International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
© Agronomy
NAAS Rating (2025): 5.20
www.agronomyjournals.com
2025; 8(9): 715-720
Received: 06-07-2025
Accepted: 07-08-2025

KV Sapkal
M.Sc., Department of Genetics and Plant Breeding, College of Agriculture, VNMKV, Parbhani, Maharashtra, India

SM Umate
Wheat and Maize Breeder, VNMKV, Parbhani, Maharashtra, India

HV Kalpande
Head of Department of Genetics and Plant Breeding, College of Agriculture, VNMKV, Parbhani, Maharashtra, India

DK Zate
Associate Professor, Department of Genetics and Plant Breeding, College of Agriculture, VNMKV, Parbhani, Maharashtra, India

PD Khadke
M.Sc., Department of Agronomy, College of Agriculture, VNMKV, Parbhani, Maharashtra, India

JR Rakhonde
M.Sc., Department of Genetics and Plant Breeding, College of Agriculture, VNMKV, Parbhani, Maharashtra, India

SP Shirale
M.Sc., Department of Agronomy, College of Agriculture, VNMKV, Parbhani, Maharashtra, India

G Praveen Kumar
Young Professional (CIMMYT-BISA), VNMKV, Parbhani, Maharashtra, India

Corresponding Author:
KV Sapkal
M.Sc., Department of Genetics and Plant Breeding, College of Agriculture, VNMKV, Parbhani, Maharashtra, India

Genetic variability studies in durum wheat (*Triticum durum* L.)

KV Sapkal, SM Umate, HV Kalpande, DK Zate, PD Khadke, JR Rakhonde, SP Shirale and G Praveen Kumar

DOI: https://www.doi.org/10.33545/2618060X.2025.v8.i9j.3842

Abstract

The study was conducted with thirty-two durum wheat genotypes along with four checks at the Wheat and Maize Research Unit, VNMKV, Parbhani during *Rabi* 2024-25. The experiment followed a randomized block design with two replications. Data were collected on yield and yield related traits to assess genetic variability, heritability, genetic advance and correlation among characters. Analysis of variance indicated significant variation among genotypes for all ten traits studied, showing the presence of sufficient diversity. Grain yield per plant showed the highest genotypic and phenotypic coefficients of variation. High heritability along with high genetic advance was noted for grain yield per plant, harvest index, biological yield per plant and grains per spike, suggesting the role of additive gene action. Genotypic correlations were generally stronger than phenotypic ones, highlighting inherent genetic associations among traits. Grain yield per plant showed positive correlations with days to heading, days to maturity, productive tillers, biological yield and harvest index. These findings suggest that direct selection for these traits may lead to effective yield improvement in durum wheat.

Keywords: Wheat, variability, heritability, genetic advance as per mean, correlation

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important food crops of the world and has been called the *"king of cereals"* because of its global acreage, productivity and role in global food trade. It is a self-pollinated crop belonging to the family *Poaceae and* genus *Triticum*. The crop is believed to have originated in the Mediterranean and Southwest Asia and its long history of domestication and polyploidy has given it wide adaptability.

Domestication of wheat and its ploidy growth had (from diploid to tetraploid to hexaploid) greatly influenced its morphology and physiology. In modern times, wheat has larger leaves, a reduced tillering phase, fewer but heavier and larger spikes and nearly no shattering (Simmons, 1987) [17]. Grain yield is mostly due to the improved distribution of above-ground mass to the grain and modern wheat depends more on photosynthates from leaves and stems for grain filling than spikes. The greater distribution of the above-ground mass to the grain in modern wheat is primarily responsible for grain production, as grain filling depends more on photosynthates from leaves and stems than from spikes (Jensen, 1978) [12]. Additionally, reported that dwarf Mexican wheat, which triggered the green revolution. In other words, the wheat revolution in India was associated with a drop in plant height.

Wheat cultivated in India is classified into three genomic categories: diploid Emmer wheat (*T. monococcum*) (AA) (2n=14), tetraploid wheat i.e. Durum wheat (*T. durum*) (AABB) (2n=28) and hexaploid wheat (*T. aestivum*) (AABBDD) (2n=42), which account for 86%, 12% and 2% of the total wheat area, respectively (Ukani *et al.* 2015) [21].

Durum wheat (*Triticum durum* Desf.) is classified within the genus *Triticum*, tribe *Triticeae*, family *Poaceae* and subfamily *Pooideae*. A 100 g serving of durum wheat has 339 calories, 71 g of carbohydrates, 14 g of protein, 2.5 g of fat, 2 g of minerals and significant amounts of vitamins (thiamine and vitamin-B) and minerals (zinc and iron) (Wolde *et al.* 2016) [22]. The tetraploid (AABB, 2n=4x=28) durum wheat (*Triticum turgidum* ssp. durum) has 14 chromosome (gamatic number) and two separate genomes: A and B. These chromosomes are organized into seven homoeologous groups, each consisting of a pair of partially homologous chromosomes one from the A genome and one from the B genome.

