Phenotypic screening of diverse wheat (*Triticum aestivum* L.) genotypes for grain yield and its component traits.

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Abstract

The present investigation was conducted during the rabi season of 2025 under late sown conditions at the research farm of FASAI, Rama University, Kanpur, with the objective of assessing genetic variability, trait associations, and selection indices for yield improvement in bread wheat (Triticum aestivum L.). A total of 104 diverse genotypes were evaluated using an augmented block design along with four standard checks for thirteen yield and yield-related traits.

Analysis of variance revealed highly significant differences among genotypes for all traits studied, indicating the existence of substantial genetic variability and considerable scope for selection. High heritability coupled with high genetic advance as percent of mean (GAM) was recorded for key traits including days to 50% flowering (h^2 = 96.3%), number of grains per spike (mean: 52.88; h^2 = 91.52%; GAM = 93.92%), grain weight per spike (GCV = 21.26%; h^2 = 88.31%; GAM = 90.71%), peduncle length (h^2 = 90.17%; GAM = 92.57%), and test weight (mean: 43.22 g; h^2 = 94.22%; GAM = 96.62%). These results indicate the predominance of additive gene action and suggest that direct phenotypic selection for these traits would be highly effective.

Grain yield per plant (mean: 15.73 g) exhibited moderate heritability (52.75%), reflecting the combined influence of genetic and environmental factors. Genotypic correlation analysis revealed that grain yield per plant had strong positive associations with test weight (0.902**), grain weight per spike (0.600**), harvest index (0.48**), and effective tillers per plant (0.274**), indicating their direct contribution to yield. Additionally, number of grains per spike showed a strong positive correlation with grain weight per spike (0.773**), emphasizing the importance of sink capacity in yield determination. In contrast, traits such as number of spikelets per spike and certain phenological characters exhibited weak or negative associations with grain yield.

Overall, grain weight per spike, number of grains per spike, test weight, and effective tillers per plant were identified as the major yield-contributing traits. Given their high heritability and strong positive association with grain yield, these traits can serve as reliable selection indices for the development of high-yielding and stable wheat cultivars under late sown conditions.

Key Words: *Wheat, GCV, PCV, Correlation, Seed yield, Heritability*

Introduction:

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops worldwide and constitutes a primary staple for a large segment of the global population. A member of the family Poaceae, it is cultivated across a wide range of agro-climatic conditions, from temperate to subtropical regions. Globally, wheat occupies approximately 220–225 million hectares, with an annual production exceeding 780 million tonnes and an average productivity of about 3.5 t ha^{-1}, positioning it among the leading cereal crops alongside rice and maize (Mohan et al., 2022). In India, wheat ranks second only to rice in terms of importance and plays a critical role in ensuring national food security. It is grown over an area of about 31–32 million hectares, producing nearly 110–112 million tonnes with an average productivity of approximately 3.5 t ha^{-1} (Anonymous, 2023). Major wheat-producing states include Punjab, Haryana, Uttar Pradesh, Madhya Pradesh, Rajasthan, and Bihar, which collectively contribute substantially to the national grain reserve.

From a nutritional perspective, wheat serves as a major source of carbohydrates (60–70%), along with moderate protein content (10–14%), dietary fiber, B-complex vitamins (notably thiamine and niacin), and essential minerals such as iron, zinc, and magnesium. The presence of gluten proteins imparts unique viscoelastic properties to wheat dough, making it highly suitable for the preparation of a wide array of food products, including bread, chapati, pasta, biscuits, and other bakery items. Economically, wheat is integral to farmers' livelihoods, rural employment, and the growth of agro-based industries. It also plays a vital role in public distribution systems and buffer stock management, thereby contributing to price stabilization and food availability.

