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Genetic Parameters and Trait Associations in Wheat Under Drought and Low Nitrogen Conditions

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Abstract: Drought and low nitrogen stress are the leading cause of low crop production and productivity worldwide. Developing drought-tolerant wheat germplasm resilient to low nitrogen conditions is essential through genetic enhancement and selection for novel traits. The objective of the research was to investigate genetic diversity, parameters, and trait relationships within a wheat genotype panel to inform drought- and low-N-tolerant variety selection. This study evaluated 50 wheat genotypes under drought-stressed and non-stressed conditions, with varying nitrogen (50 kg ha^{-1}, 100 kg ha^{-1}, and 200 kg ha^{-1}) levels across four testing sites during the 2019/2020 growing season. Statistical analysis (combined ANOVA) revealed substantial genetic variation ($p < 0.05$) for the majority of tested traits. High heritability and substantial genetic gain for KPS (97.49%, 28.10% GAM) and SE (96.48%, 14.28% GAM) were determined under drought and low nitrogen stress. Under drought-stressed and non-stressed (at 200 kg N ha^{-1}), grain yield expressed high heritability estimates of 80.43% and 75.68% and genetic advance at 21.90% and 21.56%, respectively. Positive and significant correlations ($r > 0.5$; $p < 0.001$) were measured between grain yield and yield components, implicating simultaneous direct and indirect selection of desired traits. The positive relationship between grain yield and yield components suggests that further quantitative trait loci analysis and progeny testing are crucial to guide genotype selection and breeding for drought and low-N stress-tolerant wheat genotypes.

Keywords: grain yield; heritability; variance components; wheat; yield components

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1. Introduction

Wheat (*Triticum aestivum* L.), a highly cultivated hexaploid ($2n = 6x = 42$, AABBDD), is one of the most consumed cereal crops valuable for the daily sustenance of one-third of the worldwide population [1]. It is cultivated under varied agroecologies in many countries [2], and the global demand for wheat is anticipated to escalate due to rapid population growth and urbanization. This necessitates a corresponding increase in global wheat production area by 15.4% and an increase in productivity by 6.5% under the major cropping regions [3]. In sub-Saharan Africa, the mean productivity of wheat currently stands at 2.5 t/ha [4], compared with a total average of 3.5 t/ha estimated globally [5]. South Africa's annual wheat production ranges from 1.3 to 2 million tons, with an average yield of 2 to 2.5 t/ha, positioning it as the fourth-largest producer in the region after Egypt, Morocco, and Ethiopia [5].

Wheat production is predominantly cultivated under rainfed growing regions in South Africa (e.g., Western Cape and Free State, and some parts of other provinces), where drought and low nitrogen stress occur frequently [6]. Drought is severe during the post-anthesis stage of wheat in areas with limited water supply. It is the leading cause of yield and quality losses in the country, impacting crop growth and development through poor tiller formation, stem elongation, leaf expansion, and limited stomatal conductance, among other physiological and biochemical processes governing grain improvement [7–9].

In sub-Saharan Africa, most agricultural soils have depleted nitrogen content [10,11]. Poor soil nitrogen (N) condition is another limiting factor which reduces wheat productivity. It is a crucial element required for crop growth and development. Hence, its limitation results in poor grain yield and quality. Nitrogen availability is highly influenced by drought stress, which alters plant uptake and utilization. Ahmad, Waraich [12] reported that drought stress strongly affects the N metabolism in many crop plants. Therefore, there is a need to breed nitrogen-use-efficient wheat in areas with limited soil N content. Understanding nitrogen-use efficiency (NUE) mechanisms during drought stress is essential for developing wheat cultivars tolerant to low-N stress conditions in semi-arid or arid regions [13], such as those in sub-Saharan Africa. However, there are limited studies documenting the genetic mechanisms linking drought and low-N stress conditions in wheat [14–16].

Developing low-N tolerant wheat varieties has proven to be difficult due to the intricate relationships between nitrogen acquisition, utilization, and regulation, encompassing uptake, translocation, assimilation, and re-allocation [17,18]. Research indicates that genetic diversity in NUE components is influenced by the interplay between nitrogen uptake efficiency and nitrogen utilization efficiency, both of which involve multiple genes, physiological mechanisms, and biochemical pathways [13,19,20]. Nitrogen-use efficiency is quantified as the ratio of grain dry matter (DM) yield (kg DM ha^{-1}) to nitrogen fertilizer supplied to the soil (kg N ha^{-1}) [21,22].

Enhancing NUE in wheat cultivation offers dual economic benefits such as increased yields and reduced fertilizer expenses. Additionally, improved NUE mitigates the risk of nitrate leaching and promotes environmental sustainability. In South Africa, winter wheat exhibits an average nitrogen recovery rate of 65% and NUE of 25 kg DM kg^{-1} N available, based on computations of grain-N total and N available in the soil [23]. Current recommendations suggest applying at least 130 kg N ha^{-1} to achieve five tons ha^{-1} yield and 200 kg N ha^{-1} or more for yields above eight tons ha^{-1} [5]. To optimize wheat production in arid environments, developing drought-tolerant and low-N resilient genotypes could minimize irrigation and fertilizer requirements, increasing yields while reducing environmental impact.