Genetic variability is the key to any crop improvement program. Wide range of variability among genotypes increases the chances of selecting superior recombinants. Estimating genetic parameters such as variability, heritability and genetic advance helps breeders understand the nature of gene action and the efficiency of selection. Similarly, correlation analysis provides insight into the relationship among traits, which is useful for identifying indirect selection criteria for improving yield.

Material and Methodology

The thirty-six wheat genotypes used in the experiment were obtained from the Wheat and Maize Research Unit at the College of Agriculture, VNMKV, Parbhani, Maharashtra, India (Table 1). The plot size was 6 m × 1.20 m and the inter-intra row spacing was 20 × 10 cm. In 2024-2025, the seeds were planted on 9th of November. Two replications of these genotypes were seeded using a Randomized Block Design. According to the DUS criteria, five competing plants per genotype were chosen at random for each replication and observations were documented.

Statistical Analysis

For statistical analysis, the mean values of each genotype were used. The formula proposed by Burton (1952) [4] was used to determine the genotypic and phenotypic coefficients of variance (GCV and PCV, respectively).

The formula proposed by Johnson *et al.* (1955) [13] was used to estimate the percentage of heritability in a wide sense, genetic advance and genetic advance as a per cent mean.

The formula proposed by Johnson *et al.* (1955) [13] was used to calculate the genotypic and phenotypic correlation coefficient between characters using the corresponding components of variances and co-variances.

Results and Discussion

Analysis of Variance

According to the results of the analysis of variance, there were significant differences between the thirty-six genotypes for each of the ten characters: days to 50% heading, days to maturity, number of productive tillers per plant, spike length, number of grains per spike, biological yield per plant, 1000 seed weight, grain yield per plant, plant height and harvest index (Table 2).

Estimation of Genetic Parameters

In Table 3 and Fig. 1, the genetic traits of the characters are displayed, including mean, range, PCV and GCV, heritability and genetic advance as a per cent of mean. Significant variations in mean values for all characteristics were noted in the current study. The trait days to 50 % heading from 53 days to 68 days with a general mean of 58.57 days, days to maturity 99.00 days to 108 days with general mean of 101.75 days, number of productive tillers per plant 5.4 to 7.4 with general mean 6.12, length of main spike 5.65 cm to 7.00 cm with general mean of 6.15 cm, number of grains per spike 30.50 to 51.50 with a general mean of 41.73, biological yield per plant 18.40 g to 35.00 g with a general mean of 24.58g, 1000 seed weight 39.69 g to 56.13 g with general mean of 46.25 g, grain yield per plant 5.9 g to 15.2 g with a general mean 8.29 g., plant height 73.70 cm to 97.70 cm with general mean 84.85 cm and harvest index 27.48% to 52.45% with general mean value 33.76%. The majority of the traits under study showed favourable mean performance with an immense amount of variability in the experimental material.

Estimation of Genotypic and Phenotypic Variance

Variability is a key component of crop breeding. In order to have a breeding program which succeeds, genetic variability is necessary. Genetic and environmental factors contribute to the overall diversity found in a population. For a plant breeding effort to be successful, the breeding material must have genetic variation. Genetic variability in plant populations is a major contributor of selection efficiency. Genetic variability was assessed using mean value estimation, phenotypic and genotypic coefficient of variation, heritability, genetic advance as a percentage of mean and genetic advance.

For various characters, estimates of PCV ($\sigma 2p$) and GCV ($\sigma 2g$) were calculated (Table 3, Fig. 1). For every trait, a broad range of variability is recorded. For every characteristics, the PCV estimations were greater than the corresponding GCV. For practically every character, a close relationship between GCV and PCV values indicated that the environment had less of an impact on the character's expressions. For all yield and yield related characters, phenotypic variance was greater than genotypic variance, suggesting that these traits are not significantly affected by the environment. Grain yield per plant (g) showed significant PCV and GCV. Similar outcomes for high heritability estimates were reported by (Dashora *et al.* 2020) [5] and (Gerema, 2021) [11]. The parameters number of grains per spike, biological yield per plant (g) and harvest index (%) showed considerable PCV and GCV. The present findings are consisted of (Nukasani *et al.* 2014) [15], (Neetu *et al.* 2021) [14], (Singh *et al.* 2023) [18] and (Zewdu *et al.* 2024) [23]. Whereas low PCV and GCV were found for days to 50% heading, day to maturirty, number of productive tillers per plant, spike length (cm), plant height (cm) and 1000 grain weight (g). Previous studies have also revealed comparable findings (Abinasa *et al.* 2011) [2], (Dragov *et al.* 2022) [7], (Dukamo *et al.* 2024) [8], (Ebsa *et al.* 2024) [9], (Fikir, 2024) [10], (Gerema, 2021) [11], (Neetu *et al.* 2021) [14], (Tsegaye *et al.* 2012) [20] and (Zewdu *et al.* 2024) [23]. This suggests the limited potential for improving these traits by direct selection for better performing genotypes, as environmental factors influenced the expression of these characters more than genetic factors did.

