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Genetic variability and breeding opportunities in wheat under stripe rust stress: A comprehensive analysis of morphological traits

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Abstract
Information on trait based genetic parameters play strategic role in designing breeding methodologies. Genetic variability parameters were studied in the set of 51 genotypes of diverse eco-geographical location under artificial inoculation of stripe rust stimulating disease epiphytotic using augmented block design. Phenotypic variance distribution indicates substantial genetic and environmental influences on the traits studied. High GCV and PCV were observed for traits such as number of tillers, grain yield per plant, and AUDPC, suggest existence of significant genetic and phenotypic diversity as a prerequisite for effective selection. High broad-sense heritability coupled with genetic advance for traits like days to 50% flowering, number of tillers and plant height indicates effective transfer of these traits to the progenies and low influence of the environment. The interrelationship studies revealed positive association of number of tillers per plant, spike length, thousand grain weight and negative association of days to 50% flowering with grain yield per plant highlighting the importance of these traits in enhancing yield. The findings highlight the significance of considering genetic variability parameters along with correlation in designing effective wheat breeding program under stripe rust pressure due to variable climatic patterns.

Keywords: Wheat, augmented block design, stripe rust, epiphytotic, variability, correlation

Introduction
The global demand for wheat is progressively increasing even with crop diversification for nutritional alternatives. The global agricultural landscape projects wheat cultivation over 219.15 million hectares, achieving a productivity rate of 3.69 tons/ha and a total production of 808.44 million metric tons (Anonymous, 2023) [2]. India is a major contributor to world wheat following China in terms of wheat statistics (area of 30.45 million hectares productivity of 3.54 tons/ha).
Indian wheat is continuously at the threat of climate induced stresses like stripe rust caused by the fungus *Puccinia striiformis* (Chen, 2020) [7]. The wheat bowl of India which includes North-Western Plain Zone and Northern Hills Zone including foothills of Himalayas in J&K is at continuous endemic threat of stripe rust which may take serious epidemic forms (Srinivas *et al.*, 2021) [26]. The pace of development of new wheat varieties is hindered by several factors like narrow genetic variation, the large genome size (17 gb) and environment variance (Shamuyarira *et al.*, 2019) [25]. Understanding the genetic variability within wheat population becomes crucial for the development of resilient and high yielding varieties. Grain yield is a highly complex polygenic trait dependent on component traits including the environment (Bisne *et al.*, 2009) [4]. This variable environmental component includes varying levels of stripe rust effecting grain yield. Genetic components of variability include phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability and genetic advance. These components facilitate in the selection of potential genotypes among the available germplasm and predict improvement by making selection based on effective traits. (Haq *et al.*, 2008) [12]. Before beginning any crop breeding effort, it is also critical to acquire information on the correlation between yield and yield contributing traits. The present study aims to assess the genetic variability in wheat genotypes cultivated under stripe rust epiphytotic and to identify suitable

genotypes for utilization in breeding programs.

Materials and Methods

Plant Materials and Phenotypic Evaluations

The experimental material consist of 51 wheat genotypes (25 IC lines, 20 AGP lines, 3 commercially cultivated varieties and 3 stripe rust checks) as presented in Table.1, The material was sown in Augmented Block Design with six blocks, each with 8 test genotypes and 3 checks (randomly assigned) at Research Farm, Division of Plant Breeding and Genetics, SKUAST, Jammu. Two rows of two meters each was sown using recommended agronomical practices. The experiment material was evaluated for two consecutive years, 2021-22 and 2022-23, with the average data from this period being utilized for present study. Five competitive plants per genotype were randomly selected in each replication for recording observations on eight plant traits *viz.*, number of tillers per plant, plant height (cm), spike length (cm), spikelet per spike, grain yield per plant (g), thousand grain weight (g), and area under disease progress curve (%) for stripe rust. Data for days to 50% flowering was recorded on a plot-by-plot basis.

Table 1: List of wheat genotypes

Sr. No	Genotypes	Sr. No	Genotypes	Sr. No	Genotypes
1	IC530119	18	IC553914	35	Sunlin
2	IC530005	19	IC582705	36	FH11-6-24
3	IC533416	20	lC529094	37	HAR627
4	IC539162	21	IC443759	38	Kenya Kudu
5	ICS30086	22	IC580119	39	Trophy
6	IC542117	23	ICS29908	40	Tura
7	IC543413	24	IC530086	41	Tusie
8	IC529902	25	IC529802	42	FSD -2008
9	ICS49409	26	Braewood	43	Parus
10	ICS29907	27	Carinya	44	Tatara
11	IC529943	28	Ega Stampede	45	Zarlaashta
12	IC547699	29	Giles	46	RSP 561
13	IC530058	30	Hyperno	47	JAUW 584
14	IC529894	31	Monad	48	PBW175
15	ICS30025	32	Mulgara	C1	Agra local
16	IC128153	33	Naparoo	C2	PBW 343
17	IC564090	34	Quarrion	C3	DBW 187

