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Exploring Genetic Variability, Heritability, and Interrelationship in Phenotypic Traits of Recombinant Inbred Lines in Durum Wheat (*Triticum turgidum* L. ssp. *Durum*, Desf.)

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Abstract

Durum wheat is a vital wheat species cultivated worldwide for human consumption, ranking second to bread wheat. The Ethiopian durum wheat allele pool shows wide gene diversity; however, limited improvement work has been done to exploit this diversity. Thus, this study aimed to assess the genetic variability, heritability, and interrelationship among different phenotypic traits in 210 recombinant inbred lines (RILs) using an alpha lattice design with two replications. The analysis of variance revealed a significant difference for all the measured traits. The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all the characters, which reflects that the existing range of variability within the genotypes was not only due to the varying influence of genotype but also the environment. A correlation analysis disclosed that grain yield was positively related to the traits of plant height and 1000-kernel weight, suggesting that selecting these traits could enhance yield. Path analysis revealed that days to booting, maturity, and 1000-kernel weight directly affect grain yield. Among the measured traits, early developmental traits revealed higher broad-sense heritability. The findings of this study highlight high genetic diversity among Ethiopian durum wheat genotypes, opening up opportunities to integrate these materials into future wheat-breeding programs through introgression with other germplasm sources in Ethiopia and beyond.

Keywords: durum wheat; genetic advance; heritability; recombinant inbred lines

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1. Introduction

Wheat (*Triticum* spp.) is among the most widely cultivated crops globally. It covers approximately 224.09 million hectares and yields around 794.44 million metric tons annually [1]. Ethiopia is the foremost wheat producer in sub-Saharan Africa. The cultivated wheat on 1.96 million hectares of land increased by 2.98 million hectares in 2023. This marked a 52% increment. Concurrently, the fulfillment rate of certified wheat seed demand has increased steadily from 43.1% in 2021 to 58.6% in 2023 [2]. As a result, Ethiopia's wheat production reached a record high [3]. Durum wheat (*Triticum turgidum* L. ssp. *Durum*) is inconsiderable in its production relative to bread wheat, yet it has great significance. It has grown to approximately 16 million hectares, representing about 5% of worldwide wheat production [4]. In the case of Ethiopia, durum wheat is mainly grown in the highlands, at altitudes ranging from 1800 to 2800 meters above sea level, on heavy clay soils known as vertisols [5]. Ethiopia is recognized as a major center of diversity for durum wheat by having diverse agro-climatic zones [6,7].

Genetic studies revealed that the unique diversity of durum wheat landraces maintained in farmer fields is unexploited mainly by national and international breeding [8]. The development of artificial populations recombining the diversity of Ethiopian durum wheat with that of international breeding pools gives the means to support pre-breeding of new genotypes while providing a tool of discovery to characterize the genetic basis of trait determination [9]. Recombinant inbred lines (RILs) representing this intermixed inheritance are a powerful tool for characterizing trait potential and tradeoffs in production traits. RILs resulting from landrace and elite crosses in durum wheat grab the recombination between different parental genomes, making them especially useful for genetic diversity research and bridging the gap between underutilized landrace variation and contemporary breeding populations [9].

Many agronomic traits of breeding interest are quantitative and emerge from the interaction of many component characters. Yield is paradigmatic of this complexity, so its genetic architecture can be better derived by examining its component features [10]. Due to this complexity, direct selection for yield alone may be misleading in breeding programs, and successful selection relies on knowledge of genetic variability and the relationship between morphological and agronomic traits with grain yield [11].

Correlation analysis is the most common and important tool to identify relationships between traits in genetically diverse populations that assist crop improvement [12]. These correlations are crucial in plant breeding by indicating the degree of trait dependence. In wheat breeding, simple correlation coefficients are often used to understand the relationship between grain yield and other agronomic and morphological traits.

Path analysis can also quantify the relative importance of each independent variable in predicting changes in a dependent variable. A path coefficient is a standardized partial regression coefficient that measures the direct effect of one trait on another, allowing for the separation of direct and indirect effects within correlation coefficients [13]. Path coefficients directly indicate the influence of independent variables on dependent variables [14]. In crop improvement programs, plant breeders have utilized path coefficient analysis to identify traits that are effective selection criteria for improving crop yield [13]. By better understanding the genetic relationships between grain yield and its components, plant breeders can make more effective selections and identify traits for future breeding programs [5]. Though several studies explored the genetic diversity of durum wheat from Ethiopia [15–18], information about the genetic diversity of durum wheat based on multivariate analysis, including RILs, is minimal, which motivated wheat researchers to investigate and create new traits in pre-breeding cultivars. In this study, a set of RILs of breeding relevance was selected and used to assess their genetic variability and to determine the interrelationships among various traits and their direct and indirect effects on the grain yield that had a beneficial direct influence on grain yield.