Heritability (Broad Sense) and Genetic Advance as Percent of Mean

The degree of inheritance of any given trait can be assessed by heritability estimates. However, high heritability indicates a significant proportion of variation that is heritable, which breeders can use to figure out superior genotypes. While genetic advance indicates the role of the type of gene action in the development of a specific trait, heritability predicts the transmission of characteristics from parents to offsprings. High heritability and greater genetic advance are evidence that additive gene action plays a role in both the expression and transmission of any trait and selection may work well in these situations.

According to Table 3, estimates of broad sense heritability ranged from 46.32% to 97.79%. High heritability and greater genetic advance were observed in the current investigation for harvest index (%), biological yield per plant (g), grain yield per plant (g) and number of grains per spike. However, plant height (cm), 1000 grain weight (g) and the number of tillers per plant showed high heritability and moderate genetic advance, suggesting that these traits are less affected by the environment and are controlled by both additive and non-additive gene activity. Days to maturity, spike length and day to 50% heading all indicated low genetic advance.

These results coincide with those of the study carried out by Abinasa *et al.* (2011) [2], (Dragov *et al.* 2022) [7], (Dukamo *et al.* 2024) [8], (Ebsa *et al.* 2024)[9], (Fikir, 2024) [10], (Gerema, 2021) [11], (Neetu *et al.* 2021) [14], (Nukasani *et al.* 2014)[15], (Singh *et al.* 2023)[18], (Tsegaye *et al.* 2012) [20] and (Zewdu *et al.* 2024) [23].

Estimates of Phenotypic and Genotypic Correlation Coefficients

All of the traits under study had their respective genetic and phenotypic correlation coefficients estimated (Table 4). Plant breeders place more importance on genotypic correlation than phenotypic correlation when it comes to the genetic improvement of any one character by choosing the other character that is genetically correlated with the selected trait. Phenotypic correlation is the observable correlation between two variables, including both genotypic and environmental effect. For the majority of the qualities examined in this study, genotypic correlation coefficients were found to be larger in magnitude than phenotypic correlation coefficients. This clearly demonstrated the existence of an inherent relationship between different characters. Numerous previous studies also found that phenotypic correlation coefficients were smaller than genotypic correlation coefficients, indicating that there were inherent genetic relationships between different characters and that environmental factors had less of an impact on the phenotypic expression of these traits.

Grain yield per plant was found to be significant positive correlation with day to 50% heading, day to maturity, number of productive tillers per plant, biological yield per plant and harvest index in the current research's genotypic and phenotypic correlation analysis. Days to 50% heading, on the other hand, showed a strong correlation with harvest index, biological yield per plant, days to maturity, grain yield per plant and grains per spike. Whereas, days to maturity had a significant positive correlation with days to 50% heading, harvest index, grain yield per plant.

Number of productive tillers per plant showed significant positive correlation with spike length, grain yield per plant and biological yield per plant. Number of grains per spike exhibited positive significant correlation with day to 50% heading, spike length, biological yield per plant. Spike length presented significant positive correlation with number of productive tillers per plant, number of grains per spike. Biological yield per plant disclosed significant positive correlation with day to 50% heading, number of grains per spike, 1000 grain weight, grain yield per plant and number of productive tillers per plant. However, plant height revealed positive correlation with 1000 grain weight and harvest index. Harvest index is significantly positively correlated with day to 50% heading, day to maturity and grain yield per plant. 1000 grain weight is significantly positively correlated with plant height and biological yield per plant. Selecting superior wheat varieties should place more emphasis on the inter-relationships among yield components since they will help to raise yield levels.

Similarly, it has been documented that grain yield is correlated with one or more traits by (Abdulhamid *et al.* 2017) [1], (Alemu *et al.* 2020) [3], (Dashora *et al.* 2020) [5], (Donga *et al.* (2022) [6], (Gerema, 2021) [11], (Nukasani *et al.* 2014)[15], (Sadgar *et al.* 2021) [16], (Singh *et al.* 2023) [18], (Tegenu *et al.* 2019) [19] and (Tsegaye *et al.* 2012) [20].