Statistical Analysis

Analysis of variance (ANOVA), descriptive statistics and correlation analysis for genotypes was performed by using the R version 4.3.2(package augmented RCBD and corrplot). The analysis of variance for augmented block design was carried following Federer (1956) [9], phenotypic and genotypic coefficients of variation (Burton, 1952) [5], broad sense heritability (Burton and Devane, 1953) [6], and genetic advance (Johnson *et al.*, 1955) [15].

Results and Discussion

Analysis of variance

Analysis of variance show significant variation among genotypes for all the traits under investigation suggesting the material under study had considerable genetic diversity. Table.2, reveal that Mean Sum of Squares (MSS) for all of the sources of variation, except for the blocks were statistically significant. MSS for varieties (genotypes) was significant for all traits, indicating existence of significant variation among the genotypes of wheat under study. Similar results have also been reported by Upadhyay *et al.* (2020) [27] and Prabha *et al.* (2022) [20]. Days to 50% flowering, number of tillers per plant, plant height, spike length, spikelet per spike, grain yield per plant, and thousand grain weight revealed highly significant differences between genotypes, whereas the area under the disease progress curve revealed significant differences between genotypes.

Table 2: Analysis of variance for yield and disease influencing morphological traits in wheat

Source	df	MSS							
		DF	NT	PH	SL	SS	GYP	TGW	AUDPC
Treatment/ Entries	50	54.50**	4.18**	261.43**	4.89**	8.46**	13.68**	40.27**	438167.62*
Check	2	1.87**	24.57**	1206.99**	60.68**	4.06**	103.57**	8.23 ns	754238.72*
Varieties	47	42.74**	3.36**	217.92**	2.29**	6.57**	6.67**	33.67**	306385.29*
C vs V	1	712.13**	1.80*	415.09**	15.31**	106.2**	163.26**	414.64**	5999794.99**
Block	4	0.48ns	0.43 ns	1.59 ns	0.33 ns	0.42 ns	0.69 ns	2.36 ns	71015.50 ns
Residuals	8	0.20	0.25	4.28	0.37	0.38	0.39	2.22	116232.28
CV		0.41	8.80	2.15	6.19	3.54	9.20	4.31	37.11

'*' and '**' significant at 5% and 1% respectively, df: degrees of freedom; DF: Days to 50 per cent flowering; NT: Number of tillers per plant; PH: Plant height (cm); SL: Spike length (cm); SS: Spikelet per spike: GYP: Grain yield per plant (g); TGW: Thousand grain weight (g): AUDPC: Area under disease progress curve (%).

The traits under study exhibit a spectrum of variability within the studied population and coefficients of variation (CV) provide insights into the relative dispersion of these traits. A higher coefficients of variation signifies greater variability in the trait across the sample and accordingly *viz.*, number of tillers per plant (8.8) and grain yield per plant (9.20), respectively demonstrate substantial variation. This indicates a diverse range in the number of tillers per plant and grain yield within the population. Plant height and spike length exhibit moderate coefficients of variation values, 2.15 and 6.19, respectively while days to 50% flowering, spikelet per spike, thousand grain weight, and area under disease progress curve are 0.41, 3.54, 4.31, and 37.11, respectively.

Descriptive statistics for yield and disease influencing morphological traits in wheat

The estimates of mean, range, CV, skewness, kurtosis and standard deviation for all traits under study have been presented in Table 3.

Wide range of variation in the days to 50% flowering (97.37 to 118.87), number of tillers per plant (3.19 to 14.38), plant height (68.72 to 136.89 cm), spike length (7.12 to 14.73 cm), spikelet per spike (12 to 23.44), thousand grain weight (21.58 to 48.65 g), grain yield per plant (2.19 to 14.18 g), and AUDPC (15.00 to 2112.35) were estimated based on above descriptive statistics. The true extent of variation can be achieved by comparing the relative amount of coefficient of phenotypic and genotypic variance for each trait contributing to yield.

