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RESEARCH PAPER

Genetic variability and character association studies in *Triticum* species

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Abstract: This study evaluated the variability and interrelationships among traits in 18 wheat genotypes, including10 checks and 8 advanced breeding lines, representing both *Triticum aestivum* L.(bread wheat) and *Triticum durum* (macaroni wheat). These species are vital to agriculture in the Indian subcontinent, with bread wheat primarily used for baking and durum wheat for pasta production. The analysis revealed that the phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV) across most traits. Notably, traits such as grain yield, spike length, peduncle length, 1000-grain weight, and biomass exhibited high heritability coupled with high genetic advance as a percentage of the mean, underscoring the potential for effective selection to enhance these characteristics. Correlation analysis indicated a positive and significant association between grain yield and key traits, including the number of productive tillers, spike length, and biomass. This suggests that targeted improvements in these traits could significantly boost grain yield in wheat.

Key words: Advanced breeding lines, Correlation, Heritability, Variability

Introduction

Wheat is one of the world's most important and widely cultivated cereal crop. It is primarily grown for its grain, which serves as a staple food for a large portion of the global population. Belonging to the genus *Triticum,* wheat is rich in carbohydrate and is also a significant source of dietary fiber, vitamins and minerals. The primary purpose of wheat cultivation is to produce grain, which is then grinded to flour for making bread, pasta, pastries, and other baked foods. The main types of wheat are *Triticum aestivum*, known as common wheat, and *Triticum durum*, known as durum wheat. Common wheat is mainly used for baking, while durum wheat is predominantly used for pasta production.

According to the estimates by Food and Agriculture Organization (FAO) for the year 2022, 770 million metric tons of wheat were produced globally on 221 million hectors of land (Anon., 2022). Despite these significant production figures, wheat cultivation needs increase to meet the projected global food demand for an estimated 9 billion people by 2050 (Ray *et al*., 2013).

Studying variability in crop plants like wheat is vital for enhancing genetic diversity, which serves as the basis for improving key traits such as yield, growth and quality. It allows breeders to select and develop varieties that are better adapted to diverse environments and agricultural practices. By understanding the range of genetic variation, breeders can make informed decisions toi mprove traits like grain size, nutritional content and overall performance.This helps in meeting market demands, improving crop productivity and ensuring the sustainability of wheat production across different regions and conditions.

The total variability can be divided into heritable and non-heritable components using genetic parameters such as the phenotypic (PCV) and genotypic coefficients of variation (GCV), heritability, and genetic advance as a per cent of mean. High heritability alone is insufficient for efficient selection in of advanced breeding lines unless accompanied by a significant genetic advance. Additionally, someresearchers (Kumar and Shukla, 2002 and Ismail *et al*., 2001) argue that data on genotypic and phenotypic correlations between yield and its component traits is essential for improving yield through selection programs.

Material and methods

The current experiment was carried out at the Main agriculture research station, University of Agricultural Sciences, Dharwad. The study involved 18 genotypes, consisting of 8 advanced breeding lines and 10 checks. Current experiment was laid out in Randomized Complete Block Design (RCBD) with two replications with spacing of 20 cm between rows and 2 cm between plants under field conditions during the *rabi* season. Observations were taken under field conditions included, days to fifty percent flowering, days to maturity, plant height (cm), number of productive tillers permeter, spike length, number grains per spike, thousand grain weight (g), peduncle length (cm), grain yield per plot (q ha^{-1}), biomass (qha^{-1}), Soil Plant Analysis Development (SPAD) chlorophyll content, Normalized Difference Vegetative Index (NDVI), leaf waxiness, relative water content (RWC) and the average values of each trait was further employed for statistical analysis. Some of the quality parameters studied are protein content, zinc content (ppm) and iron content (ppm).

The GCV and PCV were calculated using the formula provided by Burton and Devane (1953) and classified according to method suggested by Shivasubramanian and Menon (1973). Heritability in broad sense was computed using the following formula given by Weber and Moorthy (1952) and categorized as demonstrated by Robinson *et al.* (1949). Further, genetic advance as a percent mean were computed as suggested by Johnson *et al.*(1955).The correlation coefficient analysis among all possible character combination at phenotypic level was estimated employing the formula as suggested by Aljibouri *et al.* (1958).