Conclusion

Thirty-six wheat genotypes showed significant variations for all traits investigated, including the requirement for efficient selection. These traits are controlled by additive gene action, so direct selection for this trait will produce more effective results for increasing the grain yield through genetic improvement in wheat. High heritability and moderate genetic advancement were observed in the percent mean of the number of tillers per plant, plant height and 1000 grain weight. At both the genotypic and phenotypic levels, there was a significant positive correlation found between the harvest index, the number of productive tillers per plant, the day to maturity, the day to heading and the biological yield per plant. Therefore, selecting these characters could be used for improvement. Therefore, in future breeding programs, selection for these traits may be used to increase wheat yield.

Table 1: Pedigree name and genotype selection history details are given below

Trial	Selection History	Pedigree
AMLS3-01	ICDM19-033-0MCH-0SAN-15MCH0SAN-4MCH-0SAN-0MCH-0AML	Halab/4/Geromtel1/Icasyr1/3/Korifla/AegSpeltoides Syr//Amedakul
AMLS3-02	ICDM19-044-0MCH-0SAN-15MCH0SAN-12MCH-0SAN-0MCH-0AML	Halab/Jabal
AMLS3-03	ICDM19-132-0MCH-0SAN-15MCH0SAN-3MCH-0SAN-0MCH-0AML	Azizeraa/Farkassem
AMLS3-04	ICDM19-214-0MCH-0SAN-15MCH0SAN-4MCH-0SAN-0MCH-0AML	Gigamor/Adnham
AMLS3-05	ICDL19(f2)-012-0STR-040TR-0STR12MCH-0SAN-0MCH-0AML	Zagharin2/4/Saada3/DDS//MTL1/3/Kundermiki
AMLS3-06	ICDL19(f2)-013-0STR-040TR-0STR12MCH-0SAN-0MCH-0AML	Zagharin2/4/Saada3/DDS//MTL1/3/Bezajihan
AMLS3-07	ICDL19(f2)-041-0STR-040TR-0STR11MCH-0SAN-0MCH-0AML	Syryopis/7/Shabha/6/CandocrossH25/Bicrederaa1/3 /ICAMORTA0463//Lah/Ch12504/4/Bcrch1//Ossl1/ Stj5/5/Ysf1/Otb6
AMLS3-08	ICDL19(f2)-054-0STR-040TR-0STR9MCH-0SAN-0MCH-0AML	Margherita/Ouassara3/14/Icavert2/13/SNITAN/5/A JAIA_12/F3LOCAL (SEL.ETHIO.135.85)//PLATA_13/3/SOMAT_3/4/SOOTY_9/RASCON_37/6/SNITAN/11/CANELO_9.1/SNITAN/10/PLATA_10/6/MQUE/4/USDA573/