Skewness, kurtosis and standard deviation

The skewness and kurtosis values offer critical insights into the distribution pattern of the traits within the studied plant population. A negative skewness in days to 50 percent flowering and spikelet per spike (-0.21 and -0.13, respectively) indicates a slight asymmetry towards higher values, while positive skewness in number of tillers, grain yield per plant(1.97 and 1.22, respectively) suggests a tail towards lower values. Furthermore, kurtosis values for number of tillers, grain yield per plant (9.46 and 4.30, respectively) indicate heavier tails and more extreme values in their distributions. Plant height, spike length, thousand grain weight, and area under disease progress curve exhibit moderate skewness and kurtosis. Understanding these distributional pattern aids in characterizing the variability and potential outliers within the studied traits, which is pivotal for comprehensive assessments in breeding and crop improvement strategies.

Table. 3: Estimates of mean, range, skewness, kurtosis and standard deviation for yield and disease influencing morphological traits in wheat

Traits	Mean±S.E	Range				Skewness	Kurtosis	Std. Deviation
		Low	Genotypes	High	Genotypes			
DF	109.93 ±0.91	97.37	Kenya Kudu	118.87	IC529094	-0.21	1.62**	6.52
NT	5.73±0.27	3.19	Agra local	14.38	PBW175	1.97**	9.46**	1.92
PH	95.23±2.07	68.72	IC543413	136.89	IC443759	0.72*	3.46	14.79
SL	9.65±0.24	7.12	IC539162 and IC542117	14.73	DBW 187	0.76*	3.18	1.69
SS	18±0.37	12	IC529943	23.44	IC128153	-0.13	2.27	2.62
GYP	6.15±0.4	2.19	Naparoo	14.18	PBW175	1.22**	4.3	2.84
TGW	33.55±0.84	21.58	Ega Stampede	48.65	IC533416	0.2	2.64	5.99
AUDPC	783.9±81.34	15	Tura and Tusie	2175.00	Agra local	0.21	2.04*	580.89

'*' and '**' significant at 5% and 1%respectively, DF: Days to 50 per cent flowering; NT: Number of tillers per plant; PH: Plant height (cm); SL: Spike length (cm); SS: Spikelet per spike: GYP: Grain yield per plant (g); TGW: Thousand grain weight (g): AUDPC: Area under disease progress curve (%).

Assessment of variability parameters for yield and disease influencing morphological traits in wheat

The estimates of variances due to Genotype and Phenotype measured in terms of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) for traits studied have been presented in Table 4. The distribution of phenotypic variance (PV), genetic variance (GV), and environmental variance (EV) among traits offers important information on their nature of inheritance. Area under disease progress curve and plant height exhibit significant PV values, signifying their extensive overall variability. The significant PV for area under disease progress curve and plant height, predominantly driven by EV, suggests a significant influence of environmental factors on disease progression. Conversely, traits such as number of tillers and spike length show lower PV, indicating less influence of environment. The genetic component (GV) contributes significantly to traits such as thousand grain weight, indicating it to be heritable. Understanding these variances aids in targeted breeding strategies for improving specific traits especially those influenced by genetic factors, offering key insights for crop improvement and disease management in agriculture.

Table4: Estimates of Variability Parameters for yield and disease influencing morphological traits in wheat

Trait	PV	GV	EV	GCV	GCV. category	PCV	PCV. category	ECV	hBS	hBS. category	GA	GAM	GAM. category
DF	42.74	42.54	0.20	5.93	Low	5.95	Low	0.41	99.53	High	13.42	12.21	Medium
NT	3.36	3.11	0.25	30.79	High	32.00	High	8.72	92.58	High	3.50	61.11	High
PH	217.92	213.64	4.28	15.35	Medium	15.50	Medium	2.17	98.04	High	29.86	31.35	High
SL	2.29	1.92	0.37	14.37	Medium	15.70	Medium	6.32	83.80	High	2.62	27.14	High
SP	6.57	6.19	0.38	13.82	Medium	14.24	Medium	3.42	94.23	High	4.98	27.68	High
GYP	6.67	6.28	0.39	40.75	High	42.00	High	10.16	94.15	High	5.02	81.57	High
TGW	33.67	31.45	2.22	16.72	Medium	17.30	Medium	4.44	93.40	High	11.18	33.33	High
AUDPC	306385.29	190153.00	116232.28	55.63	High	70.61	High	43.49	62.06	High	708.71	90.41	High

DF: Days to 50 per cent flowering; NT: Number of tillers per plant; PH: Plant height (cm); SL: Spike length (cm); SS: Spikelet per spike: GYP: Grain yield per plant (g); TGW: Thousand grain weight (g): AUDPC: Area under disease progress curve (%).