Several studies were involved in breeding for drought tolerance [24–26], while breeding for concurrent selection for drought and low-N tolerance is yet to be pursued [6,23]. To develop wheat varieties resilient to drought and low nitrogen stress, researchers must conduct thorough evaluations of genetically diverse candidates in diverse environmental conditions. This rigorous testing identifies top-performing lines for breeding or cultivation. Furthermore, selecting yield components with complementary effects can significantly improve grain yield. By targeting these synergistic traits, breeders can optimize crop productivity, ultimately developing wheat cultivars tolerant to drought and low-N stress conditions [27].

Improved crop productivity can be achieved through new progeny selection with higher trait heritability and associations. Heritability estimates and the magnitude of trait relationships are vital for predicting the performance and selection of progenies [28–30]. Semahegn, and Shimelis [31] reported that drought-stressed wheat exhibited high heritability and substantial genetic gain for spike length and 1000-kernel weight. The greater magnitude of heritability and higher genetic advance indicated that these parameters were controlled by additive genetic effects, which is essential for pure-line cultivar development. Further, analyzing the relationship between agronomic traits could assist in determining the selection response.

The magnitude and trend of trait associations assessed through phenotypic and genotypic correlations guide selection in plant breeding programs. Genotypic correlation measures the extent of trait association due to independent or linked genes [3]. Duma and Shimelis [6] revealed a positive relationship between 1000-kernel weight, grain yield, and the number of productive tillers and recommended a simultaneous selection of these traits for wheat improvement. Previous research has identified tiller number, spike length, grains per spike, and 1000-kernel weight as key determinants of grain yield, influencing both phenotypic expression and genotypic potential [32–34]. Nofouzi [35] reported a negative and significant correlation between 1000-kernel weight and plant height, spike length, number of fertile tillers, and number of kernels per spike, suggesting an indirect selection of these traits. A similar method can be applied to select correlated traits for developing genotypes tolerant to drought stress and low-N content.

The African Centre for Crop Improvement (ACCI; University of KwaZulu-Natal) embarked on a pre-breeding program to develop wheat populations tolerant to drought and low-N conditions. A diverse genetic pool of bread wheat was assembled, evaluated, and selected for drought and low-N tolerance based on phenotypic analysis [6]. The data on the assessed germplasm must be evaluated for variance components and heritability estimates to determine breeding values and genetic gains through selection. This will allow for an effective germplasm characterization based on the realized genetic variation, essential for the precision selection of genotypes with high breeding values under drought and variable N tolerant conditions. Therefore, the objective of the study was to determine the extent of the genetic variability, genetic parameters, and trait associations among a panel of wheat genotypes to guide selection and production under drought and low nitrogen conditions.

2. Materials and Methods

2.1. Plant Materials, Trial Design, and Setup

Fifty wheat genotypes were assessed for their performance under varying water and nitrogen conditions. The study employed a 10 × 5 alpha lattice design with two replications across two testing sites. Each genotype was evaluated under drought-stressed and non-stressed conditions, combined with three nitrogen levels: 50 kg N ha^{-1} (low), 100 kg N ha^{-1} (intermediate), and 200 kg N ha^{-1} (recommended). The selected genotypes exhibited genetic diversity for high-yielding potential and drought tolerance. Table 1 lists the genotypes used, including leading commercial spring wheat cultivars (local checks) with proven performance in National Cultivar Evaluation trials. Two local checks (Check#1 and Check#2) were specifically chosen for their adaptability to low soil nitrogen. Nitrogen treatments were applied following South Africa's wheat production guidelines [36].

During the 2019/2020 growing season, the selected wheat genotypes were evaluated in both greenhouse and field conditions at the University of KwaZulu-Natal (UKZN). Greenhouse experiments involved planting 10 seeds per genotype in 5-L pots with composted pine bark media and automated drip irrigation for water and nitrogen application (50, 100, and 200 kg N ha^{-1}). Field experiments were conducted at Ukulinga Research Farm (29°60′ S and 30°37′ E; 596 m above sea level), where plots consisted of 1.5 m rows with 45 cm inter-row and 15 cm intra-row spacing. Custom-made plastic mulch used prevented rainfall infiltration, and basal fertilizer (10:20:10 NPK) was applied at planting. Four weeks post-planting, nitrogen treatments (50, 100, and 200 kg N ha^{-1}) were applied using urea fertilizer (34.5% N).

Drought stress was induced in both greenhouse and field experiments by withholding irrigation until soil moisture reached 35% of the field capacity. Soil moisture content was monitored using tensiometer readings from 50% heading to physiological maturity. The mean rainfall, mean minimum, and maximum temperatures during the experiment period were 80.80 mm, 15 °C, and 24 °C, respectively, while relative humidity varied from 60 to 81%. In contrast, non-stressed conditions received continuous optimal irrigation until 95% of plants reached maturity. All other agronomic practices adhered to South Africa's wheat production guidelines [36].

Table 1. List and source of wheat genotypes evaluated in this study.