2. Materials and Methods

2.1. Plant Materials and Experimental Design

This study used 210 durum wheat RILs derived from the Ethiopian nested association mapping (EtNAM) population (Table S1). The EtNAM is a multi-parental population derived from intercrossing Ethiopian durum wheat landraces with an international elite durum wheat variety released in Ethiopia under the name Asassa [9]. The 210 RILs used in this study were selected from a subset of 12 EtNAM families. The seed samples were obtained from the Amhara Agricultural Research Institute (ARARI), Bahir Dar, Ethiopia. The characterization experiment was conducted over two consecutive years (2022/23 and 2023/24) at Jamma and Woreilu test sites. Based on the recommended sowing time for each site, sowing was carried out while considering the prevailing environmental conditions. The experiments were set up with an alpha lattice design in two replications. Each plot measured 0.8 m × 2 m and consisted of four rows. The distances between the replications, plots, and rows were 1 m, 50 cm, and 20 cm, respectively. The trials were maintained following the standard agronomic practices for the sites.

2.2. Description of Experimental Site

The experimental sites Jamma and Woreilu belong to the Sirinka and Woreilu Agricultural Research Center, respectively. They are in the South Wollo Zone, Amhara Region, Ethiopia. Both sites are high-potential areas for durum wheat production and are characterized by different agroecologies (Table 1). The testing sites represent the country's major and most suitable durum wheat growing environments (Figure 1). The weather information of the mean monthly maximum and minimum temperatures and rainfall during the crop-growing season for the two consecutive years is presented in Table S2.

Table 1. Agro-ecological description of the experimental sites: Jamma and Wereilu.

Location	Longitude	Latitude	Altitude (m)	Agro-Ecology	Soil Type	Annual Rainfall (mm)	Annual Average Temperature
Jamma	39°16′20.93″ E	10°27′37.18″ N	2630	Highland	Vertisol	1200–1800	19.0
Woreilu	39°26′12.17″ E	10°37′05.11″ N	1700	Highland-mid altitude	Vertisol & clay	500–1800	21.5

Source: (Sirinka Agricultural Research Center, Woreilu Agricultural Research Center).

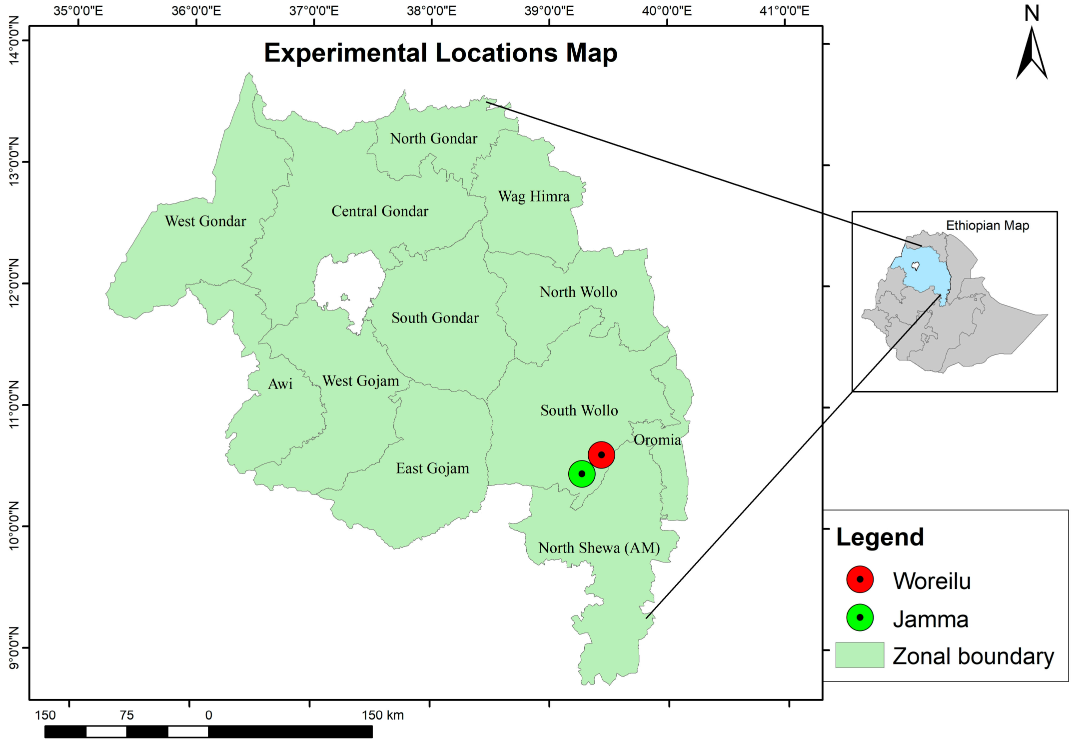


Figure 1. Map showing the geographical location of the experimental site (shaded green and red). (Note: All boundaries are approximate and do not correspond to political borders.) The map was created using the ArcGIS software suite version 10.7.1.