Figure.1 provides a graphical representation of the Phenotypic and Genotypic Coefficient of Variation of traits under study. The genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and environmental coefficient of variation (ECV) provide insights into the variation and environmental influence among studied traits. Traits with high GCV and PCV, such as number of tillers, grain yield per plant, and area under disease progress curve, indicate large genetic and phenotypic variability (Nagar *et al.*, 2018 and Bayisa *et al.*, 2020) [19, 3]. PCV and GCV values for number of tillers and grain yield per plant were not significant, while AUDPC exhibits the significantly higher PCV (70.61) compared to GCV (55.63) emphasizing the importance of considering environmental influences when studying disease dynamics which greatly impact disease progression and severity. Traits with moderate GCV and PCV, such as plant height, spike length, spikelet per spike, and thousand grain weight, exhibit less variability (Gangwar *et al.* 2019) [11]. Thousand grain weight and spike length showed relatively high ECV, in such case marker-assisted selection for specific genes influencing these traits can be used to improve them. Conversely, days to 50 percent flowering displays low GCV, PCV, and ECV, indicating lower variability and environmental influence where recurrent selection could be employed, emphasizing genotypes with desired flowering characteristics. Prasad *et al.* (2021) [21], Hassani *et al.* (2022) [13] and Shah *et al.* (2023) [24] obtained similar results on variability for different traits in wheat.

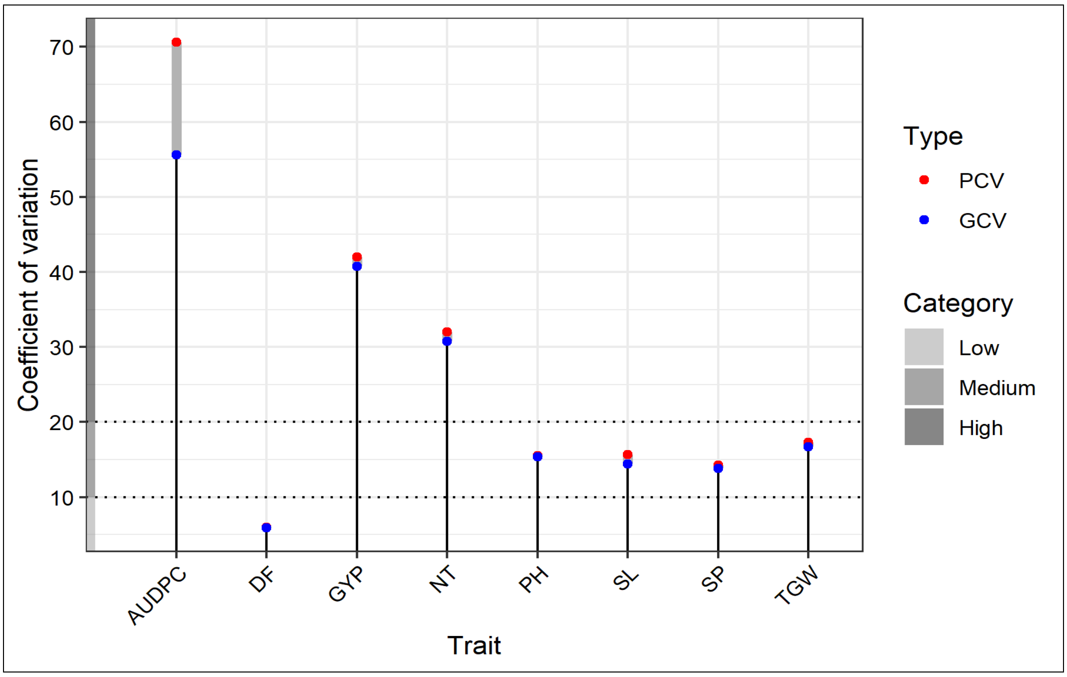

Fig 1: Graphical representation of genetic parameters of variation (GCV, PCV) for eight traits among 51 wheat accessions.

Heritability and Genetic Advance over mean

The estimates of heritability, expected genetic advance and genetic advance over mean for various traits studied are shown in Table 3. The study depicts thorough assessment of broad sense heritability (hBS) and genetic advance over mean (GAM) in a wide range of key plant traits, revealing profound insights into the genetic architecture and prospective pathways for development. The Figure 2 and 3 provides a graphical representation of broad sense heritability and genetic advance mean for the concerned traits. Days to 50% flowering emerged with a high hBS of 99.53, signifying a remarkable genetic influence coupled with intermediate genetic advance over mean (GAM) value of 12.21 suggesting a restrained pace of improvement. Breeding based on phenotypic selection is recommended for such trais. For such trait, the application of recurrent selection techniques holds promise for the fine-tuning of early-flowering genotypes. All other traits had high hBS and high GAM indicating a significant genetic contribution and highlight the promising prospects for genetic improvement. Similar to the result of this study, many researchers reported maximum heritability for numbers of tillers per plant, thousand grain weight, grain yield per plant and spike length (Fellahi *et al.*, 2013; Kumar *et al.*, 2019; Jaiswal *et al.*, 2020 and Vaghela *et al.*, 2021) [10, 17, 14, 28].

