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RESEARCH PAPER

Genetic variability and character association of yield, yield attributes and grain nutrient traits in *Triticum* species

RANJEETA A. NAIKODI[1*], SUMA S. BIRADAR[1], S. A. DESAI[1], P. U. KRISHNARAJ[2] AND S. S. CHANDRASHEKHAR[3]

[1]Department of Genetics and Plant Breeding, [2] Department of Microbiology,
[3]Department of Seed Science and Technology College of Agriculture, Dharwad
University of Agricultural Sciences, Dharwad - 580 005, India
*E -mail: ranjitanaikodi812@gmail.com

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Abstract: Wheat (*Triticum aestivum* L.) is a major global staple contributing approximately 35% to global food consumption. This study was conducted to assess genetic variability and correlations among morpho-physiological traits, yield components, and grain nutrients in 18 wheat genotypes at the Main Agricultural Research Station, UAS Dharwad, during the *rabi* season of 2023-24. The genotypes included bread wheat, durum wheat and diccocum wheat, representing different commercially grown wheat species in India. Genetic variability analysis revealed low genotypic and phenotypic coefficients of variation (GCV and PCV) for days to 50% flowering and days to maturity, indicating limited variability. In contrast, traits such as the number of productive tillers and peduncle length exhibited moderate to high GCV, PCV, heritability and genetic advance as a percentage of the mean (GAM), indicating significant genetic variability and strong selection potential.Correlation analysis identified a positive relationship between grain yield and the number of grain per spike and biomass , while grain nutrient traits such as iron and protein content exhibited a negative association with grain yield. These findings provide valuable insights for developing wheat varieties with enhanced yield and grain quality.

Key words: Correlation, Grain nutrients, Variability, Wheat

Introduction

Wheat (*Triticum aestivum* L.) is a self-pollinating, long-day crop belonging to the *Poaceae* family and is a vital global staple, thriving particularly in arid and semi-arid regions. It plays a crucial role in food security, contributing around 35% to global food consumption and ranking second in overall cereal production, following maize and ahead of rice. In India, three primary wheat species are commercially cultivated: *Triticum aestivum* L. (bread wheat), *Triticum durum* Desf. (durum or macaroni wheat), and *Triticum dicoccum* (Schrank) Schubl. (emmer or khapli wheat), which account for 95, 4 and 1 of the nation's total wheat production, respectively (Anon, 2012). India's wheat production is estimated at around 112.92 million metric tonnes from 36.2 million hectares, with an average yield of 3620 kg ha^{-1}. Uttar Pradesh emerged as the top wheat-producing state in 2022-23, with a production of 33.95 million metric tonnes. Other major wheat-producing states include Madhya Pradesh, Punjab, Haryana, Rajasthan, Bihar and Gujarat (Statista, 2023).

Wheat (*Triticum* spp.) is one of the most widely cultivated and consumed cereal crops globally, playing a significant role in food security and nutrition. Understanding genetic variability in yield, yield attributes, and grain nutrient traits among different Triticum species is crucial for breeding programs aimed at enhancing productivity and nutritional quality. Studies have shown that genetic variation exists not only among species, but also within species, affecting traits like grain yield, protein content, and mineral concentrations. Such variability is essential for selecting superior genotypes that can adapt to varying environmental conditions and meet the growing demands for quality wheat. Furthermore, the incorporation of genetic variability into breeding strategies can lead to the development of high-yielding varieties with enhanced grain nutrient profiles, thereby contributing to improved human health and agricultural sustainability.

This study evaluated genetic variability and correlation among morpho-physiological traits, yield components, and grain nutrient content in order to identify promising genotypes for crop improvement. Key variability parameters, such as range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability, and genetic advance as a percentage of the mean (GAM), were assessed. The range provides insights into the variability among genotypes, while PCV and GCV help differentiate between environmental and genetic influences on traits. A comparison of PCV and GCV clarifies the contribution of genetics to trait expression, and broad-sense heritability quantifies the proportion of genetic variance. GAM reflects the potential for genetic improvement through selection. Additionally, correlation coefficients were analyzed to explore the relationships among traits, guiding breeders in selecting genotypes that not only enhance yield but also improve grain nutritional quality. This comprehensive analysis helps in making informed decisions for crop enhancement strategies.