Despite substantial yield improvements achieved during the Green Revolution, largely due to the adoption of semi-dwarf, high-yielding varieties, sustaining and further enhancing wheat productivity under the prevailing challenges of climate change, as well as increasing biotic and abiotic stresses, remains a significant concern. In this context, the assessment of genetic variability among wheat genotypes is of paramount importance, as it forms the foundation for effective selection and crop improvement. Estimation of genetic parameters such as variability, heritability, and genetic advance provides critical insights into the nature of gene action governing key traits and aids in identifying characters amenable to selection (Zewdu et al., 2023).

Grain yield in wheat is a complex quantitative trait governed by multiple interrelated components, including days to heading, days to maturity, plant height, number of tillers per plant, spike length, number of grains per spike, and test weight. Therefore, the study of correlation and character associations is essential to elucidate the relationships among these traits and to identify those with a strong positive influence on grain yield. Such information is invaluable in formulating efficient selection strategies and in identifying indirect selection criteria for yield improvement. Moreover, the evaluation and genetic characterization of diverse wheat genotypes facilitate the identification of superior lines possessing desirable trait combinations, which can either be recommended for cultivation following multilocational evaluation or utilized as parents in hybridization programmes aimed at developing high-yielding, stable, and climate-resilient varieties.

In view of the above, the present investigation entitled "Phenotypic screening of diverse wheat (*Triticum aestivum* L.) genotypes for grain yield and its component traits." was undertaken to assess the extent of genetic variability, examine the association among yield and its component traits, and identify promising genotypes for their effective utilization in future wheat breeding programmes focused on yield enhancement and stability.

Materials and Method

The present investigation was carried out at the research farm of FASAI, Rama University, Mandhana, Kanpur-209217 during rabi 2025 under late sown condition. For experiment purpose 104 diverse wheat genotypes (Table 1.) were collected and evaluated in augmented block design with four check entries. All the recommended agronomic practices have been followed to raise the good crop. Data for all important traits related to yield parameters such as Days to 50% flowering (DFF), Days to maturity (DTM), Plant height (cm) (PHT), Tillers per plant (TPP), Spike Length (cm) (SL), Peduncle Length (PL) cm, Spikelet per spike (SPP), Grains Per Spike (GPS), Grain weight Per Spike (GWPS), Test Weight (TW) g., Biological Yield Per Plant (BYPP), Seed Yield Per Plant (SYPP) g., and Harvest Indesx (HI %) have been recorded by tagging five randomly selected competitive plant. Mean of the recorded data for each trait were calculated and subjected to statistical analysis to investigate the factful result.

Result and Discussion

Analysis of Variance

The analysis of variance revealed highly significant differences among the 104 wheat genotypes for all thirteen traits studied, indicating the presence of substantial genetic variability for yield and its component characters (Table 2.). Treatment mean squares were significant at both 5% and 1% levels for traits including days to heading, days to maturity, plant height, effective tillers per plant, spike characters, grain weight, 1000-grain weight, biological yield, grain yield per plant and harvest index, demonstrating wide variation among genotypes. The genotype component was highly significant for almost all traits, suggesting good scope for selection and genetic improvement. The significant differences observed between checks and genotypes for most yield-related traits further indicate the superiority or distinctiveness of certain experimental lines over standard varieties. The relatively low and mostly non-significant block effects, along with smaller error variances compared to treatment variances, confirm the reliability and precision of the experiment. Overall, the results highlight ample exploitable variability for effective selection in wheat breeding programmes.