It is crucial to tailor breeding strategies to the specific hBS levels with potential to choose high yielding genotypes when there is strong heritability linked to high genetic advancement for various yield components (Yadawad *et al.*, 2015) [29]. For features with high and moderately high hBS, the emphasis should be on marker-assisted selection to identify and maintain beneficial genetic components. In the case of traits with lower hBS, a combined approach involving marker-assisted selection and recurrent selection is recommended to accelerate the progression of favourable genes. The comprehension of the genetic foundations of these traits is indispensable for the formulation of precise and effective breeding programs, ultimately resulting in the development of plant varieties endowed with enhanced disease resistance, elevated yield potential, and other pivotal agronomic attributes.

Correlation coefficient analysis

The correlations coefficients of different traits under study have been presented and diagrammatically represented in Table 5 and Fig 5, respectively. The negative correlation between days to 50% flowering and grain yield per plant (-0.403*) suggests that early flowering may be associated with higher grain yield as also reported by Samar *et al.* (2019) [23]. This negative relationship implies that crops exhibiting an early flowering may have advantage of longer grain filling period and enhanced stress resistance during crucial developmental stages. The positive correlation between number of tillers and grain yield per plant (0.0331*) indicates that an increased number of tillers may contribute positively to grain yield. Significant positive association of grain yield with tillers per plant and plant height have been previously reported by Masood *et al.* (2014) [18] and Devesh *et al.* (2021) [8].

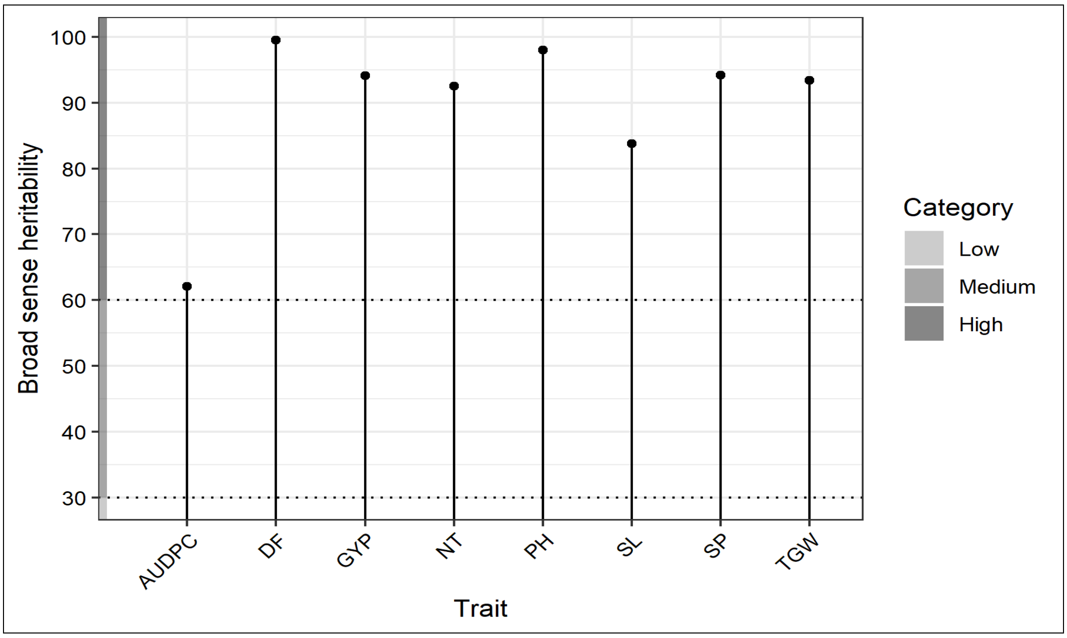

Fig 2: Graphical representation of broad sense heritability for eight traits among 51 wheat accessions

