design, along with estimation of the genotypic and phenotypic coefficients of variation, broad-sense heritability, and genetic advance (both as an absolute value and as a percentage of the mean, worked out at 5% selection intensity), was carried out using the R package 'variability', which partitions the observed phenotypic variance into its genotypic, environmental and error components and derives the associated genetic parameters directly from the fitted model. GCV and PCV were categorised as low, moderate or high following Burton and Devane [13], broad-sense heritability was categorised following Johnson *et al.* [14], and genetic advance as a percentage of the mean was likewise categorised following Johnson *et al.* [14].

Results and Discussion

Analysis of variance

Analysis of variance (ANOVA) was carried out for all the eleven quantitative traits studied in 17 bread wheat (*Triticum aestivum* L.) genotypes evaluated in a Randomized Complete Block Design (RCBD) with three replications during Rabi 2025. The ANOVA partitions the total variation into components attributable to genotypes, replications, and experimental error, thereby enabling a statistically rigorous assessment of whether observed phenotypic differences among genotypes are genuine or merely due to chance variation. The mean sum of squares (MSS) due to genotypes was found to be highly significant ($p < 0.001$) for ten of the eleven traits studied, viz. days to 50% flowering, days to maturity, plant height, effective tillers per plant, spike length, spikelets per spike, grains per spike, 1000-seed weight, harvest index, and grain yield per plant, while biological yield per plant was significant at $p < 0.05$ (Table 1). The significant differences among genotypes for all studied traits confirm the existence of adequate genetic variability among the test material, which is a prerequisite for effective selection and crop improvement. The replication MSS was non-significant for all traits, indicating uniformity of the experimental environment and the reliability of the data collect.

Table 1: Analysis of Variance (ANOVA) for yield and yield-contributing traits in 17 bread wheat genotypes

S. No.	Trait	Replication MSS (df=2)	Genotype MSS (df=16)	Error MSS (df=32)
1	Days to 50% Flowering (DFF)	0.4118	7.3971***	0.7243
2	Days to Maturity (DM)	0.0784	14.4216***	0.6826
3	Plant Height – PH (cm)	0.8057	27.1811***	1.7630
4	Effective Tillers per Plant (ETP)	0.00578	0.7744***	0.06152
5	Spike Length – SL (cm)	0.03838	1.1108***	0.08092
6	Spikelets per Spike (SPS)	0.17647	3.0368***	0.67647
7	Grains per Spike (GPS)	1.526	91.0860***	7.124
8	1000-Seed Weight – TSW	0.5981	8.4682***	0.4207
9	Biological Yield per Plant – BY	0.8532	12.6255*	0.1819
10	Harvest Index – HI	0.2712	15.1153***	0.8893
11	Grain Yield per Plant – GY (g)	0.06955	1.5983***	0.06367

*** Significant at $p < 0.001$; * Significant at $p < 0.05$

Genetic Parameters

In the present study, the genetic parameters – comprising the Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Heritability in broad sense [$h^2(bs)$], Genetic Advance (GA), and Genetic Advance as a Percentage of the Mean (GA%) – were computed for all eleven agro-morphological traits in 17 bread wheat genotypes evaluated during Rabi 2025 (Table 2). The PCV was consistently higher than or equal to GCV for all traits, reflecting the expected contribution of environmental factors to total phenotypic variation. The magnitude of the difference between PCV and GCV was small for most traits,

suggesting a relatively low influence of the environment. High heritability ($\geq 80\%$) was recorded for nine out of eleven traits, indicating that selection based on phenotypic performance would be largely effective for these traits. Traits exhibiting high heritability coupled with high GA% ($\geq 20\%$) – such as biological yield per plant, grain yield per plant, and effective tillers per plant – are governed predominantly by additive gene action and are particularly amenable to direct selection for genetic improvement. The detailed trait-wise interpretation of the genetic parameters is presented in the following sub-sections.