Genetic Variability parameters estimate

The estimates of genetic variability parameters among 104 wheat (Triticum aestivum L.) genotypes revealed substantial variation for yield and its component traits. Days to 50 per cent heading recorded a mean of 78.5 days (range: 66.2–89.2) with high heritability (96.3%) and high genetic advance as per cent of mean (98.7%), indicating strong additive gene action (Dave *et al.* 2021). Similarly, number of grains per spike (mean: 52.88; range: 31.6–74.2) exhibited high GCV (16.93%), PCV (17.75%), heritability (91.52%) and high GAM (93.92%), suggesting excellent scope for selection. Grain weight per spike showed the highest variability with GCV (21.26%) and PCV (22.69%), along with high heritability (88.31%) and GAM (90.71%). Peduncle length (mean: 37.66 cm; range: 22.67–61.9 cm) also expressed high GCV (17.12%), heritability (90.17%) and GAM (92.57%). The 1000-grain weight (mean: 43.22 g; range: 32.08–52.51 g) exhibited high heritability (94.22%) with moderate GCV (10.33%) and high GAM (96.62%). Grain yield per plant (mean: 15.73 g; range: 11.67–22.96 g) (Prasad *et al.* 2020) showed moderate variability (GCV 12.08%, PCV 16.35%) and moderate heritability (52.75%), indicating the influence of both genetic and environmental factors. In contrast, harvest index (mean: 35.78%) showed low heritability (18.18%) and low GAM (20.58%), reflecting greater environmental influence. In general, PCV values were slightly higher than GCV for all traits, indicating limited environmental effects. The presence of high heritability coupled with high genetic advance for key traits such as grains per spike, grain weight per spike, peduncle length and 1000-grain weight (Donga *et al.* 2022) suggests that these characters can be effectively utilized as selection criteria for yield improvement in wheat breeding programmes.

Correlation studies among 13 most important yield attributing traits

The genotypic (rg) and phenotypic (rp) correlation analysis among 13 traits revealed that genotypic correlations were generally higher in magnitude than phenotypic correlations, indicating strong inherent genetic associations with comparatively lower environmental influence. Grain yield per plant (SYPP) exhibited significant and positive genotypic correlations with grain weight per spike (0.600**), test weight (0.902**), harvest index (0.48**), and number of effective tillers per plant (0.274**), indicating these as major direct yield-contributing traits. At the phenotypic level, SYPP (showed strong positive associations with grain weight per spike (0.404**), test weight (0.553**) (Mekaoussi *et al.* 2021), biological yield per plant (0.657**) and harvest index (0.61**) (Alemu *et al.* 2020), suggesting their practical importance in selection programmes. Number of grains per spike was highly and positively correlated with grain weight per spike at both genotypic (0.773**) and phenotypic (0.711**) levels, reflecting the interdependence of sink components. Plant height also showed positive association with SYPP at the genotypic level (0.261**), whereas harvest index maintained a consistent positive relationship with yield. Conversely, some traits such as spikelets per spike (Regar *et al.* 2023) and certain phenological traits showed weak or negative associations with yield, indicating limited direct contribution. Overall, the results suggest that effective tillers per plant, grain weight per spike, test weight and harvest index are key yield-determining traits and can be emphasized in selection strategies for yield improvement in wheat.

Conclusion

The study identified several key yield-contributing traits with high genetic potential and practical breeding value. Grain weight per spike exhibited high variability (GCV 21.26%, PCV 22.69%), high heritability (88.31%) and strong positive genotypic correlation with grain yield per plant (0.600**), indicating its major direct contribution to yield and suitability for direct phenotypic selection. Number of grains per spike (mean 52.88; heritability 91.52%; rg with grain weight per spike 0.773**) also showed high genetic control, suggesting that improving sink capacity would substantially enhance yield. Test weight (1000-grain weight) recorded high heritability (94.22%) and very strong positive genotypic correlation with grain yield (0.902**), making it a reliable and stable selection criterion. Peduncle length (heritability 90.17%; GAM 92.57%) demonstrated high genetic advance, indicating additive gene action and its usefulness in selecting vigorous and high-yielding genotypes. Additionally, number of effective tillers per plant showed positive association with grain yield (rg 0.274**), emphasizing its importance in improving yield per unit area. In contrast, harvest index showed low heritability (18.18%), suggesting greater environmental influence and limited effectiveness of direct selection. Overall, traits with high heritability, high genetic advance and strong positive correlation with grain yield—particularly grain weight per spike, number of grains per spike and test weight—should be prioritized as key selection indices in future wheat breeding programmes aimed at developing high-yielding, stable and genetically superior cultivars.