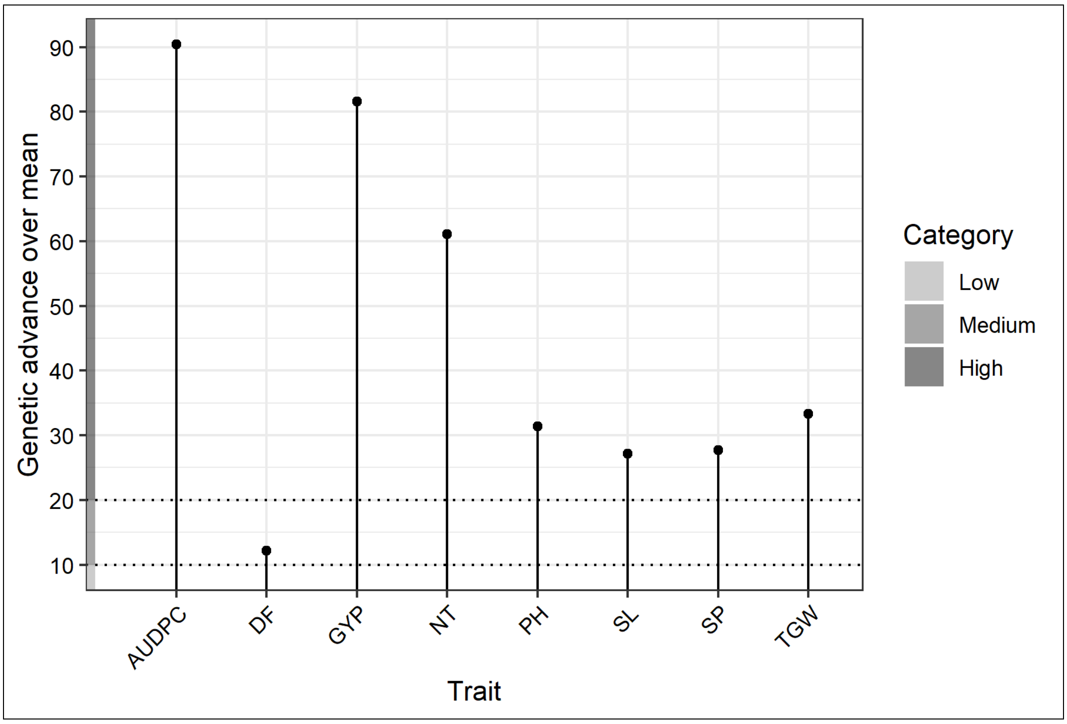

Fig 3: Graphical representation of genetic advance over mean for eight traits among 51 wheat accessions

Table 5: Genotypic correlation coefficients among morphological traits with grain yield

	DF	NT	PH	SL	SS	GYP	TGW	AUDPC
DF	--	-0.206	-0.224	-0.112	0.367	-0.403*	-0.304	-0.219
NT	-0.206	--	0.4322	0.1946	0.8388	0.0331*	0.1902	0.8234
PH	-0.224	0.4322	--	0.775	0.105	0.821	0.678	0.356
SL	-0.112	0.1946	0.775	--	0.271	0.032*	0.505	0.825
SS	0.367	0.8388	0.105	0.271	--	0.381	0.725	0.061
GYP	-0.403*	0.0331*	0.821	0.032*	0.381	--	0.027*	0.940
TGW	-0.304	0.1902	0.678	0.505	0.725	0.027*	--	0.983
AUDPC	-0.219	0.8234	0.356	0.825	0.061	0.940	0.983	--

'*' and '**' significant at 5% and 1% respectively, DF: Days to 50 per cent flowering; NT: Number of tillers per plant; PH: Plant height (cm); SL: Spike length (cm); SS: Spikelet per spike: GYP: Grain yield per plant (g); TGW: Thousand grain weight (g): AUDPC: Area under disease progress curve (%).