E. No	Genotype	Source	Attributes	E. No	Genotype	Source	Attributes
1	SBO 01	ACCI/South Africa	Drought-tolerant	26	SBO 26	ACCI/South Africa	High yielding
2	SBO 02	ACCI/South Africa	Drought-tolerant	27	SBO 27	ACCI/South Africa	High yielding
3	SBO 03	ACCI/South Africa	Drought-tolerant	28	SBO 28	ACCI/South Africa	High yielding
4	SBO 04	ACCI/South Africa	Drought-tolerant	29	SBO 29	ACCI/South Africa	High yielding
5	SBO 05	ACCI/South Africa	Drought-tolerant	30	SBO 30	ACCI/South Africa	High yielding
6	SBO 06	ACCI/South Africa	Drought-tolerant	31	SBO 31	ACCI/South Africa	Drought-tolerant
7	SBO 07	ACCI/South Africa	Drought-tolerant	32	SBO 32	ACCI/South Africa	Drought-tolerant
8	SBO 08	ACCI/South Africa	Drought-tolerant	33	SBO 33	ACCI/South Africa	High yielding
9	SBO 09	ACCI/South Africa	Drought-tolerant	34	SBO 34	ACCI/South Africa	Drought-tolerant
10	SBO 10	ACCI/South Africa	Drought-tolerant	35	SBO 35	ACCI/South Africa	Drought-tolerant
11	SBO 11	ACCI/South Africa	Drought-tolerant	36	SBO 36	ACCI/South Africa	Drought-tolerant
12	SBO 12	ACCI/South Africa	Drought-tolerant	37	SBO 37	ACCI/South Africa	Drought-tolerant
13	SBO 13	ACCI/South Africa	High yielding	38	SBO 38	ACCI/South Africa	Drought-tolerant
14	SBO 14	ACCI/South Africa	High yielding	39	SBO 39	ACCI/South Africa	High yielding
15	SBO 15	ACCI/South Africa	High yielding	40	SBO 40	ACCI/South Africa	High yielding
16	SBO 16	ACCI/South Africa	High yielding	41	SBO 41	ACCI/South Africa	Drought-tolerant
17	SBO 17	ACCI/South Africa	Drought-tolerant	42	SBO 42	ACCI/South Africa	Drought-tolerant
18	SBO 18	ACCI/South Africa	High yielding	43	SBO 43	ACCI/South Africa	Drought-tolerant
19	SBO 19	ACCI/South Africa	High yielding	44	SBO 44	ACCI/South Africa	High yielding
20	SBO 20	ACCI/South Africa	High yielding	45	SBO 45	ACCI/South Africa	High yielding
21	SBO 21	ACCI/South Africa	High yielding	46	SBO 46	ACCI/South Africa	High yielding
22	SBO 22	ACCI/South Africa	High yielding	47	Check #1	Seed Company/South Africa	Low-N tolerant
23	SBO 23	ACCI/South Africa	High yielding	48	Check #2	Seed Company/South Africa	Low-N tolerant
24	SBO 24	ACCI/South Africa	High yielding	49	Check #3	Seed Company/South Africa	High yielding
25	SBO 25	ACCI/South Africa	High yielding	50	Check #4	Seed Company/South Africa	High yielding

E. No, Entry Number; ACCI, African Centre for Crop Improvement.

2.2. Data Collection

To comprehensively evaluate wheat genotype performance, data were collected on 12 major agronomic traits. These traits included seedling emergence rate (SE), days to heading (DTH) and days to maturity (DTM), which were calculated based on the number of days between sowing and 50% emergence, spike visibility, and senescence, respectively. Additional traits assessed included productive tillers per plant (TN), plant height (PH), spike length (SL), spikelets per spike (SPS), kernels per spike (KPS), fresh plant biomass (BM), thousand kernel weight (TKW), grain yield (GY), and harvest index (HI). Plant height, spike length, and biomass were measured using standardized methods, while grain yield and harvest index were calculated from harvested grain weight and above-ground biomass.

2.3. Data Analysis

The data underwent analysis of variance (ANOVA) using Genstat® version 17. Combined analysis of variance was conducted using a general linear model (GLM) procedure which treated water regime and nitrogen treatment as fixed factors, while genotype and site were considered random factors. To ensure validity, negative variances were adjusted to zero [37], and homogeneity of variances was tested using the Levene test. Variance components and heritability estimates were calculated based on partial ANOVA (Table 2) following [38]. Genotypic and phenotypic variances were performed according to [39,40]. Broad-sense heritability (H^2) was calculated as the ratio of genotypic variance ($\sigma^2{}_g$) to total phenotypic variance ($\sigma^2{}_p$), expressed in percentage as described by Allard [41]. The phenotypic variance was calculated as:

$$\sigma^2{}_p = \sigma^2{}_g + \sigma^2{}_{gl}/l + \sigma^2{}_{gw}/w + \sigma^2{}_{gn}/n + \sigma^2{}_{glwn}/lwn + \sigma^2{}_e/rlwn;$$

where $\sigma^2{}_g$ = genotypic variance, $\sigma^2{}_{gl}$ = genotype × location interaction variance, $\sigma^2{}_{gw}$ = genotype by water regime interaction variance, $\sigma^2{}_{gn}$ = genotype by nitrogen interaction variance, $\sigma^2{}_{glwn}$ = genotype × location × water regime × nitrogen treatment interaction variance, $\sigma^2{}_e$ = environmental variance, r = replication. The genetic correlations (r_G) between two characters, x_1 and x_2 under each water regime and nitrogen treatment were estimated according to Kwon and Torrie [42] and their significance were tested using the Student *t* test [43].

$$r_G = \frac{COV_{G(X_1X_2)}}{\sqrt{V_{G(X_1)}}\cdot\sqrt{V_{G(X_2)}}}$$

where $COV_{G(X_1X_2)} = Genetic\ covariance\ among\ traits\ x_1\ and\ x_2$

$V_{G(X_1)}\ and\ V_{G(X_2)} = Genetic\ variance\ for\ trait\ x_1\ and\ x_2, respectively.$

Table 2. Partial Analysis of variance table for 50 wheat genotypes tested across two sites, three nitrogen levels, and two water regimes with two replications.