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Table 1. List of diverse genotypes collected from different research institute

S. No.	Name of Genotypes	Source of Genotypes	S. No.	Name of Genotypes	Source of Genotypes
1	RUWL-1	FASAI, RU, Kanpur	53	RUWL-53	FASAI, RU, Kanpur
2	RUWL-2	FASAI, RU, Kanpur	54	RUWL-54	FASAI, RU, Kanpur
3	RUWL-3	FASAI, RU, Kanpur	55	RUWL-55	FASAI, RU, Kanpur
4	RUWL-4	FASAI, RU, Kanpur	56	RUWL-56	FASAI, RU, Kanpur
5	RUWL-5	FASAI, RU, Kanpur	57	RUWL-57	FASAI, RU, Kanpur
6	RUWL-6	FASAI, RU, Kanpur	58	RUWL-58	FASAI, RU, Kanpur
7	RUWL-7	FASAI, RU, Kanpur	59	RUWL-59	FASAI, RU, Kanpur
8	RUWL-8	FASAI, RU, Kanpur	60	RUWL-60	FASAI, RU, Kanpur
9	RUWL-9	FASAI, RU, Kanpur	61	RUWL-61	FASAI, RU, Kanpur
10	RUWL-10	FASAI, RU, Kanpur	62	RUWL-62	FASAI, RU, Kanpur
11	RUWL-11	FASAI, RU, Kanpur	63	RUWL-63	FASAI, RU, Kanpur
12	RUWL-12	FASAI, RU, Kanpur	64	RUWL-64	FASAI, RU, Kanpur
13	RUWL-13	FASAI, RU, Kanpur	65	RUWL-65	FASAI, RU, Kanpur
14	RUWL-14	FASAI, RU, Kanpur	66	RUWL-66	FASAI, RU, Kanpur
15	RUWL-15	FASAI, RU, Kanpur	67	RUWL-67	FASAI, RU, Kanpur