2.3. Data Collection

Data were recorded for the following traits: days to booting (DB, in days), days to heading (DH, in days), days to flowering (DF, in days), days to maturity (DM, in days), plant height (PH, in meters), spike length (SL, in cm), number of spikelet per spike (NSPS, in numbers), kernel number per spike (KNPS, in numbers), 1000-kernel weight (TKW, in grams), and grain yield (GY, in tons). DB, DH, DF, and DM were recorded at the plot level, with DB, DH, and DF based on the stage when 50% of plants reached the respective development stages, while DM was recorded when 90% reached maturity. PH, SL, NSPS, and KNPS were measured from the middle rows of 10 plants per plot. TKW was determined by doubling the weight of 500 kernels, and GY was estimated by calculating the total seed harvest weight from the middle rows of each plot.

2.4. Statistical Analysis

The collected data were checked for normal distribution using the visual methods of histogram and a Q–Q Plot (Quantile–Quantile Plot). The effects of genotype, replication, block, location, and genotype by location interaction were tested via analysis of variance (ANOVA) using the general linear model. Phenotypic and genotypic correlations were performed SAS software version 9.3 and the path analysis was worked through the metan package in R software version 4.4.2.

2.5. Estimation of Variance Components

The components of environmental, genotypic, and phenotypic variance, along with their coefficients of variation, were computed following the method depicted by Singh and Chaudhary [19]:

$$\text{Genotypic variance } (\sigma_g{}^2) = \frac{MSg - MSgxl}{rl} \tag{1}$$

$$\text{Genotype by location interaction variance } (\sigma_{g\times l}{}^2) = \frac{Msg - Mse}{r} \tag{2}$$

$$\text{Environmental variance} \left(\sigma_e^2\right) = \text{MSe} \tag{3}$$

$$\text{Phenotypic variance } (\sigma_p{}^2) = \boldsymbol{\sigma_g^2} + \boldsymbol{\frac{Msgxl}{l}} + \boldsymbol{\frac{\sigma_e^2}{rl}} \tag{4}$$

where MSg is the mean square of genotype, MSgxl is the mean square due to genotype by location interaction, MSe is the error mean square, r is the number of replications, and l is the number of locations.

The genotypic and phenotypic coefficient of variation was calculated as described in Johnson et al. [20]:

$$\text{Genotypic coefficient of variation (GCV)} = \boldsymbol{\frac{\sqrt{\sigma_g^2}}{\mu} \times 100} \tag{5}$$

$$\text{Phenotypic coefficient of variation (PCV)} = \boldsymbol{\frac{\sqrt{\sigma_p^2}}{\mu} \times 100} \tag{6}$$

$$\mu = \text{population mean}$$

The PCV and GCV are crucial genetic parameters that help determine the environment's influence on a genotype's performance. Classification of coefficient of variance based on percentages: Low is less than 10%, moderate is 10–20% and high is more than 20% [21].

2.6. Estimation of Broad-Sense Heritability and Genetic Advance

Broad sense heritability (H^2) was expressed as the percentage of the ratio of the genotypic variance (σ^2 g) to the phenotypic variance (σ^2 p) as described by Allard [22]:

$$\text{Heritability (H)} = \frac{\textit{Genotypic variance } \left(\sigma_g^2\right)}{\textit{Phenotypic variance } \left(\sigma_p^2\right)} \times 100 \tag{7}$$

Heredity and environment are very important in determining the expression of the traits [22]. Heritability indicates the capacity to transfer traits from parents to progeny. Estimating heritability provides information on the level of genetic influence over the expression of specific features and the capacity of phenotypes to translate into breeding value. According to Johnson et al. [20], the values of broad-sense heritability are classified as low (Hb < 30%), moderate (30% < Hb < 60%), and high (Hb > 60%).

Genetic advance under selection (GA): expected genetic advance for each character at 5% selection intensity computed by the methodology described in Johnson et al. [20]:

$$\text{Genetic advance (GA)} = \mathrm{k} * \sigma\mathrm{p} * \boldsymbol{H}^2 \tag{8}$$

K is a constant value at a selection intensity of 5% (k = 2.06).

To compare the extent of the predicted advance of different traits under selection, genetic advance as a percentage of the mean was calculated according to Falconer and Mackay [23]:

$$\text{Genetic advance mean (GAM)} = \frac{GA}{\mu} * 100 \tag{9}$$

The GAM can be categorized into low (0–10%), moderate (10–20%), and high (≥20%) levels [20,23].

3. Results

3.1. Genetic Variability in Durum Wheat RILs

The combined mean performance of RILs showed significant genetic variation across test sites (Supplementary Table S1). The analysis of variance for the genotypes (G) showed highly significant differences for all measured traits (Table 2). Significant variation was also observed in all traits among environments (E) and G × E interaction. The test was significant ($p \leq 0.01$) for all the variables studied. This might be the genetic background of the genotype, which is highly varied. The coefficient variations for measured phenotypic traits ranged from 4.01% in DM to 22.57% in GY.