Source of Variation	Degrees of Freedom	Expected Mean Square
Site (l)	l − 1	–
Nitrogen treatment (n)	n − 1	–
Water regime (w)	w − 1	–
Genotype (g)	g − 1	σ^2e + rσ^2gwln + rwσ^2gln + rnσ^2glw + rlσ^2gnw + rwlσ^2gn + rlnσ^2gw + rnwσ^2gl + σ^2g
gl	(g − 1)(l − 1)	σ^2e + rσ^2gwln + rwσ^2gln + rnσ^2glw + rnwσ^2gl
gn	(g − 1)(n − 1)	σ^2e + rσ^2gwln + rlσ^2gwn + rwσ^2gln + rwlσ^2gn
gw	(g − 1)(w − 1)	σ^2e + rσ^2gwln + rlσ^2gwn + rnσ^2glw + rnlσ^2gw
gln	(g − 1)(l − 1)(n − 1)	σ^2e + rσ^2gwln + rwσ^2gln
glw	(g − 1)(l − 1)(w − 1)	σ^2e + rσ^2gwln + rnσ^2glw
gnw	(g − 1)(w − 1)(n − 1)	σe^2 + rσ^2gwln + rlσ^2gwn
glnw	(g − 1)(l − 1)(n − 1)(w − 1)	σ^2e + rσ^2gwln
Replication within sites, water regime and nitrogen	lwn (r − 1)	–
MEe	lwn (g − 1)(r − 1)	σ^2e

σ^2e environmental variance, σ^2g genotypic variance, σ^2gl genotype by site interaction variance, σ^2gn genotype by nitrogen interaction variance, σ^2gw genotype by water regime interaction variance, σ^2gln genotype by site by nitrogen interaction variance, genotype by site by water regime interaction (glw), σ^2gwn genotype by water regime by site interaction variance, σ^2glwn genotype by site by water regime by nitrogen interaction, r replication.

3. Results

3.1. Analysis of Variance

The combined analysis of variance indicated significant differences ($p < 0.05$) among the evaluated traits. Significant interaction effects were computed among wheat genotypes, water regime, and nitrogen treatments for days to 50% heading and maturity, plant height, number of productive tillers, 1000-kernel weight, and grain yield (Table 3). No significant first-order interactions were detected for the number of productive tillers and 1000-kernel weight. However, significant interaction effects were observed between genotypes and water regimes, and between genotypes and nitrogen treatment were detected for these two important traits. Considerable variability of mean values was recorded for all the assessed traits under varying water regimes and nitrogen treatments and is reported elsewhere [6]. Under non-stress conditions, 95% of genotypes surpassed the mean grain yield of standard checks, whereas 75% outperformed the standard checks under drought stress.

3.2. Variance Components, Heritability and Genetic Advance

The variance components, heritability and genetic advance of grain yield, and key agronomic traits of wheat genotypes are described in Table 4. A significant proportion ($\geq$50%) of the phenotypic variation was attributed to genotypic differences for SE (96.48%), DTH (83.75%), TKW (74.23%), SPS (63.53%), DTM (63.22%), KPS (57.49%), GY (55.08%), and HI (51.22%) under drought stress and low N (50 kg ha^{-1}). A relatively greater proportion of the genetic advance was observed for KPS (28.10%), followed by DTH and SE with values of 15.89% and 14.28%, respectively. For non-stress and low-N (50 kg ha^{-1}) conditions, the genotypic variance attributed higher phenotypic variation for DTH (84.37%), SPS (71.64%), TKW (70.37%), and KPS (60.53%). A low to moderate genetic advance was achieved for SL (10.80%), HI (10.28%), BM (6.36%), and PH (3.55%).

The estimated heritability values for traits under drought and intermediate N (100 kg ha^{-1}) conditions ranged between 32.12 and 95.13% compared with 41.18–92.84% obtained under non-stress and intermediate N (100 kg ha^{-1}). A genotypic variance contributed, i.e., $\geq$50%, to total phenotypic variations, with a greater proportion recorded for SE (95.13%) and DTH (83.67%) under drought and intermediate N (100 kg ha^{-1}) conditions. While under non-stress and intermediate N (100 kg ha^{-1}) conditions, HI and TN contributed 92.84% and 66.92%, respectively. The highest genetic advance (GAM > 20.00) was observed for PH, TKW, and HI, while moderate GAM values were observed for BM (15.73%), SL (13.04%), and SE (11.82%) under drought and intermediate N (100 kg ha^{-1}). For non-stress and intermediate N (100 kg ha^{-1}) conditions, DTM, TN, and GY revealed greater genetic advancement estimated at 22.38%, 21.14%, and 21.06%. The lowest genetic advance estimate was recorded for HI (1.64%), followed by TKW (1.67%), SPS (2.01%), PH (2.40%) and SE (4.90%).