Table 2: Estimates of Genetic Parameters for Agro-morphological Traits in 17 Bread Wheat Genotypes

S. No.	Trait	PCV (%)	GCV (%)	$h^2(bs)$ %	GA	GA as % of Mean
1	Days to 50% Flowering (DFF)	2.1623	1.8781	75.44	2.6684	3.36
2	Days to Maturity (DM)	2.0095	1.8746	87.03	4.1126	3.60
3	Plant Height – PH	3.3784	3.0737	82.78	5.4554	5.76
4	Effective Tillers/Plant (ETP)	10.8356	9.6576	79.44	0.895	17.73
5	Spike Length – SL	5.1618	4.6436	80.93	1.0858	8.61
6	Spikelets per Spike (SPS)	6.1386	4.5013	53.77	1.3399	6.80
7	Grains per Spike (GPS)	10.1764	9.0856	79.71	9.7299	16.71
8	1000-Seed Weight – TSW	3.6922	3.4329	86.44	3.1369	6.57
9	Biological Yield/Plant – BY	10.4588	10.2368	95.80	4.1064	20.64
10	Harvest Index – HI	6.9329	6.3620	84.21	4.1165	12.03
11	Grain Yield/Plant – GY	11.1936	10.5556	88.93	1.3893	20.50

PCV = Phenotypic Coefficient of Variation; GCV = Genotypic Coefficient of Variation; $h^2(bs)$ = Heritability (Broad Sense); GA = Genetic Advance at 5% selection intensity; GA% = Genetic Advance as % of Mean. $h^2(bs)$

Correlation Coefficient Analysis

Correlation analysis provides a quantitative measure of the degree and direction of mutual association between pairs of traits and is fundamental to understanding the interdependence of yield-contributing characters in wheat. In the present investigation, both genotypic (rg) and phenotypic (rp) correlation coefficients were estimated among all possible pairs of eleven agro-morphological traits in 17 bread wheat genotypes. The genotypic correlations generally exceeded the corresponding phenotypic correlations in magnitude for most trait pairs, suggesting that the associations are primarily governed by the

genotypes' underlying genetic constitution rather than by environmental factors — a pattern widely reported in wheat. Positive and significant correlations among traits indicate that simultaneous improvement through indirect selection is feasible, whereas negative correlations imply a trade-off that must be managed in a breeding programme. The complete matrices of genotypic and phenotypic correlation coefficients are presented in (Tables 4 and 5, respectively, and are discussed trait-wise in the following sub-sections with reference to grain yield per plant as the primary trait of economic importance.

Table 4: Genotypic Correlation Coefficients among Quantitative Traits in 17 Bread Wheat Genotypes

Genotypic Correlation											
Traits	DFE	DM	PH	ETP	SL	SPS	GPS	TSW	BY	HI	GY
DFE	1 **	0.6497 **	0.5985 *	-0.4057	0.4238	0.315	0.2013	0.2816	-0.2034	0.3417	0.0054
DM	0.6497 **	1 **	0.7797 **	-0.1609	0.5557 *	0.5149 *	0.1612	0.112	0.0533	-0.1154	0.0224
PH	0.5985 *	0.7797 **	1 **	-0.1812	0.4459	0.3779	0.2415	0.2252	0.0192	-0.1562	-0.046
ETP	-0.4057	-0.1609	-0.1812	1 **	-0.3949	-0.3427	-0.465	-0.152	0.1607	-0.286	-0.0712
SL	0.4238	0.5557 *	0.4459	-0.3949	1 **	0.7463 **	0.4051	0.4355	-0.2374	0.0768	-0.0983
SPS	0.315	0.5149 *	0.3779	-0.3427	0.7463 **	1 **	0.5744 *	0.4929 *	-0.1834	-3.00E-04	-0.0831
GPS	0.2013	0.1612	0.2415	-0.465	0.4051	0.5744 *	1 **	0.7809 **	-0.0049	0.0666	0.0961
TSW	0.2816	0.112	0.2252	-0.152	0.4355	0.4929 *	0.7809 **	1 **	0.1218	0.3361	0.4105
BY	-0.2034	0.0533	0.0192	0.1607	-0.2374	-0.1834	-0.0049	0.1218	1 **	-0.4552	0.8121 **
HI	0.3417	-0.1154	-0.1562	-0.286	0.0768	-3.00E-04	0.0666	0.3361	-0.4552	1 **	0.1886
GY	0.0054	0.0224	-0.046	-0.0712	-0.0983	-0.0831	0.0961	0.4105	0.8121 **	0.1886	1 **

Table 5: Phenotypic Correlation Coefficients among Quantitative Traits in 17 Bread Wheat Genotypes