Table 2. Combined analysis of variance for traits at Jamma and Woreilu locations for two consecutive years (2022/23–23/24).

	Location	**REP**	**Block**	**Genotype**	**Gen: Loc**	**Mean**	**CV%**	**R^2**
	(DF) = 1	**(DF = 209)**	**(DF = 28)**	**(DF = 1)**	**(DF = 209)**			
DB	237.91 **	188.90 *	3.79 **	4.69 **	1.35 **	69.60	6.95	0.83
DH	173.53 **	195.82 **	3.60 **	4.61 **	1.35 **	76.40	6.36	0.81
DF	239.77 **	194.60 **	3.66 **	4.34 **	1.40 **	85.38	5.84	0.82
DM	523.76 **	110.35 **	2.58 **	3.83 **	1.23 **	128.65	4.01	0.84
PH	850.88 **	51.20 **	0.69	3.30 **	1.32 **	1.03	10.08	0.87
SL	136.82 **	17.26 **	1.15	2.88 **	1.29 **	6.24	11.87	0.71

Table 2. *Cont.*

	Location	REP	Block	Genotype	Gen: Loc	Mean	CV%	R^2
	(DF) = 1	(DF = 209)	(DF = 28)	(DF = 1)	(DF = 209)			
NSPS	119.37 **	4.23 *	1.15	2.25 **	1.42 **	17.43	8.41	0.70
KNPS	85.17 **	140.74 **	1.12	2.81 **	1.93 **	41.81	13.09	0.74
TKW	867.72 **	0.16	1.84 **	4.00 **	2.08 **	41.50	11.24	0.86
GY	349.30 **	73.14 **	1.36	2.06 **	1.59 **	4.56	22.57	0.79

**, * = significance at 0.1% and 0.5% probability level, DF = degrees of freedom of each level, R^2 = coefficient of determination, CV = coefficient of variation, DB = days to booting, DH = Days to heading, DF = days to flowering, DM = days to maturity, PH = plant height, SL = spike length, NSPS = number of spikelets per spike, KNPS = kernel number per spike, TKW = 1000-kernel weight GY = grain yield.

3.2. Genotypic and Phenotypic Coefficient of Variation (GCV and PCV)

The parameters such as GCV, PCV, heritability, genetic advance, and genetic advance as a percentage of the mean were worked out and are presented in Table 3. The results show that the GCV ranged from 2.28 DM to 5.5 TKW and the PCV ranged from 2.77 DM to 11.39 GY. Except for the PCV of grain yield, all traits had low PCV and GCV, and the PCV was greater than the GCV for all scored characters.

Table 3. Estimation of variance components of the traits for 210 RILs of durum wheat genotypes.

	DB	DH	DF	DM	PH	SL	NSPS	KNPS	TKW	GY
$\sigma_g{}^2$	9.70	9.63	9.14	8.66	0.00	0.10	0.22	3.28	5.21	0.06
$\sigma_e{}^2$	31.69	31.91	34.92	32.73	0.01	0.71	3.05	57.92	45.28	1.68
$\sigma_{gxe}{}^2$	4.14	4.12	5.02	3.06	0.00	0.08	0.45	13.96	11.76	0.32
$\sigma_p{}^2$	13.65	13.61	13.51	12.75	0.00	0.20	0.61	10.52	10.88	0.27
GCV (%)	4.47	4.06	3.54	2.28	4.95	5.26	2.72	4.33	5.50	5.48
PCV (%)	5.30	4.82	4.30	2.77	6.40	7.09	4.46	7.75	7.94	11.39
H^2 (%)	71.06	70.00	67.67	67.94	60.46	55.1	37.19	31.00	48.02	23.06
GA	5.40	5.32	5.12	4.99	0.08	0.05	0.10	2.07	3.27	0.25
GAM	7.75	6.96	5.99	3.88	7.92	8.08	3.41	4.95	7.89	5.42

$\sigma_g{}^2$, $\sigma_e{}^2$, $\sigma_{gxe}{}^2$, and $\sigma_p{}^2$ indicate genotypic, environment, genotypic environment, and phenotypic variances, respectively. GCV (%), PCV (%), H^2 (%), GA, and GAM are the genotypic coefficient of variation, phenotypic coefficient of variation, broad-sense heritability, genetic advance, and genetic advance as a percentage of the mean at 5% selection intensity, respectively. DB = days to booting DH = days to heading, DF = days to flowering, DM = days to maturity, PH = plant height, SL = spike length, NSPS = number of spikelets per spike, KNPS = kernel number per spike, TKW = 1000-kernel weight, GY = grain yield.