Under drought and recommended N (200 kg ha^{-1}) conditions, higher heritability values were calculated for DTH at 78.05%, followed by HI (69.70%), SL (65.46%), SE (65.52%), SPS (61.70%), TKW (59.24%), BM (53.33%), and PH (52.16%). The greater proportion of genetic advance was computed for DTM (21.67%) and GY (21.90%), while moderate genetic advance was recorded for SE (17.87%), SL (13.03%), and HI (10.99%). The findings revealed that genotypic variance contributed substantially ($\geq$50%) to the total phenotypic variation for most traits under non-stress and recommended N (200 kg ha^{-1}) conditions, with high values computed for DTH (85.47%) and SE (74.67%). The lowest proportion of the heritability estimates were recorded for KPS and TN, with values of 40.46% and 47.37%, respectively. Under non-stress and recommended N (200 kg ha^{-1}) conditions, the highest genetic advance was recorded for DTH at 26.44%, followed by SPS, GY, and SE with 22.54%, 21.56%, and 20.71%, respectively. The genetic advance ranged between 10.72% and 13.38%, with a greater proportion recorded for SL (13.38%), followed by KPS and HI with 10.93% and 10.72%, respectively.

Table 3. Analysis of variance for 12 phenotypic traits among 50 wheat genotypes evaluated across two sites, two water regimes, and three nitrogen levels.

		Traits											
Source of Variation	**DF**	**SE**	**DTH**	**DTM**	**PH**	**TN**	**SL**	**SPS**	**KPS**	**TSW**	**GY**	**BM**	**HI**
Incomplete block	1	0.541	94.230	101.042	9.100	269.544	7.543	5.890	68.110	4.631	89.782	124.531	0.045
Sites (S)	1	0.003 *	187.230 ^{ns}	1708.850 **	2144.740 **	333.910 ^{ns}	1.273 **	7.643 *	947.430 ^{ns}	6.005 **	96,250.490 **	278,121.200 **	1.338 ^{ns}
Water Regimes (WR)	1	0.013 ^{ns}	104.430 ^{ns}	371.850 **	1650.480 **	2643.300 ^{ns}	9.569 **	9.852 *	155.510 *	1.415 ^{ns}	11,688.270 **	31,382.600 **	0.322 **
Nitrogen Treatment (NT)	2	19.570 ^{ns}	1255.763 **	562.120 **	642.290 ***	4503.290 **	46.486 ***	30.090 **	123.140 ^{ns}	28.782 *	3615.800 **	76,065.600 ***	0.470 **
Genotype (G)	49	11.528 ***	35.440 ***	79.580 ***	214.410 ***	50.910 ***	10.679 ***	7.124 ***	73.810 ***	4.854 ***	155.820 ***	716.100 ***	0.016 **
G*S	49	0.003 **	34.591 **	48.940 **	64.300 **	35.390 **	9.394 *	3.786 **	32.750 **	1.755 *	142.130 **	789.400 **	0.009 **
G*W	49	1.285 **	3.723 ^{ns}	41.660 *	53.010 **	35.010 ^{ns}	8.679 *	3.406 *	51.960 ^{ns}	5.080 **	60.100 **	451.700 **	0.009 *
G*N	98	1.886 **	31.005 **	30.030 **	39.550 **	29.630 *	5.411 **	3.720 **	43.290 *	2.699 **	70.650 **	341.100 **	0.011 **
G*S*W	49	0.003 ^{ns}	6.080 **	35.570 ^{ns}	32.220 ^{ns}	34.770 **	8.878 ^{ns}	2.773 ^{ns}	36.810 **	1.445 ^{ns}	45.400 **	408.800 *	0.012 ^{ns}
G*S*N	98	0.003 ^{ns}	18.260 **	24.910 **	37.750 **	29.660 ^{ns}	4.990 *	3.731 ***	34.070 **	4.566 ^{ns}	64.760 **	375.200 **	0.016 **
G*W*N	98	1.393 **	7.758 **	25.680 **	39.500 **	27.700 **	5.225 **	4.032 *	36.800 **	3.068 **	65.380 **	414.400 **	0.016 **
G*S*W*N	98	0.003 ^{ns}	5.679 **	27.620 **	32.220 **	37.700 **	5.429 ^{ns}	3.269 **	44.800 **	4.346 **	63.110 **	433.000 **	0.012 **
Error	679	0.705	7.609	33.080	43.480	35.100	6.293	3.388	48.060	3.937	70.920	447.200	0.012

DF, degrees of freedom; SE, number of seedlings emerged; DTH, days to 50% heading; DTM, days to maturity; PH, plant height; TN, number of productive tillers; SL, spike length; SPS, number of spikelet per spike; KPS, number of kernels per spike; TKW, thousand kernel weight; GY, grain yield; HI, harvest index; *, $p < 0.05$; **, $p < 0.01$ level; ***, $p < 0.001$ level; ns, non-significant.

Table 4. Variance components for 12 phenotypic traits of 50 wheat genotypes assessed across two sites, two water regimes, and three nitrogen levels with two replications.