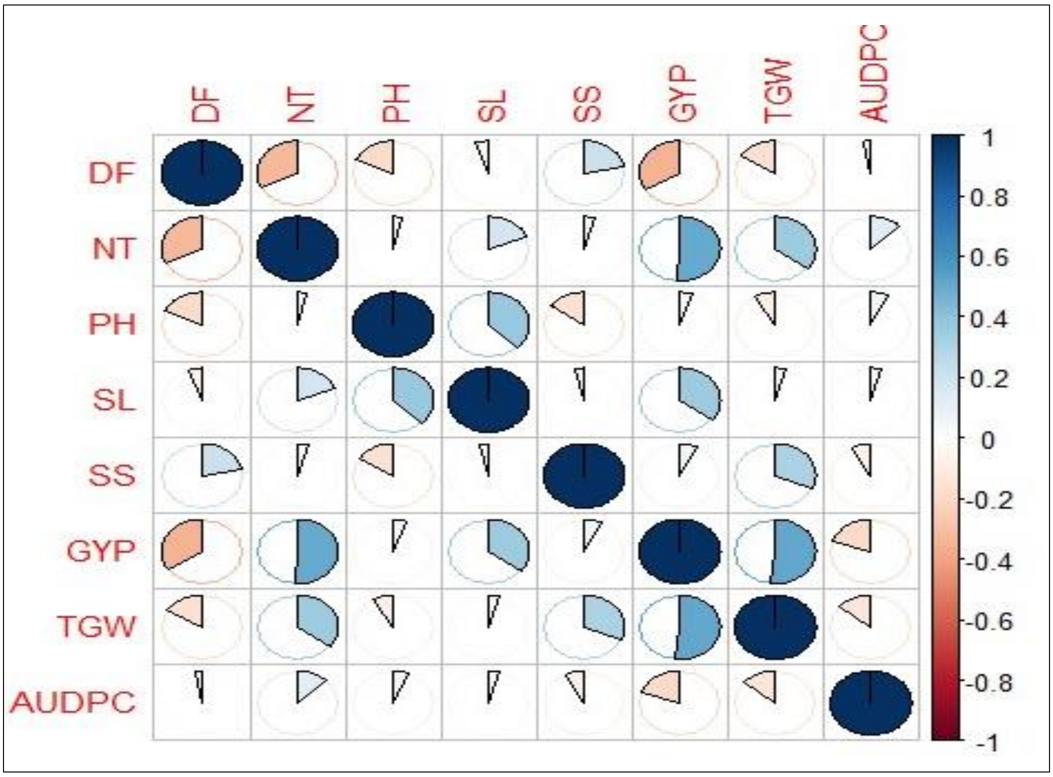

Fig 4: Genotypic correlation among morphological with grain yield in wheat genotypes.

Pictorial correlation aligns with the common understanding that a higher tiller count can result in more reproductive structures, potentially leading to greater grain production per plant. Similarly, the positive correlations of grain yield per plant with spike length and thousand grain weight (0.032* and 0.027* respectively) further underscore the importance of these morphological traits in predicting grain yield. Other researchers also reported the similar results (Ahmad *et al.* 2016; Khan *et al.* 2017) [1, 16]. Rehman *et al.* (2015) [22] also reported positive association between thousand grain weight, spike length, and grain yield. Longer spike length and greater thousand grain weight appear to be associated with higher grain yield, emphasizing the significance of these characteristics in breeding programs aimed at improving yield potential.

Conclusion

Significant genetic variability was reported in wheat genotypes under stripe rust disease pressure for yield attributing traits thereby emphasizing huge potential for selecting desired genotypes that can contribute either directly or indirectly to crop enhancement efforts. The traits with moderate to high heritability and genetic advance should be given attention to produce an effective response to yield enhancement. Stabilizing selection allow accumulation of alleles exhibiting additive gene action. Selection and hybridization of genotypes with high genotypic coefficient of variation, heritability, and genetic advance over mean can be recommended for further bread wheat yield enhancement in a specific area. The study also highlights the need to evaluate the genetic variation present in bread wheat populations to identify potential sources of resistance to tackle the threat of evolving new virulence of pathogens, especially stripe rust pathogens. The correlation coefficient analysis highlights valuable relationships between agronomic traits, providing a foundation for targeted breeding strategies. These findings contribute to the ongoing efforts to enhance crop productivity and resilience in the face of evolving agricultural challenges. Further, research is warranted to illuminate the underlying mechanisms driving these correlations and to validate the potential implications for crop improvement programs.

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Reference

1. Ahmad I, Mahmood N, Khan N. Genetics analysis for five important morphological attributes in wheat. Journal of Animal and Plant Sciences. 2016;26(3):725-730.
2. Anonymous. Food and Agriculture Organization of the United Nations. Global Food Outlook: Statistical Report 2022. Food and Agriculture Organization; c2023.
3. Bayisa T, Tefera H, Letta T. Genetic variability, heritability and genetic advance among bread wheat genotypes at South Eastern Ethiopia. Agriculture, Forestry and Fisheries. 2020;9(4):128.
4. Bisne R, Sarawgi AK, Verulka SB. Study of heritability, genetic advance and variability for yield contributing characters in rice. Bangladesh Journal of Agricultural Research. 2009;34(2):175-179.
5. Burton GW. Quantitative inheritance in grasses. Proceedings of the 6th Grassland Congress. 1952;1:356-363.
6. Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
7. Chen X. Pathogens which threaten food security: *Puccinia striiformis*, the wheat stripe rust pathogen. Food Security. 2020;12(2):239-251.