		/QFN/AA_7/3/ALBAD/5/AVO/HUI/7/PLATA_13/8/THKNEE_11/9/CH EN/ALTAR 84/3/HUI/POC//BUB/RUFO/4/FNFOOT/12/CBC 509
AMLS3-09	ICDL19(f2)-077-0STR-040TR-0STR2MCH-0SAN-0MCH-0AML	Icamoram7/Simeto.Lr19[R5A83(R5210HOM+)]/5/J k/Ch1604//Ysf1/Otb6/3/Adnan2/Berghouata1/4/Hal ab
AMLS3-10	ICDL19(f2)-079-0STR-040TR-0STR8MCH-0SAN-0MCH-0AML	Icamoram7/Simeto.Lr19[R5A83(R5210HOM+)]/8/I caghram/7/PLATA_7/ILBOR_1//SOMAT_3/3/CA BECA_2/PATKA_4//BEHRANG/5/ARMENT//SR N_3/NIGRIS_4/3/CANELO_9.1/4/VITROMAX/6/ SOOTY_9/RASCON_37//GUAYACAN INIA
AMLS3-11	ICDL19(f2)-092-0STR-040TR-0STR6MCH-0SAN-0MCH-0AML	Icamoram7/Simeto.Lr19[R5A83(R5210HOM+)]/9/ Terbol975/Geruftel2/7/Icasyr1//Mrf2/T.dids20123/6 /319ADDO/5/D68193A1A//Ruff/Fg/3/Mtl5/4/Lahn/ 8/Icaverve
AMLS3-12	ICDL19(f2)-092-0STR-040TR-0STR11MCH-0SAN-0MCH-0AML	Icamoram7/Simeto.Lr19[R5A83(R5210HOM+)]/9/ Terbol975/Geruftel2/7/Icasyr1//Mrf2/T.dids20123/6 /319ADDO/5/D68193A1A//Ruff/Fg/3/Mtl5/4/Lahn/ 8/Icaverve
AMLS3-13	ICDL19(f2)-097-0STR-040TR-0STR11MCH-0SAN-0MCH-0AML	Levante/7/Mrb3/Tboeoticum500648//IcamorTA046 2/Maamouri3/3/Mgnl3/Ainzen1/4/Ter1/3/Stj3//Bcr/ Lks4/5/Marsyr3//Lgt3/Bcrch1/6/Halab
AMLS3-14	ICDL19(f2)-107-0STR-040TR-0STR2MCH-0SAN-0MCH-0AML	Levante//Icaltagy/Zeina
AMLS3-15	ICDL19(f2)-108-0STR-040TR-0STR10MCH-0SAN-0MCH-0AML	Levante//Icaltagy/Sahi
AMLS3-16	ICDL19(f2)-115-0STR-040TR-0STR7MCH-0SAN-0MCH-0AML	Levante//Wasihun/Bezater
AMLS3-17	ICDL19(f2)-117-0STR-040TR-0STR7MCH-0SAN-0MCH-0AML	Levante/7/Wasihun/6/Icasyr1/3/Gcn//Stj/Mrb3/5/M gnl3/Ainzen1/3/ICAMORTA0463//H.mouline/Sbl2/ 4/Mgnl3/Ainzen1
AMLS3-18	ICDL19(f2)-123-0STR-040TR-0STR4MCH-0SAN-0MCH-0AML	Adnham/8/Ouasloukos1/5/Azn1/4/BEZAIZSHF//S D19539/Waha/3/Gdr2/6/Tilling/ch113/7/UAD0951 096
AMLS3-19	ICDL19(f2)-185-0STR-040TR-0STR12MCH-0SAN-0MCH-0AML	Zaghramy//Swaghost/Zeina
AMLS3-20	ICDL19(f2)-191-0STR-040TR-0STR11MCH-0SAN-0MCH-0AML	Zaghramy//Sahi/Cucaraja
AMLS3-21	ICDL19(f2)-197-0STR-040TR-0STR8MCH-0SAN-0MCH-0AML	Saragolla//Halab/Icaverve
AMLS3-22	ICDTR(f2)14-0470-0STR-020TR-0STR0TR-1AML-0AML-2AML-0AML0AML	Tilling/ch1- 7/4/MorlF38//Bcrch1/Kund1149/3/Bicrederaa1/Miki/5/Ouas bar-1/Jamile-2
AMLS3-23	ICDL17-136-0STR-015TR-0STR-1TR0STR-1TR-0STR-0AREC-0AML	Zeina/Cucaraja
AMLS3-24	ICDM16-305-0SAN-0MCH-015MCH0SAN-2MCH-0SAN-1MCH-0SAN0AREC-0AML	Margherita//DBA_Aurora/
AMLS3-25	ICDTR15-133-0STR-015TR-0STR0TR-2AML-0AML	Ouassara1/7/Ossl1/Stj5/5/Bidra1/4/BezaizSHF//SD 19539/Waha/3/Stj/Mrb3/6/Icajihan2
AMLS3-26	ICDM16-324-0SAN-0MCH-015MCH0SAN-4MCH-0SAN-1MCH-0SAN0AREC-0AML	Azeghar2//Jandaroi/Orenburgskaya10 ig:AUS23755
AMLS3-27	ICDTR15-160-0STR-015TR-0STR05ALT-015MCH-0SAN-3MCH-0SAN1MCH-0SAN-0AREC-0AML	Icamoram7/Saintly
AMLS3-28	ICDTR15-132-0STR-015TR-0STR0TR-3AML-0AML	Ouassara1/4/Msbl1//Awl2/Bit/3/T.dicoccoidesSYRI G117889
AMLS3-29	ICDM19-143-0MCH-0SAN-15MCH0SAN-2MCH-0SAN-0MCH-0AML	Syryopis/Berghouata1
AMLS3-30	ICDM19-236-0MCH-0SAN-15MCH0SAN-4MCH-0SAN-0MCH-0AML	Joudille/Castore
AMLS3-31	ICDL19(f2)-063-0STR-040TR-0STR1MCH-0SAN-0MCH-0AML	Margherita/Ouassara3//Kenzera/Sebatel1
AMLS3-32	ICDL19(f2)-085-0STR-040TR-0STR1MCH-0SAN-0MCH-0AML	Icamoram7/Simeto.Lr19[R5A83(R5210HOM+)]//M ammachan/Icaqinzen
AMLS3-33	Indore	HI8177/HI8158//HI8498
AMLS3-34	Indore	HD4672/PDW233
AMLS3-35	Indore	HD 4672/ PDW 233
AMLS3-36	Dharwad	DWR-185/DWR-2006//UAS-419

Table 2: Analysis of variance for thirty six genotypes for yield and yield attributing characters of wheat.