	Drought stress, Low N (50 kg ha^{-1})																							
	Traits																							
	SE		DTH		DTM		PH		TN		SL		SPS		KPS		TSW		GY		BM		HI	
Components	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%
Genotype (G)	69.70	76.57	13.45	48.33	4.73	27.15	11.63	18.37	5.53	12.96	0.84	8.70	0.54	27.55	9.36	23.07	4.12	42.83	14.54	25.73	16.00	18.38	0.21	21.65
G*Site (S)	4.86	5.34	1.25	4.49	1.34	7.69	2.22	3.51	0.10	0.23	0.34	3.52	0.15	7.65	0.55	1.36	0.93	9.67	7.92	14.01	14.50	16.66	0.11	11.34
G*Water regime (WR)	0.02	0.02	0.00 ^{1}	0.00 ^{1}	0.67	3.85	1.13	1.78	0.24	0.56	1.11	11.50	0.00 ^{1}	0.00 ^{1}	1.93	4.76	0.41	4.26	1.04	1.84	5.10	5.86	0.00 ^{1}	0.00 ^{1}
G*Nitrogen treatment (NT)	15.24	16.74	1.28	4.60	0.88	5.05	0.00 ^{1}	0.00 ^{1}	0.32	0.75	0.04	0.41	0.00 ^{1}	0.00 ^{1}	2.15	5.30	0.00 ^{1}	0.00 ^{1}	0.45	0.80	0.03	0.00 ^{1}	0.01	1.03
G*S*W	0.00 ^{1}	0.00 ^{1}	0.08	0.29	1.33	7.63	0.00 ^{1}	0.00 ^{1}	0.75	1.76	0.51	5.28	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.04	0.05
G*S*N	0.00 ^{1}	0.00 ^{1}	3.26	11.71	0.00 ^{1}	0.00 ^{1}	1.39	2.19	0.00 ^{1}	0.00 ^{1}	0.12	1.24	0.12	6.12	0.00 ^{1}	0.00 ^{1}	0.05	0.52	0.41	0.73	0.04	0.05	0.00 ^{1}	0.00 ^{1}
G*W*N	0.74	0.81	0.57	2.05	0.00 ^{1}	0.00 ^{1}	1.83	2.89	0.00 ^{1}	0.00 ^{1}	0.23	2.38	0.20	10.20	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.55	0.97	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}
G*S*W*N	0.03	0.03	0.00 ^{1}	0.00 ^{1}	0.02	0.12	0.00 ^{1}	0.00 ^{1}	0.10	0.23	0.01	0.10	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.00 ^{1}	0.24	2.50	0.00 ^{1}	0.00 ^{1}	0.05	0.06	0.00 ^{1}	0.00 ^{1}
Residual	0.44	0.48	7.94	28.53	8.45	48.51	45.12	71.26	35.62	83.50	6.45	66.84	0.95	48.47	26.59	65.52	3.87	40.23	31.60	55.92	51.33	58.85	0.60	61.86
Total variance	91.03	100	27.83	100	17.42	100	63.32	100	42.66	100	9.65	100	1.96	100	40.58	100	9.62	100	56.51	100	87.05	100	0.97	100
δ^2p	72.24		16.06		7.51		24.02		14.49		2.62		0.85		16.28		5.55		26.40		36.08		0.41	
H^2 (%)	96.48		83.75		63.22		48.42		38.16		32.06		63.53		97.49		74.23		55.08		44.44		51.22	
GAM (%)	14.28		15.89		13.02		4.12		2.53		7.91		1.02		28.10		3.05		4.91		4.62		10.57	

Table 4. *Cont.*

Drought stress, Intermediate N (100 kg ha^{-1})																								
	Traits																							
	SE		DTH		DTM		PH		TN		SL		SPS		KPS		TSW		GY		BM		HI	
Components	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%
Genotype (G)	48.10	69.24	14.40	50.70	4.25	10.08	4.25	16.68	3.41	14.00	4.30	32.06	2.24	16.70	0.36	6.13	0.24	10.53	0.98	14.39	16.90	33.77	0.02	7.69
G*Site (S)	4.55	6.55	1.56	5.49	1.44	3.42	2.12	8.32	0.97	3.98	0.37	2.76	0.08	1.28	0.54	9.20	0.15	6.58	0.63	9.25	9.54	19.06	0.00 [1]	0.00 [1]
G*Water regime (WR)	0.13	0.19	0.00 [1]	0.00 [1]	0.77	1.83	1.44	5.65	0.21	0.86	1.12	8.35	0.00 [1]	0.00 [1]	1.72	29.30	0.44	19.30	1.89	27.75	5.19	10.37	0.00 [1]	0.00 [1]
G*Nitrogen treatment (NT)	15.32	22.05	1.45	5.11	0.68	1.61	0.00 [1]	0.00 [1]	0.32	1.31	0.04	0.30	0.00 [1]	0.00 [1]	2.31	39.35	0.00 [1]	0.00 [1]	0.65	9.54	0.03	0.06	0.09	34.61
G*S*W	0.00 [1]	0.00 [1]	0.18	0.63	1.94	4.60	0.00 [1]	0.00 [1]	0.77	3.16	0.55	4.10	0.08	1.28	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.08	30.77
G*S*N	0.00 [1]	0.00 [1]	2.56	9.01	0.00 [1]	0.00 [1]	1.87	7.34	0.00 [1]	0.00 [1]	0.12	0.89	0.12	1.92	0.00 [1]	0.00 [1]	0.09	3.95	0.77	11.31	0.12	0.24	0.00 [1]	0.00 [1]
G*W*N	0.54	0.78	0.13	0.46	0.01	0.02	1.80	7.06	0.02	0.08	0.24	1.79	0.24	3.85	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.12	1.76	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]
G*S*W*N	0.08	0.11	0.00 [1]	0.00 [1]	0.04	0.10	0.00 [1]	0.00 [1]	0.10	0.41	0.01	0.07	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.89	39.03	0.00 [1]	0.00 [1]	0.06	0.12	0.00 [1]	0.00 [1]
Residual	0.75	1.08	8.12	28.59	33.05	78.41	14.00	54.94	18.54	76.17	6.66	49.66	3.48	55.77	0.94	16.01	0.47	20.61	1.77	25.99	18.21	36.38	0.07	26.92
Total variance	69.47	100	28.40	100	42.15	100	25.48	100	24.34	100	13.41	100	6.24	100	5.87	100	2.28	100	6.81	100	50.05	100	0.26	100
δ^2p	50.56		17.21		13.23		8.81		8.26		6.15		3.15		0.86		0.43		1.74		26.22		0.04	
H^2 (%)	95.13		83.67		32.12		48.24		41.28		69.92		71.11		41.86		55.81		56.32		64.45		50.00	
GAM (%)	11.82		6.10		2.04		22.49		2.06		13.04		2.21		0.68		20.64		1.29		15.73		20.18	