Results and discussion

Variability

The estimates of genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability (H^2), genetic advance as a per cent of mean (GAM) are presented in Table 1. The PCV values were slightly higher than the respective GCV for all the characters denoting little influence of environmental factors on their expression, means that these traits were less influenced by environment.

The study revealed a range of genetic and phenotypic variability across the traits analyzed, offering valuable insights for wheat improvement programs. For days to 50 percent flowering, lower estimates of GCV (4.46) and PCV (4.60) were observed, accompanied by high heritability (94.29) but low GAM (8.93). This suggests that the trait is influenced by non-additive genetic factors, making direct selection less effective, as high heritability does not always translate into significant genetic gains. Similar results have been reported by Poudel *et al.* (2021), Bhanu *et al.* (2018) and Islam *et al.* (2017). Days to maturity showed low variability, with a PCV of 2.1 and a GCV of 2.67, along side high heritability (60) and low GAM (3.1). Despite the high heritability, the low GAM indicates that the trait is controlled primarily by additive gene action, offering limited potential for improvement through selection. This suggests that the diversity for this trait among the studied genotypes is minimal, making it less suitable for significant genetic improvement.

Table 1. The percentage of genetic variability parameters, heritability and GAM for morpho-physiological traits, yield and yield components and micronutrient contents in different species of wheat genotypes

Characters	GCV(%)	PCV(%)	H^2(%)	GAM
DFF	4.46	4.60	94.29	8.93
DM	2.1	2.67	60.00	3.1
PH	10.82	13.15	67.74	18.35
NPT	8.94	10	79.8	16.45
SL	17.73	18.62	90.61	34.76
PL	27.3	28.39	92.41	54.05
GPS	11.81	17.93	43.38	16.02
TGW	17.28	18.39	88.2	33.42
GY	20	21.53	73.84	32.75
BMS	19.13	19.61	95.11	38.43
HI	13.56	18.22	55.35	20.78
NDVI I	3.83	4.71	66.25	6.42
NDVI II	19	22.05	74.26	33.73
SPADII	6.96	7.43	87.73	13.44
RWC	4.57	5.46	70.25	7.9
Protein	3.61	6.72	28.77	3.98
Zn	13.13	16.81	61.02	21.13
Fe	3.33	7.48	19.81	3.05

DFF-days to 50 per cent flowering, DM-Days to maturity, PH-plant height(cm), NPT-Number of productive tiller spermeter, SL-spike length (cm), PL-peduncle length (cm),TGW- thousand grain weight, YLD - grain yield (q ha^{-1}), BMS- biomass (q ha^{-1}),GPS- number of grains per spike, HI- harvest index, NDVI I – NDVI at anthesis, NDVI II- NDVI at grain filling, SPAD II- SPAD at grain filling, RWC- relative water content, Zn- Zinc content (ppm), Fe- Iron content (ppm)

Plant height demonstrated moderate variability, with GCV(10.82) and PCV(13.15),high heritability (67.74) and moderate GAM (18.35). The moderate GCV implies a genetic contribution to the observed variability, while the slightly higher PCV indicates some environmental influence. The high heritability combined with moderate GAM suggests that the trait is governed by additive gene effects, making it favorable for selection. These findings are in agreementwith Arifuzzaman *et al.* (2020) and Mkhabela *et al.* (2019).The number ofproductive tillers per meter exhibited low GCV (8.94) and moderate PCV (10), with high heritability (79.8) and moderate GAM (18.35), suggesting that the population may have been previously selected for this trait, limiting further genetic variability. These results are consistent with the findings of Thapa *et al.* (2019). Spike length, which is crucial for crop yield due to its influence on the number of spikelets, exhibited moderate GCV (17.73) and PCV (18.62), high heritability (90.61) and high GAM (34.76), indicating that the trait is highly influenced by genetic factors and is ideal for selection. These findings align with those reported by Islam *et al.* (2017), Sharma *et al.* (2018), and Porte *et al.* (2021). Peduncle length recorded high PCV (28.39) and GCV (27.3), with high heritability (92.41) and high GAM (54.05), suggesting that this trait is primarily controlled by genetic factors and offers considerable variation for selection, making it favorable for breeding. Rehman *et al.* (2015) reported similar results.