16	RUWL-16	FASAI, RU, Kanpur	68	RUWL-68	FASAI, RU, Kanpur
17	RUWL-17	FASAI, RU, Kanpur	69	RUWL-69	FASAI, RU, Kanpur
18	RUWL-18	FASAI, RU, Kanpur	70	RUWL-70	FASAI, RU, Kanpur
19	RUWL-19	FASAI, RU, Kanpur	71	RUWL-71	FASAI, RU, Kanpur
20	RUWL-20	FASAI, RU, Kanpur	72	RUWL-72	FASAI, RU, Kanpur
21	RUWL-21	FASAI, RU, Kanpur	73	RUWL-73	FASAI, RU, Kanpur
22	RUWL-22	FASAI, RU, Kanpur	74	RUWL-74	FASAI, RU, Kanpur
23	RUWL-23	FASAI, RU, Kanpur	75	RUWL-75	FASAI, RU, Kanpur
24	RUWL-24	FASAI, RU, Kanpur	76	RUWL-76	FASAI, RU, Kanpur
25	RUWL-25	FASAI, RU, Kanpur	77	RUWL-77	FASAI, RU, Kanpur
26	RUWL-26	FASAI, RU, Kanpur	78	RUWL-78	FASAI, RU, Kanpur
27	RUWL-27	FASAI, RU, Kanpur	79	RUWL-79	FASAI, RU, Kanpur
28	RUWL-28	FASAI, RU, Kanpur	80	RUWL-80	FASAI, RU, Kanpur
29	RUWL-29	FASAI, RU, Kanpur	81	RUWL-81	FASAI, RU, Kanpur
30	RUWL-30	FASAI, RU, Kanpur	82	RUWL-82	FASAI, RU, Kanpur
31	RUWL-31	FASAI, RU, Kanpur	83	RUWL-83	FASAI, RU, Kanpur
32	RUWL-32	FASAI, RU, Kanpur	84	RUWL-84	FASAI, RU, Kanpur
33	RUWL-33	FASAI, RU, Kanpur	85	RUWL-85	FASAI, RU, Kanpur
34	RUWL-34	FASAI, RU, Kanpur	86	RUWL-86	FASAI, RU, Kanpur
35	RUWL-35	FASAI, RU, Kanpur	87	RUWL-87	FASAI, RU, Kanpur
36	RUWL-36	FASAI, RU, Kanpur	88	RUWL-88	FASAI, RU, Kanpur
37	RUWL-37	FASAI, RU, Kanpur	89	RUWL-89	FASAI, RU, Kanpur
38	RUWL-38	FASAI, RU, Kanpur	90	RUWL-90	FASAI, RU, Kanpur
39	RUWL-39	FASAI, RU, Kanpur	91	RUWL-91	FASAI, RU, Kanpur
40	RUWL-40	FASAI, RU, Kanpur	92	RUWL-92	FASAI, RU, Kanpur
41	RUWL-41	FASAI, RU, Kanpur	93	RUWL-93	FASAI, RU, Kanpur
42	RUWL-42	FASAI, RU, Kanpur	94	RUWL-94	FASAI, RU, Kanpur
43	RUWL-43	FASAI, RU, Kanpur	95	RUWL-95	FASAI, RU, Kanpur
44	RUWL-44	FASAI, RU, Kanpur	96	RUWL-96	FASAI, RU, Kanpur
45	RUWL-45	FASAI, RU, Kanpur	97	RUWL-97	FASAI, RU, Kanpur
46	RUWL-46	FASAI, RU, Kanpur	98	RUWL-98	FASAI, RU, Kanpur
47	RUWL-47	FASAI, RU, Kanpur	99	RUWL-99	FASAI, RU, Kanpur
48	RUWL-48	FASAI, RU, Kanpur	100	RUWL-100	FASAI, RU, Kanpur
49	RUWL-49	FASAI, RU, Kanpur	101	HD 3407	IARI, New Delhi
50	RUWL-50	FASAI, RU, Kanpur	102	PBW 902	IIWR, Karnal
51	RUWL-51	FASAI, RU, Kanpur	103	PBW 870	PAU, Ludhiana
52	RUWL-52	FASAI, RU, Kanpur	104	HD 3440	PAU, Ludhiana

Table 2. Analysis of variance of 13 Different traits of 104 genotypes

S. No.	Character	Block	Treatment	Check	Genotype	C v/s G	Error
		[4]	[103]	[3]	[99]	[1]	[12]
1	DFF	1.69	39.25**	105.99**	38.56**	6.04*	1.89
2	DTM	2.5	15.50**	14.14**	16.49**	18.80**	2.65
3	PHT (cm)	8.35	82.10**	55.77*	82.77**	7.89	14.98

4	TPP	0.49*	0.36**	0.68**	0.30**	8.90**	0.14
5	PL (cm)	6.6	38.44**	47.63**	35.19**	143.27**	3.88
6	SL (cm)	1.88	2.96**	28.88**	2.33**	4.99	1.45
7	SPP	6.88*	4.21**	13.65**	2.87*	2.82	2.5
8	GPS	3.25	78.86**	152.83**	75.77**	8.28	7.31
9	GWPS (g)	0.07	0.39**	0.55**	0.44**	7.01**	0.05
10	TW (g)	2.87	20.79**	5.70*	18.78**	79.50**	1.37
11	BYPP (g)	2.86	26.06**	110.34**	22.22**	165.28**	10.48
12	SYPP (g)	2.5	6.13**	15.84**	5.00**	95.21**	2.42
13	HI (%)	10.45	20.71**	97.27**	17.09	168.24**	14.19

* Significant at P = 0.05, **Significant at P = 0.01

Table 3. Estimates of Genetic variability parameters for yield and its attributing traits