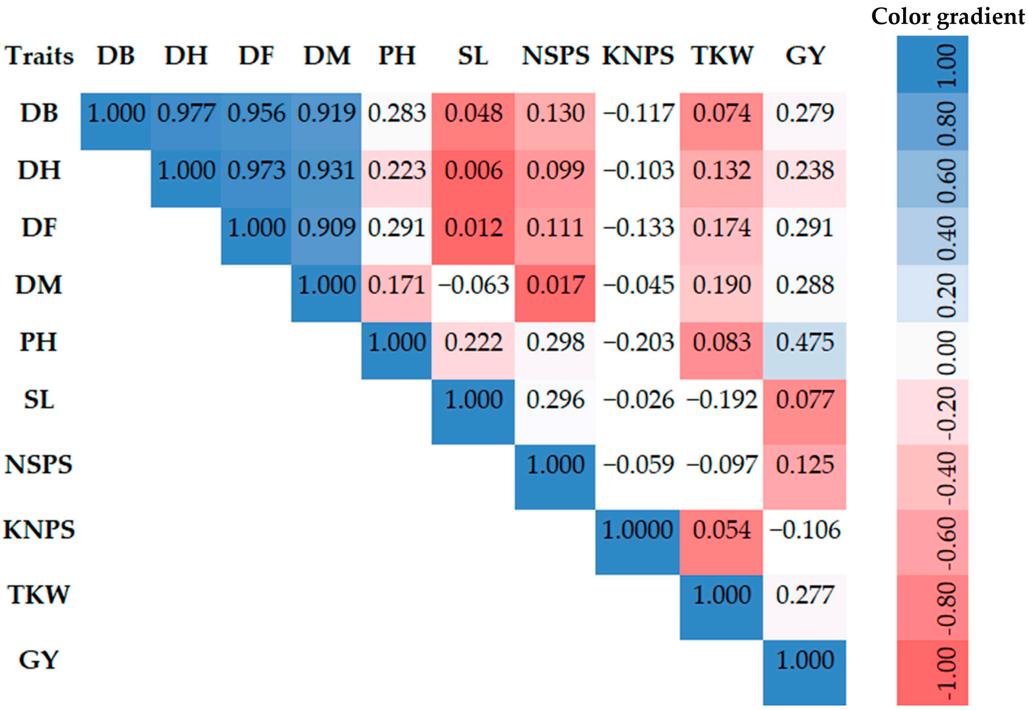
3.3. Broad-Sense Heritability and Genetic Advance as a Percentage Mean

In the present study, heritability estimates ranged widely from a low of 23.06% to a high of 71.06% for GY and DB, respectively. High heritability was observed for DB (71.06%), DH (70%), DF (67.67%), DM (67.94%), and PH (60.46%). Medium heritability was recorded for TKW (48.02%), SL (55.1%), NSPS (37.19%), and KNPS (31%). Low heritability was shown for trait GY (23.06%). The GAM ranged from 3.4% for NSPS to 8.8% for GY.

3.4. Phenotypic and Genotypic Correlation Analysis

The present study presents the predictable values of phenotypic and genotypic correlation coefficients among pairs of traits in Figures 2 and 3, respectively. GY has a positive and highly significant ($p < 0.01$) phenotypic correlation with PH ($r_p = 0.475$), DF ($r_p = 0.291$), DM ($r_p = 0.288$), DB ($r_p = 0.279$), and TKW ($r_p = 0.277$). The SL ($r_p = 0.077$) and NSPS ($r_p = 0.125$) showed weak positive correlations with GY, whereas the KNPS ($r_p = -0.106$) exhibited a negative correlation. Phenological traits showed strong positive associations among DB, DH, DF, and DM. Particularly, DB exhibited notably great correlations with DH

(r_p = 0.977), DF (r_p = 0.956), and DM (r_p = 0.919), whereas DH was strongly linked to DM (r_p = 0.931) and DF (r_p = 0.973). DF similarly had a high link with DM (r_p = 0.909). PH was modestly positively correlated with DB r_p = 0.283), DH (r_p = 0.223), DF(r_p = 0.291), DM (r_p = 0.171), SL (r_p = 0.222), and NSPS (r_p = 0.298), but inversely correlated with KNPS (r_p = −0.203). TKW, however, had negative associations with SL (r_p = −0.192) and NSPS (r_p = −0.097) and just a small link with KNPS (r_p = 0.054).