Sr. No.	**Characters**	**Mean sum of squares**		
		Replication (df=1)	**Genotypes (df=35)**	**Error (35)**
1.	Days to 50% heading	0.68	21.58**	4.05
2.	Days to maturity	2.72	5.07**	2.72
3.	Number of Tillers/plant	0.04	0.48**	0.09
4.	Plant height (cm)	11.00	52.69**	8.57
5.	Spike length(cm)	0.20	0.23**	0.10
6.	Number of grain/Spike	2.35	63.51**	2.39
7.	Biological Yeild/Plant(g)	0.64	30.78**	1.23
8.	1000-grain weight (g)	0.41	30.79**	0.68
9.	Grain yield per plant(g)	0.29	6.36**	0.28
10.	Harvest index (%)	21.03	39.20**	6.23

*, ** Signifcant at P = 0.05 and P = 0.01 levels of probability, respectively.

Table 3: Estimates of variability parameters for yield and yield contributing characters for ten characters in thirty six genotypes of wheat

S. No.	**Characters**	**Mean**	**Range**		**Phenotypic Variance**	**Genotypic Variance**	**PCV (%)**	**GCV (%)**	**Heritability in broad sense (H^2) (%)**	**Genetic Advance as % of mean**
			Min	Max						
1	Days to 50% heading	58.57	53.00	68.00	10.78	8.76	5.60	5.05	81.22	9.38
2	Days to maturity	101.75	99.00	108.00	2.53	1.17	1.56	1.07	46.32	1.49
3	Number of Tillers/plant	6.12	5.40	7.40	0.24	0.20	8.06	7.27	81.58	13.51
4	Plant height (cm)	84.85	73.70	97.70	26.34	22.05	6.52	5.54	83.73	10.43
5	Spike length (cm)	6.15	5.65	7.00	0.12	0.07	5.52	4.18	57.57	6.54
6	Number of grain/Spike	41.73	30.50	51.50	31.75	30.56	13.50	13.25	96.24	26.77
7	Biological Yeild/Plant	24.58	18.40	35.00	15.39	14.78	15.95	15.64	96.02	31.56
8	1000-grain weight (g)	46.25	39.69	56.13	15.39	15.06	8.48	8.39	97.79	17.03
9	Harvest index (%)	33.76	27.48	52.45	19.60	16.49	13.12	12.03	72.60	22.72
10	Grain yield/plant (g)	8.29	5.90	15.20	3.18	3.04	21.50	21.01	95.50	42.30

GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation.