Material and methods

The present study was conducted during the *rabi* season of 2023-24 at the All India Coordinated Wheat and Barley Improvement Project, Main Agricultural Research Station, UAS

Dharwad, located in the northern transitional zone of Karnataka. The aim was to evaluate genetic variability in wheat by exploring diversity for enhanced yield and quality traits. The experimental material comprised of 18 genotypes, including six bread wheat, six durum wheat, and six dicoccum wheat, along with check varieties, as presented in Table 1. A randomized complete block design (RCBD) was employed for field evaluation and standard cultural practices were followed. Plots were kept free from weeds, pests and diseases through appropriate agrochemical applications and furrow irrigation was provided every 10-12 days to maintain optimal growth conditions. Observation were recorded on morphological traits like early vigour, days to fifty percent flowering, Days to maturity, Plant height (cm), Number of productive tillers per meter, Spike length (cm), Number of spikelets per spike, Peduncle length (cm), Number grains per spike, Thousand grain weight (g), Grain filling duration, Biomass, Grain yield per plot, Harvest index and physiological traits like SPAD (Soil Plant Analysis Development for chlorophyll content) meter reading, NDVI (Normalized Difference Vegetation Index).

Results and discussion

Genetic variability parameters

Genetic variability parameters are key to assessing diversity and guiding breeding decisions. The Genotypic Coefficient of Variation (GCV) shows genetic influence, while the Phenotypic Coefficient of Variation (PCV) reflects both genetic and environmental effects. High GCV and PCV indicate strong potential for genetic improvement. The Mean, Range, GCV, PCV, heritability and GAM for yield, yield attributes, and grain nutrient traits are presented in Table 2. Low GCV (9.34%) and PCV (9.65%) for days to 50% flowering suggesting limited variability, but high heritability and moderate Genetic Advance as a per cent of (GAM) were observed, showing that high heritability doesn't always lead to high genetic gain. Similar findings were noted by Islam *et al*. (2017), Bhanu *et al*. (2018), and Poudel *et al*. (2021). For days to maturity, low GCV (7.74%) and PCV (8.15%) were observed with high heritability and moderate GAM, aligning with Bayisa *et al*. (2020), suggesting moderate genetic progress.

For the number of productive tillers, moderate GCV (14.12%) and PCV (14.90%) values were recorded along with high heritability and high GAM, suggesting significant potential for genetic improvement. Similar findings were reported by Singh *et al*. (2013) and Suryakanth *et al*. (2011), who highlighted high heritability and GAM for traits associated with tiller production. Peduncle length exhibited high GCV (32.38%) and PCV (32.95%), heritability, and GAM, indicating substantial genetic variability and strong selection potential for this trait. This observation is consistent with the findings of Zewdu *et al*. (2024), who noted that high heritability coupled with high GAM is indicative of additive gene actions, making the trait suitable for improvement through direct selection.

Table 1. List of different speices of wheat genotypes employed in the current investigation along with their pedigree and salient features