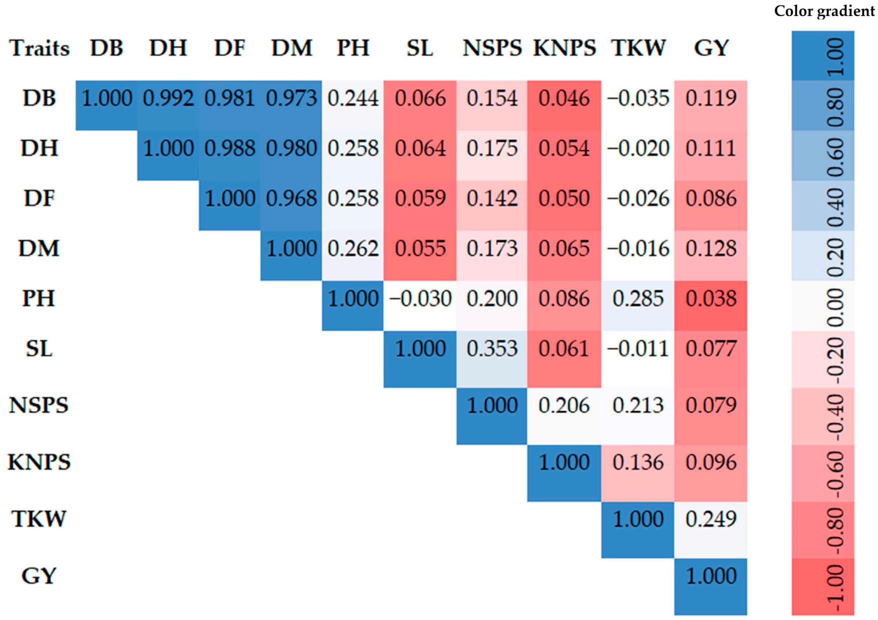


Traits	DB	DH	DF	DM	PH	SL	NSPS	KNPS	TKW	GY
DB	1.000	0.977	0.956	0.919	0.283	0.048	0.130	−0.117	0.074	0.279
DH		1.000	0.973	0.931	0.223	0.006	0.099	−0.103	0.132	0.238
DF			1.000	0.909	0.291	0.012	0.111	−0.133	0.174	0.291
DM				1.000	0.171	−0.063	0.017	−0.045	0.190	0.288
PH					1.000	0.222	0.298	−0.203	0.083	0.475
SL						1.000	0.296	−0.026	−0.192	0.077
NSPS							1.000	−0.059	−0.097	0.125
KNPS								1.0000	0.054	−0.106
TKW									1.000	0.277
GY										1.000

Figure 2. Phenotypic correlation coefficients of measured phenotypic traits for 210 recombinant inbred lines (RILs).

GY showed a significant positive association with TKW (r_p = 0.249) at the genotypic level (Figure 3). The PH showed a significant positive association with DB (r_g = 0.244), DH (r_g = 0.258), DF (r_g = 0.258), DM (r_g = 0.262), NSPS (r_g = 0.2), and TKW (r_g = 0.285) at the genotypic level. SL (r_g = 0.077) and PH (r_g = 0.038) had weak positive correlations with GY. The genotypic correlation analysis showed powerful positive associations among DB, DH, DF, and DM. DB was almost perfectly correlated with DH (r_g = 0.992), and also highly correlated with DF (rg = 0.981) and DM (rg = 0.973). Similarly, DH exhibited strong genotypic correlations with DF (r_g = 0.988) and DM (r_g = 0.98), while DF was also highly correlated with DM (r_g = 0.968). In contrast, PH genotypic correlations with the phenological traits ranged from 0.244 to 0.262, and were also positive for NSPS r_g = 0.2) and TKW (r_g = 0.285).

However, phenotypic correlation coefficient values were greater for most of the characters than their corresponding genotypic correlation coefficient values, which implies a strong environmental influence on the expression of these traits. As with the phenotypic correlation, the genotypic correlation matrix shows extremely high positive values among the phenological traits.



Traits	DB	DH	DF	DM	PH	SL	NSPS	KNPS	TKW	GY
DB	1.000	0.992	0.981	0.973	0.244	0.066	0.154	0.046	−0.035	0.119
DH		1.000	0.988	0.980	0.258	0.064	0.175	0.054	−0.020	0.111
DF			1.000	0.968	0.258	0.059	0.142	0.050	−0.026	0.086
DM				1.000	0.262	0.055	0.173	0.065	−0.016	0.128
PH					1.000	−0.030	0.200	0.086	0.285	0.038
SL						1.000	0.353	0.061	−0.011	0.077
NSPS							1.000	0.206	0.213	0.079
KNPS								1.000	0.136	0.096
TKW									1.000	0.249
GY										1.000

Figure 3. Genotypic correlation coefficients of measured phenotypic traits for 210 recombinant inbred lines (RILs).

Both phenotypic and genotypic correlations were observed on DB, DH, DF, and DM with PH. TKW correlated with GY at the phenotypic and genotypic levels. PH correlated with NSPS at the phenotypic and genotypic levels.

3.5. Path Coefficient Analysis

The highest positive direct effect was imposed by DB (0.798), followed by DM (0.456) and TKW (0.273), but the indirect effect of them was very low (Table 4). The SL (0.079) and KNPS (0.057) also had a low positive direct effect on the GY. All other traits, such as DF (−0.993), DH (−0.128), PH (−0.049), and NSPS (−0.048), had a negative direct effect and were not non-significantly correlated with GY, hence may not be statistically significant (Table 4).