The number of grains per spike exhibited moderate GCV (17.93) and PCV (11.81), with low heritability (43.38) and moderate GAM (16.02), indicating limited predictability in selection but some potential for improvement. The findings were consistent with those of Porte *et al.*(2020). Thousand grain weight demonstrated moderate PCV (18.39) and GCV (17.28), with high heritability (88.2) and high GAM (33.42), aligning with the results of Poudel *et al.* (2021). Grain yield per plot exhibited high GCV (20) and PCV (21.53), suggesting substantial variability within the panel. High heritability (73.84) and high GAM (32.75) indicate significant genetic control, making the trait suitable for selection, consistent with Thapa *et al.* (2019). Biomass exhibited moderate GCV (19.13) and PCV (19.61), with high heritability (95.11) and high GAM (38.43), indicating potential for genetic improvement through selection. The high heritability suggests that the observed variability is largely due to genetic factors, making it a strong candidate for breeding programs. The harvest index demonstrated moderate GCV (13.56) and PCV (18.22), moderate heritability (55.35) and high

Table 2. Phenotypiccorrelationsamongvariousmorpho-physiologicaltraits,yield,yieldcomponentsandmicronutrientcontentindifferent species of wheat genotypes

	DFF	DM	PH	NPT	SL	PL	GPS	TGW	BMS	HI	NDVII	NDVIII	SPADII	RWC	LW	PROTEIN	Zn	Fe	YLD
DFF	1**	0.919**	0.427**	-0.055	-0.016	-0.066	-0.022	-0.103	-0.164	0.139	0.121	0.409*	0.396*	-0.066	-0.081	0.051	-0.068	-0.527**	-0.126
DM		1**	0.333*	-0.272	0.041	-0.064	-0.028	-0.153	-0.105	0.065	0.216	0.356*	0.269	0	-0.165	0.065	-0.183	-0.566**	-0.226
PH			1 **	0.32	0.305	-0.109	0.158	-0.318	-0.117	0.153	0.049	0.385*	0.358*	-0.093	0.374*	-0.2	-0.053	-0.388*	0.159
NPT				1 **	-0.017	0.012	0.065	0.166	-0.137	0.363*	-0.246	0.117	0.332*	-0.13	0.384*	-0.27	0.3	0	0.585**
SL					1**	-0.165	0.176	-0.101	-0.176	0.049	0.315	-0.034	-0.118	0.097	0.398*	-0.092	-0.228	0.01	-0.034
PL						1**	-0.237	0.223	0.144	-0.094	0.124	0.075	0.262	0.002	-0.096	0.046	0.202	0.23	-0.148
GPS							1**	0.007	0.066	0.264	0.121	-0.283	-0.134	0.26	0.26	-0.043	-0.005	0.003	0.213
TGW								1**	-0.125	-0.093	0.177	-0.061	-0.248	-0.293	-0.132	-0.187	0.145	0.023	0
BMS									1**	-0.087	-0.259	-0.198	0.03	0.25	-0.164	0.032	-0.036	0.087	-0.189
HI										1**	-0.048	0.268	0.441**	0.126	0.322	0.186	0.084	-0.103	0.524**
NDVII										1**	-0.025	-0.132	0.011	0.14	-0.327	-0.18	-0.18	-0.203	
NDVIII												1**	0.437**	-0.226	-0.178	0.144	0.161	-0.29	-0.072
SPADII													1 **	0.294	0.259	0.109	0.246	-0.004	0.069
RWC														1**	0.362*	-0.129	-0.027	0.159	0.125
LW															1**	-0.227	-0.19	0.178	0.517**
PROTEIN																1**	0.107	0.226	-0.26
Zn																	1**	0.152	0.128
Fe																		1**	-0.038
YLD																			1**

*Significant at 5% level; **Significant at 1% DFF- days to 50 per cent flowering, DM- Days to maturity, PH- plant height (cm), NPT- No of productive tillers per meter, SL- spike length(cm),PL-pedunclelength(cm),TGW-thousandgrainweight,YLD -grainyield(qha-1),BMS-biomass (qha-1),GPS-numberofgrains perspike,HI-harvestindex,NDVII– NDVIatanthesis, NDVIII-NDVIatgrainfilling, SPAD II-SPAD atgrainfilling, LW-leafwaxiness, RWC-relative watercontent, Zn-Zinc content(ppm), Fe-Iron content (ppm)

GAM (20.78), indicating moderate progress in improving this trait. This suggests that consistent selection pressure and environmental management are needed to enhance its genetic potential.