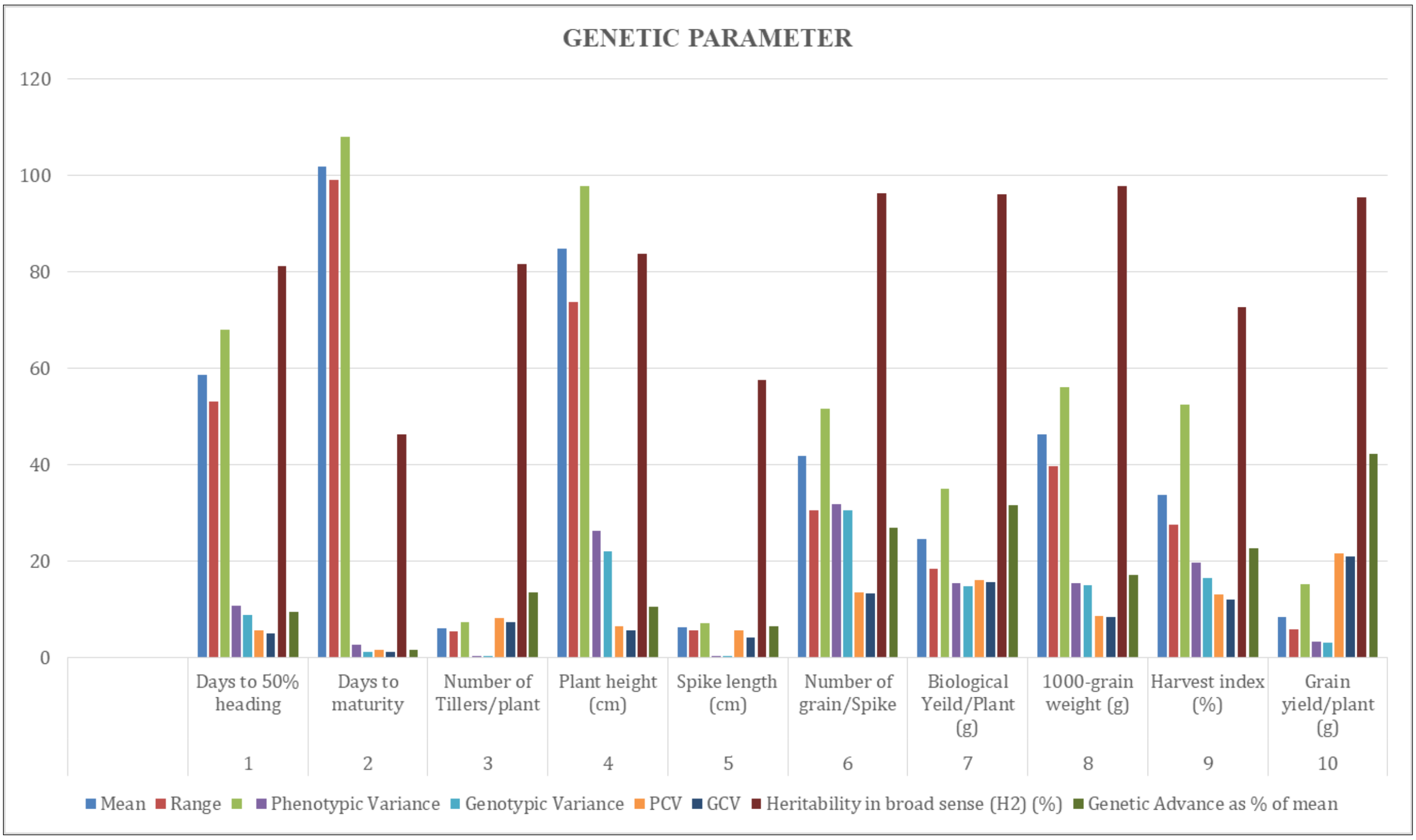

Fig 1: Genetic parameters and components of variance present among various traits of wheat genotypes.

Table 4: Genotypic correlation (Above diagonal) and phenotypic (below diagonal) correlation coefficients of wheat genotypes

	DH	DM	TL/PL	PH	SPL	Gs/Sp	Bi/PL	TW	HI	Gr/PL
DH	1	0.4525 **	-0.2363 *	-0.2276 *	-0.0606	0.2539 *	0.2329 *	0.0159	0.1847 *	0.2772 *
DM	0.4446 **	1	-0.0744	0.0281	-0.0199	0.1076	-0.0246	-0.3539 **	0.2507 *	0.1812 *
TL/PL	-0.0944	0.0955	1	-0.3337 **	0.4143 **	0.1452	0.5114 **	-0.2647 *	-0.1813 *	0.2768 *
PH	-0.1504	-0.0422	-0.1697 *	1	-0.0692	-0.3188 *	-0.0832	0.2381 *	0.2144 *	0.0692
SPL	-0.0793	-0.02	0.2074 *	-0.0143	1	0.6236 **	0.1658	0.0223	-0.4857 **	-0.1838 *
Gs/Sp	0.1928 *	0.0053	0.1258	-0.2406 *	0.37 **	1	0.2515 *	-0.2528 *	-0.1659	0.0977
Bi/PL	0.2179 *	0.0423	0.4736 **	-0.0375	0.1321	0.215 *	1	0.1821 *	0.0579	0.7851 **
TW	0.0092	-0.1425	-0.2216 *	0.1788 *	0.01	-0.2281 *	0.1683	1	-0.191*	0.0051
HI	0.1239	0.0538	-0.1696 *	0.1538	-0.2741 *	-0.1478	-0.0429	-0.1632	1	0.6769 **
Gr/PL	0.2366 *	0.0712	0.2284 *	0.0586	-0.0881	0.0732	0.7102 **	-0.0082	0.6527 **	1

**- Significant at p = 0.01 *- Significant at p = 0.05

DH- Days to 50% heading, DM- Days to maturity, TL/PL- Number of Tillers/plant, PH- Plant height (cm), SPL- Spike length (cm), Gs/Pl- Number of grain/Spike, Bi/PL- Biological Yeild/Plant (g), TW- 1000-grain weight (g), Gr/PL- Grain yield/plant (g), HI- Harvest index (%).