Drought stress, Recommended N (200 kg ha^{-1})																								
	Traits																							
	SE		DTH		DTM		PH		TN		SL		SPS		KPS		TSW		GY		BM		HI	
Components	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%
Genotype (G)	32.25	34.81	12.66	45.70	2.68	10.73	4.71	20.02	1.24	18.84	4.44	30.26	1.20	25.00	1.54	7.73	1.25	16.78	2.98	15.50	13.14	21.47	0.46	25.84
G*Site (S)	9.89	10.67	1.89	6.82	1.10	4.40	4.02	17.09	1.98	30.09	0.56	3.82	0.26	5.42	1.01	5.07	0.10	1.34	4.41	22.94	5.43	8.87	0.36	20.22
G*Water regime (WR)	0.48	0.52	0.02	0.07	0.15	0.60	1.14	4.85	0.21	0.3.19	1.15	7.84	0.00 [1]	0.00 [1]	1.32	6.62	1.04	13.96	1.28	6.66	5.47	8.94	0.14	0.00 [1]
G*Nitrogen treatment (NT)	13.01	14.04	2.22	8.01	1.10	4.40	0.05	0.21	0.12	1.82	0.75	5.11	0.05	1.04	3.77	18.91	0.11	1.48	0.51	2.65	0.18	0.29	0.00 [1]	0.00 [1]
G*S*W	0.00 [1]	0.00 [1]	0.10	0.36	1.25	5.00	0.11	0.47	0.04	0.61	0.16	1.09	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.67	8.99	0.05	0.26	0.23	038	0.09	5.06
G*S*N	0.00 [1]	0.00 [1]	4.71	17.00	0.00 [1]	0.00 [1]	2.84	12.07	0.09	1.37	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.05	0.25	0.03	0.40	0.84	4.37	0.14	0.23	0.00 [1]	0.00 [1]
G*W*N	0.00 [1]	0.00 [1]	0.83	3.00	0.00 [1]	0.00 [1]	1.41	5.99	0.02	0.30	0.51	3.48	0.81	16.87	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.19	1.00	1.29	2.11	0.17	9.55
G*S*W*N	0.24	0.26	0.01	0.04	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	1.01	15.35	0.04	0.27	0.02	0.42	0.00 [1]	0.00 [1]	1.01	13.56	0.22	1.14	0.15	0.24	0.48	26.97
Residual	36.77	39.69	5.26	18.99	18.70	74.86	9.24	39.28	1.87	28.42	7.06	48.12	2.46	51.25	12.24	61.41	3.24	43.49	8.74	45.47	35.17	57.47	0.08	4.49
Total variance	92.64	100	27.70	100	24.98	100	23.52	100	6.58	100	14.67	100	4.80	100	19.93	100	7.45	100	19.22	100	61.20	100	1.78	100
δ^2p	46.39		16.22		7.90		9.03		2.70		6.48		1.94		5.10		2.11		7.37		24.64		0.66	
H^2 (%)	65.52		78.05		33.90		52.16		45.97		68.46		61.70		30.17		59.24		80.43		53.33		69.70	
GAM (%)	17.87		6.50		21.67		2.73		1.32		13.03		1.51		1.19		1.50		21.90		4.60		10.99	