The Normalized Difference Vegetation Index (NDVI) I exhibited low GCV (3.83) and PCV(4.71), with high heritability (66.25) and low GAM (6.42), similar to the results obtained by Shehrawat and Kumar (2021). NDVI II exhibited moderate GCV (19) with high PCV (22.05), high GAM (), and high heritability (), consistent with Ramya *et al.* (2015). At the grain-filling stage, SPAD II readings exhibited low GCV (6.96) and PCV(7.43), with high heritability (87.73) and moderate GAM (13.44), indicating limited variability but significant genetic influence, suggesting incremental improvements could be achieved through breeding. Relative water content exhibited low PCV (5.46) and GCV (4.57), with high heritability (70.25) but low genetic advance (7.9), which is in line with the findings of Al-Ashkar *et al.* (2021). Protein content showed low GCV (3.61) and PCV (6.72), with low heritability (28.77) and low GAM (3.98), consistent with the results of Meles *et al.* (2017).

Estimation of association patterns among morpho-physiological and yield related traits

Grain yield exhibited a significant positive correlation with several traits, including the number of productive tillers, harvest index and relative water content. This indicates that an increase in these traits contributes directly to higher grain yield, a finding that aligns with Fellahi *et al.* (2024) who reported a significant positive correlation between grain yield and harvest index, reinforcing the critical role of harvest efficiency in yield enhancement. Additionally, plant height showed significant positive association with NDVIII (0.385), SPADII (0.358) and relative water content (0.374), highlighting the relationship between plant vigor and water content. However, plant height exhibited asignificant negative correlation with iron content (-0.388), suggesting that taller plants may have reduced iron accumulation, a finding that warrants further investigation into nutrient management strategies.

The number of productive tillers demonstrated a significant positive correlation with traits such as the harvest index (0.366), SPAD II (0.332), relative water content (0.384) and yield (0.585). This suggests that enhancing the number of productive tillers could indirectly improve yield through its association with traits like water content and photosynthetic capacity. In contrast, a negative correlation was observed between grain yield and days to fifty percent flowering. This observation aligns with findings by Gonzalez *et al.* (2007), who also reported a negative correlation between yield and phenological traits. Furthermore, a negative correlation between yield and NDVI II was noted, consistent with the results of Gurumurthy *et al.* (2019), indicating that higher vegetative index values may not always translate into higher grain yields.

Interestingly, a non-significant relationship was found between SPAD II and yield, which is in line with the findings of Zhang *et al.* (2018), suggesting that chlorophyll content, as measured by SPAD, may not be a direct predict or of yield in this case. However, a significant positive correlation between yield and relative water content was observed, highlighting the importance of water retention for grain production. This finding corroborates the results of Kettani *et al.*(2023), who also emphasized the role of relative water content in maintaining crop performance under varying environmental conditions.

Conclusion

In conclusion, the study identified traits with varying levels of genetic and phenotypic coefficient of variation, heritability, and genetic advance. Traits such as spike length, peduncle length, and biomass showed high potential for genetic improvement due to high heritability and GAM. On theother hand, traits such as days to maturity and relativewater contentexhibited low variability and limited genetic advance, indicating less potential for significant improvement. These findings provide important insights for breeding programs aimed at enhancing wheat productivity and adaptability. The correlation analysis provides important insights into the relationships between key agronomic traits and grain yield. Traits such as the number of productive tillers, harvest index, and relative water content emerged as critical factors influencing yield, while negative associations with phenological trait and NDVI II suggest that optimizing these traits requires a balance between vegetative growth and reproductive efficiency. These findings offer valuable direction for future wheat breeding programs aimed at improving yield potential under diverse growing conditions.

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