References

1. Abdul Hamid MIE, Qabil N, El Saadony FMA. Genetic variability, correlation and path analyses for yield and yield components of some bread wheat genotypes. J Plant Prod. 2017;8(8):845-852.
2. Abinasa M, Ayana A, Bultosa G. Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum* L. var. *durum*) genotypes. Afr J Agric Res. 2011;6(17):3972-3979.
3. Alemu YA, Anley AM, Abebe TD. Genetic variability and association of traits in Ethiopian durum wheat (*Triticum turgidium* L. var. *durum*) landraces at Dabat Research Station, North Gondar. Cogent Food & Agriculture. 2020;6:1778604.
4. Burton GW. Quantitative inheritance in grass. Proceedings of International Grass Land Congress. 1952;1:17-23.
5. Dashora A, Urmila, Gupta A, Khatik C. Assessment of genetic variability and correlation for yield and its components traits in durum wheat (*Triticum durum* Desf.). Int J Curr Microbiol Appl Sci. 2020;9(6):548-554.
6. Donga A, Prajapati K, Goswami P, Gajjar K. Study of genetic diversity and principal component analysis under limited irrigation in durum wheat (*Triticum durum* L.). Life Sci Res. 2022;8:124-131.
7. Dragov R, Uhr Z, Dimitrov E. Genetic variability, heritability and genetic advance for important quantitative traits of durum wheat: Part I. Bulg J Agric Sci. 2022;28(4).
8. Dukamo BH, Degu HD, Abitie AG, Asfaw BT. Genetic diversity analysis and population structure of selected Ethiopian durum wheat (*T. turgidum* subsp. *durum*) landraces using DArTSeq markers. J Agric Food Res. 2024;18:101529.
9. Ebsa MA, Tesso B, Letta T. Genetic analysis and quality assessment of durum wheat (*Triticum turgidum* L.) landraces in Ethiopia. Cogent Food & Agriculture. 2024;10(1):2303804.
10. Fikir Desalew. Evaluation of genetic variability in bread wheat (*Triticum aestivum* L.) genotypes at Holeta, Central Ethiopia. Genetic Molecular Research. 2024;23(3).
11. Gerema G. Evaluation of durum wheat (*Triticum turgidum*) genotypes for genetic variability, heritability, genetic advance and correlation studies. J Agric Nat Resour. 2021;3(2):150-159.
12. Jensen NF. Limits to growth in world food production. Science. 1978;201:317-320.
13. Johnson HW, Robinson HF, Comstock RE. Estimates of Genetic and Environmental Variability in Soybeans. Agron J. 1955;47:314-318.
14. Neetu Yadav, Abhay Dashora, Urmila Choudhary, Mayur Dave, Jyotsana Rathore. Assessment of genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.) Genotypes. Pharma Innov. 2021;10(9):528-530.
15. Nukasani V, Potdukhe NR, Bharad S, Deshmukh S, Shinde SM. Genetic variability, correlation and path analysis in wheat. J Cereal Res. 2014;5(2):48-51.
16. Sadgar T, Gadekar D, Viju-Amolic RB. Assessment of genetic diversity studies for yield and yield contributing characters in durum wheat (*Triticum durum* Desf.) under limited irrigation condition. 2021.
17. Simmons SR. Growth, development and physiology in wheat and wheat improvement E.G Heyne (ed), Agronomy No. 13. 1987;77-133.
18. Singh PK, Singh L, Singh SV, Nath S, Yadav V, Mishra A, *et al.* Estimation of Genetic Variability, Correlation and Path Analysis for Yield and Some Yield Contributing Traits in Bread Wheat (*Triticum Aestivum* L.). Int J Environ Clim Chang. 2023;13(11):2429-2440.
19. Tegenu Z, Lule D, Nepir G. Correlations and path analysis of some quantitative and qualitative characters in durum wheat (*Triticum turgidum* L.) accession in Western Oromia, Ethiopia. J Biol Agric Healthc. 2019;9:2224-3208.
20. Tsegaye D, Dessalegn T, Dessalegn Y, Share G. Analysis of genetic diversity in some durum wheat (*Triticum durum* Desf) genotypes grown in Ethiopia. Afr J Biotech. 2012;11(40).
21. Ukani JD, Patel JB, Dabhi KH, Ribadia KH. Development of identification keys on the basis of plant morphological characters in wheat. AGRES -Int. e-J. 2015;4(3):290-300.
22. Wolde T, Eticha F, Alamerew S, Assefa E, Dutamo D. Genetic variability, heritability and genetic advance for yield and yield related traits in durum wheat (*Triticum durum* L.) accessions. Sky J Agric Res. 2016;5(3):42-47.
23. Zewdu D, Mekonnen F, Geleta N, Abebe K. Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits of Bread Wheat (*Triticum aestivum* L.) Genotypes. Int J Econ Plants. 2024;11(1):38-47.