Name	Species	Pedigree	Salient features
HTW 6 (IC029007A)	*Triticum aestivum*	Genetic stock	High zinc content
MP 1378	*Triticum aestivum*	18HRWYT218/DBW17	High zinc content
UAS 334	*Triticum aestivum*	SITE/MO/4/NAC/TH. AC//3*PVN/3/ MIRL O/BUC	Released and notified for irrigated condition of Karnataka and Maharashtra
UAS 3020	*Triticum aestivum*	UAS 320 X (QUAIU#3//MILAN/AMSEL)	High yielding genotype for irrigated condition
HD 2888	*Triticum aestivum*	C306/*T.sphaerococcum*//HW 2004	Low zinc content
KRL 283	*Triticum aestivum*	CPAN 3004/ KHARCHIA65//PBW 343	Low zinc content
HI 8777	*Triticum durum*	B93/HD4672// HI8627	High zinc content
UASQ 332	*Triticum durum*	Gamma irradiation (150gy) of F1 (DDK 1001/HD 4501)	High zinc content
UAS DW 31442	*Triticum durum*	Korifla/AegSpeltoidesSyr// Heider	Low zinc content
UAS DW 31260	*Triticum durum*	HI 8693 X DWR 1006	Low zinc content
UAS 428	*Triticum durum*	GREEN-14/YAV- 10/AUK/UAS402	Released and notified for irrigated condition of Karnataka and Maharashtra
MACS 3949	*Triticum durum*	STOT//ALTAR84/AL D/3/THB/CEP7780// 2*MUSK_4	Released and notified for irrigated condition of Karnataka and Maharashtra
DDK-50931	*Triticum diccoccum*	NP 200 X GPM DIC90	High zinc content
DDK 508031	*Triticum diccoccum*	HW-5016 x HW-1098	High zinc content
GPM DIC 20	*Triticum diccoccum*	DDK-50337	Low zinc content
DDK 51182	*Triticum diccoccum*	DDK 1029 X NIDW 295	Low zinc content
DDK 1029	*Triticum diccoccum*	DDK 1012/HW 1093//276-15	Released and notified for irrigated condition of Karnataka and Maharashtra
HW 1098	*Triticum diccoccum*	NP 201 (Mutant developed through 20 Kr irradiation)	Released and notified for irrigated condition of Karnataka and Maharashtra

Table 2. Summary of mean, range, and genetic variation parameters for different traits in wheat genotypes.

Characters	Range		Mean	GCV	PCV	h^2_{bs}	GAM
	Min	Max		(%)	(%)		
EV	0.56	0.72	0.65	6.61	7.07	87.35	12.73
DFF	58	78	65	9.34	9.65	93.76	18.63
DM	92	114	100	7.74	8.15	90.07	15.12
NPT	65	124.75	98.52	14.12	14.9	89.76	27.55
PL	7.55	21.4	12.53	32.38	32.95	96.54	65.53
PH	64.7	98.8	80.87	12.53	12.94	93.84	25.01
SL	5.4	9.55	7.9	15.48	15.69	97.35	31.47
SPS	14	24.6	18.44	15.93	16.78	90.17	31.16
GPS	28.5	57.67	41.49	18.41	20.52	80.5	34.03
GFD	20.5	31.5	26.83	10.23	12.09	71.51	17.81
SPAD I	35.4	58.3	48.25	11.62	14.35	65.56	19.38
SPAD II	31.9	49.8	36.41	8.44	14.08	35.94	10.43
NDVI I	0.32	0.63	0.43	22.47	25.19	79.59	41.3
NDVI II	0.22	0.53	0.33	28.37	31.58	80.71	52.51
TGW	31.23	53.16	43.68	14.64	16.23	81.37	27.21
GY	25.17	51.94	41.37	14.02	17.1	67.26	23.69
BMS	73.61	133.33	109.54	12.64	20.19	39.19	16.3
HI	0.29	0.46	0.36	12.75	15.83	64.85	21.15
Protien%	11.94	17.96	14.07	10.1	10.7	89.08	19.64
Zn ppm	20.85	33	26.84	11.59	15.69	54.58	17.64
Fe ppm	33.85	48.5	38.59	9.94	10.13	96.33	20.1

GCV - Genotypic coefficient of variation PCV – Phenotypic coefficient of variation