Table 4. Path coefficient showing direct (diagonal) and indirect effect (off-diagonal) of different traits on grain yield in RILs of Ethiopian durum wheat.

	DB	DF	DH	DM	KNPS	PH	SL	NSPS	TKW	Linear
DB	0.798	−0.974	−0.127	0.444	0.003	−0.012	0.005	−0.007	−0.01	0.119
DF	0.783	−0.993	−0.127	0.442	0.003	−0.013	0.005	−0.007	−0.007	0.086
DH	0.792	−0.981	−0.128	0.447	0.003	−0.013	0.005	−0.008	−0.005	0.111
DM	0.776	−0.962	−0.126	0.456	0.004	−0.013	0.004	−0.008	−0.004	0.128
KNPS	0.037	−0.049	−0.007	0.03	0.057	−0.004	0.005	−0.01	0.037	0.096
PH	0.196	−0.26	−0.033	0.122	0.005	−0.049	−0.002	−0.009	0.076	0.045
SL	0.053	−0.059	−0.008	0.025	0.004	0.001	0.079	−0.017	−0.003	0.075
NSPS	0.123	−0.141	−0.023	0.079	0.012	−0.009	0.028	−0.048	0.058	0.079
TKW	−0.028	0.026	0.003	−0.007	0.008	−0.014	−0.001	−0.001	0.273	0.249 **

** = significance at 0.1% probability level, DB = Days to booting, DH = days to heading, DF = days to flowering, DM = days to maturity, PH = plant height, SL = spike length, NSPS = number of spikelets per spike, KNPS = kernel number per spike, TKW = 1000-kernel weight,.

4. Discussion

4.1. Genetic Variability and Heritability

The combined analysis of variance for 210 RILs for the traits of DB, DH, DF, DM, PL, SL, NSPS, KNSP, and TKW revealed significant differences ($p < 0.01$) among the genotypes and environments (Table 2), which implies the RILs were heterogeneous. In the study of Kidane et al. [9], the genotypes differed and varied in agro-morphological traits. High variability in the breeding lines enhances the probability of producing desirable recombinants in successive generations. Especially for breeders, variation is crucial to increase the possibility of selecting and creating cultivars that respond appropriately to biotic and abiotic stresses. It is important to enhance the likelihood of finding desired features through selection. Moreover, this genotypic difference is vital for heterosis breeding, whereby hybrid vigor can enhance performance and resiliency [24]. The significant genotype × environment (G × E) interactions indicated that the performance of specific genotypes considerably depends on environmental factors [6,25–30]. The environment has a notable impact on phenotypic traits. In similar studies, genotypic and genotype-by-environment interaction influences were remarkable for most traits [29,31,32]. The coefficient of variation for the phenotypic traits also indicated a wide range of variation across the traits.

The findings show the PCV was slightly higher than GCV across all traits (Table 3), suggesting an environmental impact that affected trait expression. The gap between the PCV and GCV was narrow, indicating the trait is under genetic control with minimal environmental influence. This aligns with the previous study, which states that environmental and genetic factors are critical to phenotypic outcomes [25]. Except for the PCV of grain yield, all traits had low PCV and GCV. Consistent studies were conducted by Dagnew [29] for low PCV and GCV for traits of DH, DM, NSPS, and PH. Bhushan et al. [33] also found DH and DM, while Donga et al. [30] found DH, DM, and PH. Azene and Menzir [27] also found the traits of DM and DH. Even if the low GCV and PCV reduce the scope for genetic improvement, it does not mean there is no space for improvement. They might be able to make considerable progress by thoughtfully analyzing the factors affecting the traits and using suitable breeding approaches.

Heritability indicates the capacity to transfer traits from parents to progeny. Estimating heritability provides information on the level of genetic influence over the expression of specific features, and the capacity of phenotypes translates into breeding value. All the measured traits showed from high to moderate heritability, except GY. Specifically, the phenological traits had higher heritability. The current results were similar to some of the earlier studies by Amha et al. [26], which found high heritability for DH, DF, and PH, and low heritability for GY. Ozukum et al. [34] obtained high heritability for PH along with low heritability for GY in bread wheat. Dagnaw et al. [29] found high heritability for DH and PH and stated that these traits were comparatively stable across various environmental conditions. Direct selection for high heritability of traits in early segregating generations is likely to be successful and beneficial in breeding programs. Conversely, low heritability for GY implies that this trait was prone to environmental influences. Moderate heritability indicates that environmental factors also significantly impact trait expression, even if the genetic condition is dominant. A good breeding approach should be planned for successful breeding results by considering genetic potential and environmental factors. However, heritability is not enough to choose and improve genotypes. Genetic advance is also a key factor in predicting change in target traits, which must be considered along with [35]. The result of GAM indicates that environmental factors play a stronger role in the traits of the RILs. Therefore, breeders should focus more on heritability and genetic advance when planning selection strategies.