Phenotypic Correlation											
Traits	DFE	DM	PH	ETP	SL	SPS	GPS	TSW	BY	HI	GY
DFE	1 **	0.598 **	0.4685 **	-0.2922 *	0.3483 *	0.1858	0.1545	0.2317	-0.154	0.2418	-0.0414
DM	0.598 **	1 **	0.6785 **	-0.1125	0.4796 **	0.2645	0.1771	0.1146	0.0608	-0.1596	0.0161
PH	0.4685 **	0.6785 **	1 **	-0.1814	0.3339 *	0.2408	0.2422	0.2287	0.0385	-0.1232	-0.035
ETP	-0.2922 *	-0.1125	-0.1814	1 **	-0.2218	-0.2484	-0.3865 **	-0.1657	0.1136	-0.2059	-0.052
SL	0.3483 *	0.4796 **	0.3339 *	-0.2218	1 **	0.4194 **	0.2627	0.3433 *	-0.1982	0.121	-0.1242
SPS	0.1858	0.2645	0.2408	-0.2484	0.4194 **	1 **	0.3644 **	0.2815 *	-0.1571	0.015	-0.1345
GPS	0.1545	0.1771	0.2422	-0.3865 **	0.2627	0.3644 **	1 **	0.6498 **	0.0089	-0.0114	0.112
TSW	0.2317	0.1146	0.2287	-0.1657	0.3433 *	0.2815 *	0.6498 **	1 **	0.1188	0.2488	0.3724 **
BY	-0.154	0.0608	0.0385	0.1136	-0.1982	-0.1571	0.0089	0.1188	1 **	-0.4129 **	0.7513 **
HI	0.2418	-0.1596	-0.1232	-0.2059	0.121	0.015	-0.0114	0.2488	-0.4129 **	1 **	0.1522
GY	-0.0414	0.0161	-0.035	-0.052	-0.1242	-0.1345	0.112	0.3724 **	0.7513 **	0.1522	1 **

Path Coefficient Analysis

Path coefficient analysis, introduced by Wright (1921) and elaborated for plant breeding by Dewey and Lu (1959), partitions the genotypic and phenotypic correlation coefficient between each causal trait and the effect variable (grain yield per plant) into direct and indirect effects via all other traits in the system. This approach overcomes the limitation of simple correlation, which cannot distinguish whether a trait influences yield directly or merely through its association with other traits. In the present investigation, path coefficients were computed at both genotypic and phenotypic levels for all ten causal traits — Days to 50% Flowering (DFE), Days to Maturity (DM), Plant Height

(PH), Effective Tillers per Plant (ETP), Spike Length (SL), Spikelets per Spike (SPS), Grains per Spike (GPS), 1000-Seed Weight (TSW), Biological Yield per Plant (BY), and Harvest Index (HI) — towards grain yield per plant (GY) as the effect variable. The residual effects at the genotypic and phenotypic levels were 0.0512 and 0.1346, respectively, indicating that the ten traits together explain approximately 97.4% of the genotypic variation and 81.9% of the phenotypic variation in grain yield per plant — a remarkably high degree of explanation that validates the comprehensiveness of the trait set included in the analysis. The complete genotypic and phenotypic path coefficient matrices are presented in Tables 6 and 7 respectively.

Table 6: Genotypic path coefficient analysis showing direct and indirect effects of component traits on seed yield in bread wheat

Genotypic Path											
Traits	DFE	DM	PH	ETP	SL	SPS	GPS	TSW	BY	HI	
DFE	-0.3471	0.31452	-0.1076	0.21627	-0.1221	-0.0109	-0.1492	0.26946	-0.1486	0.0906	
DM	-0.2255	0.48411	-0.1402	0.0858	-0.1601	-0.0177	-0.1195	0.10713	0.03895	-0.0306	
PH	-0.2077	0.37747	-0.1798	0.0966	-0.1285	-0.013	-0.179	0.21542	0.014	-0.0414	
ETP	0.14079	-0.0779	0.03259	-0.5331	0.11376	0.01181	0.34471	-0.1454	0.11743	-0.0758	
SL	-0.1471	0.26904	-0.0802	0.21053	-0.2881	-0.0257	-0.3003	0.41662	-0.1734	0.02035	
SPS	-0.1093	0.24926	-0.068	0.18268	-0.215	-0.0345	-0.4258	0.47157	-0.134	-9E-05	
GPS	-0.0699	0.07804	-0.0434	0.24792	-0.1167	-0.0198	-0.7413	0.74713	-0.0036	0.01766	
TSW	-0.0978	0.05421	-0.0405	0.08101	-0.1255	-0.017	-0.5789	0.95672	0.08899	0.08908	
BY	0.07058	0.0258	-0.0035	-0.0857	0.06838	0.00632	0.00366	0.11652	0.73068	-0.1207	
HI	-0.1186	-0.0559	0.02809	0.15249	-0.0221	0.00001	-0.0494	0.3215	-0.3326	0.26509	
Residual = 0.0512											