GAM - Genetic advance over mean h^2_{bs} – Broad sense heritability

EV-early vigour, DFF-days to 50 per cent flowering, DM-days to maturity, NPT-number of productive tillers per meter, PL-peduncle length (cm), PH-plant height (cm), SPS-number of spikelets per spike, SL-spike length (cm), GPS-number of grains per spike, GFD-Grain filling duration, SPAD I and II-chlorophyll content at anthesis and grain filling stage, respectively, NDVI I and II-normalized difference vegetation index at anthesis and grain filling stage, respectively, TGW- Thousand grain weight (g), GY-grain yield (q/ha), BMS-biomass (q/ha), HI-harvest index, Zn (ppm)-Zinc parts per million, Fe (ppm) –Iron parts per million

Plant height exhibited moderate GCV (12.53%) and PCV (12.94 %), High heritability coupled with high GAM, suggesting that the trait could be effectively improved through selection, as observed by Devesh *et al*. (2018). For spike length, moderate GCV (15.48%) and PCV (15.69%) were recorded, along with high heritability and high GAM, supporting findings by Abrar *et al*. (2020). In the case of the number of spikelets per spike, moderate GCV (15.93%) and PCV (16.78%) were observed, accompanied by high heritability and GAM, consistent with Krishna *et al*. (2020) mentioned that Heritability estimate is more reliable when coupled with genetic advance values and aids in effective selection.The number of grains per spike showed moderate GCV (18.41%) and high PCV (20.52%) with moderate heritability and high GAM, reflecting findings by Kaur *et al*. (2023). For grain filling duration, showed moderate GCV (10.23%) and low PCV (12.09%) were noted, along with high heritability and moderate GAM, which aligns with the findings of Bayisa *et al.* (2020).

Thousand-grain weight and grain yield had moderate GCV and PCV, with high heritability and GAM, suggesting strong genetic improvement potential, similar to Dabi *et al*. (2019) and Rana *et al*. (2019). Biomass showed moderate GCV (12.64%) and high PCV (20.19%), with moderate heritability and GAM, indicating environmental influence but scope for selection. Harvest index also had moderate GCV and PCV with high heritability and GAM, aligning with Saxena *et al*. (2007). Protein content exhibited moderate GCV, PCV and high heritability, confirming genetic control (Arati *et al*., 2015; Naik *et al*., 2015). Zinc content showed moderate GCV, PCV, high heritability, and moderate GAM, echoing Heidari *et al*. (2016) and Fyroj *et al.* (2017). Iron content revealed low GCV (9.94%), moderate PCV (10.13%), high heritability and GAM, supporting potential for genetic gains (Naik *et al*., 2015).

Correlation response of yield with yield components

Grain yield, a complex polygenic trait, requires indirect selection strategies based on its component traits. This study analyzes correlations between yield, yield attributes and grain nutrients across wheat genotypes are shown in Table 3. The biomass showed a highly significant positive correlation with grain yield, aligning with Abderrahmane *et al*. (2013) and number of grains per spike demonstrated a significant positive correlation with grain yield. This indicates that this trait can be a reliable criterion for selecting and improving grain yield in wheat, as supported by Bhutto *et al.* (2016). Traits like days to fifty percent flowering, days to maturity, spike length, and spikelets per spike, number of productive tillers and harvest index had non-significant positive correlations, similar to findings by Abdul *et al*. (2014), Heidari *et al*. (2016) and Wahidy *et al*. (2016).

Association of grain yield with grain nutrients

Iron content showed a negative correlation with yield, aligning with Oury *et al*. (2006), suggesting a trade-off between nutrient content and yield. Protein content also exhibited a

Table 3. Character association for morpho-physiological, yield and yield attributes, and grain nutrients in different species of wheat genotypes