4.2. Association and Path Coefficient Study

From the phenotypic correlation result of this study, a consistent study by Kandel et al. [12] found that GY had positive and significant correlations with PH. The positive significant associations between GY and PH are because these tall genotypes generally excel in their capacity to support kernel growth by stem reserve mobilization [36]. Therefore, selection for tall plants tends to increase grain yield per plant. Another study, whose result aligns with the present study, was [37,38], which stated that GY had a significant positive correlation with TKW. Not only did PH influence the yield, but TKW also had a crucial effect on the RILs' productivity.

In durum wheat RILs, the positive correlations between GY with PH and TKW are consistent with other results, reinforcing their function as general yield elements in self-pollinated crop improvement across other RIL populations in cereal and crops. The correlations observed in different crops using RILs and related populations showed the importance of yield-related traits in determining GY performance. In bread wheat, RIL populations consistently show that kernel yield is significantly and positively correlated with PH and TKW. Likewise, maize RILs were assessed and the association result implied that PH, 1000-kernel weight and other biochemical traits showed a significant positive association with GY. This suggests that both morphological and biochemical traits connectively enhance productivity [39]. Consistent results were also reported in bread wheat RILs; GY positively correlated with PH and test weight under supplemental irrigation conditions. Similar results were also revealed between GY and PH, and test weight in a dryland environment [40]. This implies the indirect selection target PH and/or TKW offers for improving self-pollinated plants' yields.

Knowing the inherent genetic correlation of the traits enables the breeders to create a strategic plan for selection. The significant genotypic effects indicate genetic variability among genotypes and the potential for genetic improvement in most traits. GY is significantly associated with TKW at the genotypic level (Figure 3). Therefore, positive correlation coefficients of GY with the traits implied that improving this trait could result in high grain yield [41].

Strong genotypic correlations between GY and TKW in several RILs and related populations indicated the usefulness of indirect selection to raise yields. Bread wheat genotypes including national advanced lines varieties in Ethiopia showed a highly significant genotypic correlation between GY and TKW [42]. Besides this, populations in durum wheat RILs revealed TKW influences GY [43]. These results show that TKW serves as a dependable indirect predictor of GY in both bread and durum wheat, and adding it to selection criteria for breeding would help efficiency.

TKW positively correlated with GY in both genotypic and phenotypic correlation coefficients. This implies that plants with higher TKW produce more grain overall. Because this association was also present at the genetic level, choosing plants with greater TKW might be a wise approach to boost output in future breeding programs. Moreover, phenotypic correlation coefficient values were greater for most of the characters than their corresponding genotypic correlation coefficient values, implying a more substantial environmental influence on the expression of these traits.

Path analysis is another effective statistical technique to determine the relationships between dependent and independent variables [13]. The present study uses path analysis to understand dependent variables' direct and indirect effects on GY and how these traits interact. Table 3 shows that the highest positive direct effect was observed for DB (0.798), followed by DM (0.456) and TKW (0.273). Some findings align with the current study, which stated that DM had the highest impact on GY [33,44]. This implies that timely maturation is vital for producing a high-yield product, while Baranwal et al. [45] observed a direct positive effect of TKW on GY, and Dogan [38] reported a similar result for the trait of KNPS and TKW. Other studies by Ali et al. [46], Dogan [38], and Subhashchandra et al. [47] also identified PH, NSPS, KNPS, and TKW as key traits that made a higher contribution to GY. This partially supports the present findings. Based on these study results, it is recommended that DB, DM, and TKW traits be prioritized, as these traits positively influenced RILs' yield.

5. Conclusions

This study used 210 RILs, and the results from all measured phenotypic traits revealed that all traits had high variance estimates, heritability ranging from high to low, and low GAM. GY was positively associated with PH and TKW, indicating that higher TKW and taller plants increase yield. Path coefficient analysis validated that GY is most strongly directly influenced by DB, DM, and TKW. The main factor in determining yields in durum wheat breeding initiatives was the direct positive influence of TKW. The path and correlation analyses helped us see trait contributions better; TKW and phenological traits are top candidates for selection. Durum wheat breeding should therefore use a multi-trait selection strategy emphasizing traits closely correlated with grain yield. Breeding programs should maximize these features and ensure that selected RILs exhibit overall agronomic stability. Moreover, great care should be taken in selecting RILs with high heritability for traits like DB, DH, DF, DM, and PH; these traits are more likely to be known as genetic improvements. By genetic means, this approach allows breeders to increase grain yield in durum wheat while maintaining the adaptability and stability of the genotypes, hence accomplishing some significant genetic progress. Future studies should combine GWAS with marker-assisted selection to verify these results and find reliable QTLs associated with phenotypic traits.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/crops5050071/s1, Table S1. The combined mean performance of 210 RILs evaluated at two major Durum wheat growing areas (Jama and Wereilu) for two consecutive years(2021/22 and 2022/23) during the main cropping season. Table S2. Description of mean monthly weather information of test sites during crop growing season for two consecutive years.

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