S. No.	Character	Mean	Range		GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
			Min.	Max.					
1	DFF	78.5	66.2	89.2	8.87	9.06	96.3	97.5	98.7
2	DTM	129.5	121.2	142.2	3.89	4.18	83.03	84.23	85.43
3	PHT (cm)	91.6	64.74	123.38	10.26	11.2	83.14	84.34	85.54
4	TPP	5.55	5.2	7.6	9.51	13.19	49.27	50.47	51.67
5	PL (cm)	37.66	22.67	61.9	17.12	18.07	90.17	91.37	92.57
6	SL (cm)	12.45	8	16.06	9.05	14.25	37.35	38.55	39.75
7	SPP	20.44	17	31	5.66	9.99	26.9	28.1	29.3
8	GPS	52.88	31.6	74.2	16.93	17.75	91.52	92.72	93.92
9	GWPS (g)	3.71	3.05	5.7	21.26	22.69	88.31	89.51	90.71
10	TW (g)	43.22	32.08	52.51	10.33	10.66	94.22	95.42	96.62
11	BYPP (g)	42.55	30.6	50.8	9.92	12.77	57.98	59.18	60.38
12	SYPP (g)	15.73	11.67	22.96	12.08	16.35	52.75	53.95	55.15
13	HI (%)	35.78	31.22	46.35	6.1	13.09	18.18	19.38	20.58

Table No. 4 Estimates of genotypic and phenotypic correlation coefficient analysis for 13 characters under study.

Characters	r	DFF	DTM	PHT (cm)	TPP	PL (cm)	SL (cm)	SPP	GPS	GWPS	TW (g)	BYPP (g)	HI (%)	SYPP (g)
DFF	rg.	1	0.456**	0.059	0.1	-0.06	0.04	0.705**	0.289**	0.188	-0.22*	0.15	-0.12	0.110
	rp	1	0.424**	0.074	0.206	-0.05	0.06	0.374**	0.292*	0.144	-0.21*	0.08	-0.1	0.011
DTM	rg		1	0.559**	0.812**	0.375**	0.448**	0.955**	0.188	0.155	0.493**	0.369**	-0.474**	**0.117**
	rp		1	0.368**	0.455**	0.371**	0.526**	0.574**	0.08	0.116	0.437**	0.17	0.14	**0.06**
PHT (cm)	rg			1	0.651**	0.588**	0.672**	0.355**	0.265*	0.278**	-0.272*	0.375**	-0.286**	**0.261****
	rp			1	0.340**	0.659**	0.335**	0.574**	0.295**	0.249*	-0.16	0.251*	-0.202*	0.003
TPP	rg				1	0.570**	0.05	0.416	0	0.155	-0.299**	0.271*	0.18	**0.274****
	rp				1	0.433*	0.14	0.415	-0.04	-0.035	-0.284*	0.329**	0	**0.225***
PL (cm)	rg					1	0.411**	0.650**	0.01	0.197	-0.16	0.17	-0.02	0.180
	rp					1	0.115	0.235**	0	0.145	-0.11	0.1	-0.12	0.010
SL (cm)	rg						1	1.001	0.743**	0.199	0.02	1.1	-2.306**	-0.223*
	rp						1	0.377**	0.399**	0.12	-0.138	0.329**	-0.19	0.090
SPP	rg							1	0.576**	0.497**	-0.616**	0.453**	-1.717**	-0.333**
	rp							1	0.334**	0.254*	-0.353**	0.07	-0.19*	-0.080
GPS	rg								1	0.773**	0.01	0.526**	-0.15	0.114
	rp								1	0.711**	0	0.423*	0	0.118
GWPS	rg									1	0.488**	0.564**	0.13	**0.600****
	rp									1	0.544**	0.736**	0.719**	**0.404****
TW (g)	rg										1	0.347**	1.19	**0.902****
	rp										1	0.536**	0.303**	**0.553****
BYPP (g)	rg											1	0.331**	1.0
	rp											1	-0.20*	**0.657****
HI (%)	rg												1	**0.48****
	rp												1	**0.61****
SYPP (g)	rg													1
	rp													1

* Significant at P = 0.05, **Significant at P = 0.01, r= correlation, rg= genotypic correlation, rp= phenotypic correlation