	EV	DFF	DM	NPT	PL	PH	SL	SPS	GPS	GFD	SPADI	SPADII	NDVII	NDVIII	TGW	Biomass	HI	Protein	Zn	Fe	GY
EV	1**	0.24	0.136	0.201	-0.258	-0.177	0.168	0.3	0.199	-0.072	0.129	0.267	0.248	0.153	-0.265	0	0.259	-0.162	-0.082-	0.076	0.134
DFF		1**	0.760**	0.083	-0.697**	0.257	0.677**	0.800**	-0.251	-0.085	-0.2	-0.119	0.814**	0.764**	0.074	-0.119	0.498**	-0.054	0.279	0.567**	0.142
DM			1**	0.118	-0.514**	0.152	0.660**	0.662**	-0.218	0.393*	-0.155	0.013	0.798**	0.673**	0.21	-0.231	0.458**	0.126	0.268	0.486**	0.116
NPT				1**	-0.189	-0.005	0.099	0.157	0.357*	0.097	0.198	-0.053	0.177	0.118	-0.061	0.218	0.113	0.235	-0.266`	-0.185	0.242
PL					1**	0.073	-0.845**	-0.777**	-0.057	0.162	0.341*	0.019	-0.680**	-0.659**	0.204	-0.187	-0.372*	0.124	0.1	-0.3	-0.386*
PH						1**	-0.077	0.215	-0.294	0.051	-0.134	-0.01	0.112	0.22	0.493**	-0.036	-0.161	0.379*	0.565**	0.686**	-0.289
SL							1**	0.741**	-0.068	-0.103	-0.203	-0.005	0.606**	0.628**	-0.138	-0.029	0.313	-0.158	-0.108	0.395*	0.179
SPS								1**	-0.301	0.015	-0.288	0.032	0.712**	0.619**	0.14	0.017	0.357*	0.022	0.315	0.511**	0.217
GPS									1**	-0.138	0.06	-0.27	-0.157	-0.109	-0.517**	0.06	0.204	-0.123	-0.573**	-0.426**	0.333*
GFD										1**	0.236	0.202	0.164	-0.023	0.361*	-0.05	0.086	0.173	0.198	0.086	0.125
SPADI											1**	0.308	-0.274	-0.278	0.069	-0.004	0.015	-0.194	-0.192	-0.103	-0.002
SPADII												1**	-0.091	-0.065	0.016	0.096	-0.253	0.137	0.045	0.016	-0.185
NDVII													1**	0.858 **	0.165	-0.157	0.512**	0.008	0.215	0.333*	0.166
NDVIII														1**	0.028	-0.178	0.424**	-0.002	0.242	0.467**	0.057
TGW															1**	-0.027	-0.217	0.383*	0.606**	0.324	-0.186
Biomass																1**	-0.469**	0.232	-0.208-	0.076	0.474**
HI																	1**	-0.262	-0.125	0.088	0.308
Protein																		1**	0.197	0.146	-0.014
Zn																			1**	0.515**	-0.329
Fe																				1**	-0.137
GY																					1**

**. Correlation is significant at the 0.01 level, *. Correlation is significant at the 0.05 level.EV-early vigour, DFF-days to 50 per cent flowering, DM-days to maturity, NPT-number of productive tillers per meter, PL-peduncle length (cm), PH-plant height (cm), SPS-number of spikelets per spike, SL-spike length (cm), GPS-number of grains per spike, GFD-Grain filling duration, SPAD I and II-chlorophyll content at anthesis and grain filling stage, respectively, NDVI I and II-normalized difference vegetation index at anthesis and grain filling stage, respectively, TGW- Thousand grain weight (g), GY-grain yield (q/ha), BMS-biomass (q/ha), HI-harvest index, Zn (ppm)-Zinc parts per million, Fe (ppm) –Iron parts per million

non-significant negative correlation with yield, consistent with Blanco *et al*. (2012), highlighting the challenge of balancing quality traits like protein with yield in wheat breeding.

Conclusion

The study highlights variability in key traits and their implications for wheat breeding. Traits like peduncle length, spike length and productive tillers showed high heritability and genetic advance, indicating strong potential for improvement through direct selection. However, traits such as days to 50% flowering and days to maturity exhibited low variability despite high heritability, suggesting limited genetic progress. Correlation analysis showed that the number of grain per spike and biomass was strongly linked to grain yield, while nutrient traits like iron and protein content had a negative relationship with yield, underscoring the challenge of balancing yield and nutritional quality in breeding efforts.

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