Conclusion

The present investigation demonstrated substantial and exploitable genetic variability among the 17 bread wheat genotypes for most of the agro-morphological traits studied, providing a sound genetic base for selection. High broad-sense heritability accompanied by high genetic advance as percentage of mean was recorded for biological yield per plant ($h^2 = 95.80\%$, $GAM = 20.64\%$) and grain yield per plant ($h^2 = 88.93\%$, $GAM = 20.50\%$), indicating that these two traits are governed predominantly by additive gene action and are therefore the most responsive to direct phenotypic selection. Correlation analysis further corroborated this, with biological yield per plant showing the strongest and only consistently significant association with grain yield per plant at both the genotypic ($r_g = 0.8121$) and phenotypic ($r_p = 0.7513$) levels, while 1000-seed weight was significantly correlated with grain yield at the phenotypic level alone ($r_p = 0.3724$). Path coefficient analysis, which explained nearly 97% of the genotypic and 82% of the phenotypic variation in grain yield (residual effects of 0.0512 and 0.1346, respectively), resolved these associations into their causal components and identified 1000-seed weight (genotypic direct effect = +0.9567) and biological yield per plant (phenotypic direct effect = +0.8914) as the principal direct determinants of grain yield, with harvest index and days to maturity making additional positive direct contributions. Notably, the large negative direct effect of grains per spike (−0.7413) was almost entirely neutralised by its strong positive indirect effect via 1000-seed weight, underscoring the grain number–grain weight trade-off as a key physiological constraint that breeders must reconcile rather than a barrier to yield improvement. Taken together, these findings indicate that grain yield in the present material is governed by a relatively compact and well-defined genetic architecture centred on biomass production, grain weight, and partitioning efficiency, rather than by spike architecture or phenological traits, which exerted their influence largely through indirect pathways. Accordingly, a composite selection strategy that simultaneously targets high biological yield per plant, high 1000-seed weight, and high harvest index, supported by genotypes with adequate maturity duration, is recommended as the most efficient and genetically sound route to enhancing grain yield in bread wheat under the agro-climatic conditions of the Satpura Plateau zone of Madhya Pradesh, and merits validation across multiple environments and breeding cycles to confirm its stability before large-scale deployment.

References

1. Bhutto AH, Sial MA, Arain MA, Arzani A, Naqvi MH. Genetic variability and correlation studies in bread wheat (*Triticum aestivum* L.) germplasm. *Pak J Bot*. 2016;48(4):1394-1396.
2. Anonymous. Agricultural statistics at a glance 2022. New Delhi: Directorate of Economics and Statistics, Ministry of Agriculture and Farmers Welfare, Government of India; 2022.
3. Lupton FGH, editor. Wheat breeding: Its scientific basis. Chapman and Hall; 1987.
4. Bayisha A, Mulatu K, Dechassa N. Genetic diversity analysis of bread wheat (*Triticum aestivum* L.) genotypes using morpho-agronomic traits. *Cogent Food Agric*. 2020;6(1):1741462. doi:10.1080/23311932.2020.1741462
5. Das BK. Wheat. In: Singh DP, Singh HB, editors. *Advances in agronomy*. Vol. 2. Agrobios (India); 2008. p. 121-165.
6. Kaur V, Mavi GS, Kaur S. Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.) genotypes. *Electron J Plant Breed*. 2019;10(2):618-624. doi:10.5958/0975-928X.2019.00079.3
7. Sharma I, Sendhil R. Recent advances in wheat research in India: a perspective. Karnal: ICAR-Indian Institute of Wheat and Barley Research; 2016.
8. Ministry of Agriculture and Farmers Welfare. Second advance estimates of production of major crops for 2025-26 [Internet]. New Delhi: Government of India; 2026 Mar 10 [cited 2026 Sep 6]. Available from: <https://pib.gov.in>
9. Anonymous. Vision 2050. Karnal: Indian Institute of Wheat and Barley Research; 2015.
10. Government of Madhya Pradesh. Agriculture statistics: Madhya Pradesh. Bhopal: Directorate of Agriculture; 2023.
11. Mary SS, Gopalan A. Dissection of fluctuating yield in bhendi [*Abelmoschus esculentus* (L.) Moench]. *J Agric Biol Sci*. 2006;1(2):17-22.
12. Khan AA, Alam MA, Alam MK, Alam MJ, Sarker ZI. Correlation and path analysis of some yield traits in wheat. *Online J Biol Sci*. 2003;3(9):823-826. doi:10.3923/jbs.2003.823.826
13. Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron J*. 1953;45(10):478-481.
14. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agron J*. 1955;47(7):314-318.