8. Devesh P, Moitra PK, Shukla RS. Correlation and path coefficient analysis for yield, yield components and quality traits in wheat. Electronic Journal of Plant Breeding. 2021;12(2):388-395.
9. Federer WT. Augmented designs. Hawaiian Planters' Record. 1956;55:191-208.
10. Fellahi Z, Hannachi A, Guendouz A, Bouzerzour H, Boutekrabt A. Genetic variability, heritability and association studies in bread wheat (*Triticum aestivum* L.) genotypes. Electronic Journal of Plant Breeding. 2013;4(2):1161-1166.
11. Gangwar OP, Kumar S, Bhardwaj SC, Prasad P, Kashyap PL, Khan H, Singh GP, Savadi S. Virulence and molecular diversity among *Puccinia striiformis* f. sp. *tritici* pathotypes identified in India between 2015 and 2019. Crop Protection. 2019;148:105717.
12. Haq W, Malik MF, Rashid M, Munir M, Akram Z. Evaluation and estimation of heritability and genetic advancement for yield related attributes in wheat lines. Pakistan Journal of Botany. 2008;40(4):1699-1702.
13. Hassani I, Nimbal S, Singh V, Noori A. Genetic variability analysis and correlation studies of bread wheat (*Triticum aestivum* L.) genotypes. Ekin Journal of Crop Breeding and Genetics. 2022;8(2):139-145.
14. Jaiswal R, Gaur SK, Jaiswal KS, Kumar A. An estimate of variability, heritability and genetic advance for grain yield and yield components in bread wheat (*Triticum aestivum* L.). Current Journal of Applied Science and Technology. 2020;39(12):1-6.
15. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47:314-318.
16. Khan AS, Hassan G. Heritability and correlation studies of yield and yield related traits in bread wheat. Sarhad Journal of Agriculture. 2017;33(1):103-107.
17. Kumar M, Avinashe H, Dubey N, Kaur S, Kalubarme S, Reddy P. Heritability and correlation studies of yield and yield related traits in bread wheat (*Triticum aestivum* L.). Journal of Pharmacognosy and Phytochemistry. 2019;8:97-101.
18. Masood SA, Ahmad S, Kashif M, Ali Q. Correlation analysis for grain and its contributing traits in wheat (*Triticum aestivum* L.). Natural Science. 2014;12(11):168-176.
19. Nagar SS, Kumar P, Vishwakarma SR, Singh G, Tyagi BS. Assessment of genetic variability and character association for grain yield and its component traits in bread wheat (*Triticum aestivum* L.). Journal of Applied and Natural Science. 2018;10(2):797-804.
20. Prabha AA, Avinashe H, Dubey N, Reddy JP, Reddy BT. Genetic studies on F3 population of bread wheat (*Triticum aestivum* L.) for yield and its components traits. Electronic Journal of Plant Breeding. 2022;13(2):369-376.
21. Prasad J, Dasora A, Chauhan D, Rizzardi DA, Bangarwa SK, Nesara K. Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.) genotypes. Genetics and Molecular Research. 2021, 20(2).
22. Rehman S, Abid MA, Bilal M, Ashraf J, Liaqat S, Ahmed RI, Qanmber G. Genotype by trait analysis and estimates of heritability of wheat (*Triticum aestivum* L.) under drought and control conditions. Basic Research Journal of Agricultural Science and Review. 2015;4(4):127-134.
23. Samar PV, Pathak VN, Verma OP. Interrelationship between yield and its contributing traits in wheat (*Triticum aestivum* L.). International Journal of Current Microbiology and Applied Sciences. 2019;8(2):3209-3215.
24. Shah N, Sharma P, Kumar D. Estimation of variability, heritability and genetic advance of yield contributing traits in bread wheat (*Triticum aestivum* L.). The Pharma Innovation Journal. 2023;12(3):1404-1407.
25. Shamuyarira KW, Shimelis H, Tapera T, Tsilo TJ. Genetic advancement of newly developed wheat populations under drought-stressed and non-stressed conditions. Journal of Crop Science and Biotechnology. 2019;22:169-176.
26. Srinivas K, Moizur RS, Yadav M, Sharma M. Brown and yellow rust of wheat in India - significance of climate on its races and resistance. International Journal of Environment and Climate Change. 2021;11(11):72-91.
27. Upadhyay P, Krishna S, Thakur P, Agrawal N, Yadav P, Prasad LC, Mishra VK. Identification of genetic variability and diversity in selected wheat (*Triticum aestivum* L.) germplasm under three different dates of sowing. Journal of Pharmacognosy and Phytochemistry. 2020;9(2):82-86.
28. Vaghela GK, Patel JM, Rahevar P. Assessment of genetic variability and character association for morpho-chemical traits in bread wheat (*Triticum aestivum* L.). Emergent Life Sciences Research. 2021;7:14-20.
29. Yadawad A, Hanchinal RR, Nadaf HL, Desai SA, Biradar S, Naik RV. Genetic variability for yield parameters and rust resistance in F2 population of wheat (*Triticum aestivum* L.). The Bioscan. 2015;10:707-710.