Table 4. *Cont.*

	Non-stress, Low N (50 kg ha^{-1})																							
	Traits																							
	SE		DTH		DTM		PH		TN		SL		SPS		KPS		TSW		GY		BM		HI	
Components	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%
Genotype (G)	6.20	10.70	14.62	56.60	2.61	20.53	7.11	24.88	0.77	20.98	0.44	10.76	0.24	21.82	2.81	19.29	3.04	31.34	1.70	18.30	1.09	9.38	0.05	16.67
G*Site (S)	4.51	7.78	1.53	5.92	1.42	11.17	2.67	9.34	0.32	8.72	0.59	14.42	0.08	7.27	0.62	4.25	0.12	1.24	0.82	8.83	0.50	4.30	0.00 [1]	0.00 [1]
G*Water regime (WR)	4.11	7.08	0.00 [1]	0.00 [1]	0.32	2.52	0.45	1.57	0.29	7.90	1.16	28.36	0.00 [1]	0.00 [1]	1.90	13.04	0.68	7.01	2.05	22.07	6.40	3.44	0.00 [1]	0.00 [1]
G*Nitrogen treatment (NT)	19.08	32.93	1.33	5.15	0.90	7.08	0.00 [1]	0.00 [1]	0.22	5.99	0.04	0.98	0.00 [1]	0.00 [1]	3.15	21.62	0.00 [1]	0.00 [1]	0.49	5.27	0.80	6.88	0.00 [1]	0.00 [1]
G*S*W	0.00 [1]	0.00 [1]	0.01	0.04	1.02	8.02	0.54	1.89	0.16	4.36	0.28	6.85	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.04	13.33
G*S*N	0.00 [1]	0.00 [1]	3.21	12.43	0.00 [1]	0.00 [1]	1.60	5.60	0.00 [1]	0.00 [1]	0.41	10.02	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.04	0.41	0.41	4.41	0.09	0.77	0.00 [1]	0.00 [1]
G*W*N	4.32	7.46	0.49	1.90	0.02	0.16	1.15	4.02	0.00 [1]	0.00 [1]	0.31	7.58	0.46	41.82	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.55	5.92	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]
G*S*W*N	0.14	0.24	0.00 [1]	0.00 [1]	0.02	0.16	0.00 [1]	0.00 [1]	0.24	6.54	0.05	1.22	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.94	9.69	0.00 [1]	0.00 [1]	0.10	0.86	0.00 [1]	0.00 [1]
Residual	19.58	33.79	7.77	30.08	6.40	50.35	15.06	52.69	1.67	45.50	0.81	19.80	0.32	29.09	6.09	41.80	4.88	50.31	3.27	35.20	2.64	22.72	0.21	70.00
Total variance	57.94	100	25.83	100	12.71	100	28.58	100	3.67	100	4.09	100	1.10	100	14.57	100	9.70	100	9.29	100	11.62	100	0.30	100
δ^2p	13.35		17.32		4.92		12.21		1.35		0.94		0.33		4.64		4.32		2.93		2.00		0.10	
H^2 (%)	46.44		84.37		53.05		58.23		57.14		46.81		71.64		60.53		70.37		58.07		44.50		50.00	
GAM (%)	2.94		26.12		2.06		3.55		1.16		10.80		0.72		2.30		22.55		1.74		6.36		10.28	

	Non-stress, Intermediate N (100 kg ha^{-1})																							
	Traits																							
	SE		DTH		DTM		PH		TN		SL		SPS		KPS		TSW		GY		BM		HI	
Components	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%
Genotype (G)	16.00	16.14	18.46	30.17	4.55	14.87	3.63	19.97	0.90	15.05	1.74	24.51	2.18	27.66	0.77	12.98	1.42	26.39	0.61	11.03	13.65	32.38	0.94	72.87
G*Site (S)	12.21	12.32	1.23	2.01	2.30	7.52	2.84	15.62	0.12	2.01	0.61	8.59	1.02	12.94	0.50	8.43	0.58	10.78	0.14	2.53	7.10	16.85	0.08	6.20
G*Water regime (WR)	9.66	9.74	0.00 [1]	0.00 [1]	0.81	2.65	1.40	7.70	0.33	5.52	1.13	15.91	0.00 [1]	0.00 [1]	1.21	20.40	0.64	11.90	2.04	36.89	3.19	7.57	0.00 [1]	0.00 [1]
G*Nitrogen treatment (NT)	18.29	18.45	1.20	1.96	0.06	0.20	0.00 [1]	0.00 [1]	0.40	6.69	0.04	0.56	0.00 [1]	0.00 [1]	2.36	39.80	0.00 [1]	0.00 [1]	0.42	7.59	0.21	0.50	0.01	0.77
G*S*W	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	1.40	4.58	0.00 [1]	0.00 [1]	0.12	2.01	0.88	12.39	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.01	0.77
G*S*N	0.00 [1]	0.00 [1]	4.74	7.75	0.00 [1]	0.00 [1]	1.95	10.73	0.00 [1]	0.00 [1]	0.16	2.25	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.14	2.60	0.09	1.63	0.94	2.23	0.00 [1]	0.00 [1]
G*W*N	0.41	0.41	0.91	1.49	0.00 [1]	0.00 [1]	1.10	6.05	0.00 [1]	0.00 [1]	0.31	4.37	0.84	10.66	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.87	15.72	0.00 [1]	0.00 [1]	0.12	9.30
G*S*W*N	0.09	0.09	0.00 [1]	0.00 [1]	0.06	0.20	0.00 [1]	0.00 [1]	0.29	4.85	0.01	0.14	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.56	10.41	0.00 [1]	0.00 [1]	0.05	0.12	0.00 [1]	0.00 [1]
Residual	42.48	0.48	34.64	56.62	21.41	69.99	7.62	41.91	3.82	63.88	2.22	31.27	3.84	48.73	1.09	18.38	2.04	37.92	1.36	24.59	17.10	40.57	0.13	10.08
Total variance	99.14	100	61.18	100	30.59	100	18.18	100	5.98	100	7.10	100	7.88	100	5.93	100	5.38	100	5.53	100	42.15	100	1.29	100
δ^2p	32.72		27.73		11.05		6.96		1.91		2.60		3.65		1.29		2.22		1.02		21.47		1.01	
H^2 (%)	48.89		66.56		41.18		52.19		47.00		66.92		59.73		59.57		63.96		59.80		63.56		92.84	
GAM (%)	4.90		16.17		22.38		2.40		21.14		1.89		2.01		10.19		1.67		21.06		15.19		1.64	

Table 4. *Cont.*

	Non-stress, Recommended N (200 kg ha^{-1})																							
	Traits																							
	SE		DTH		DTM		PH		TN		SL		SPS		KPS		TSW		GY		BM		HI	
Components	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%	Var	%
Genotype (G)	19.53	35.82	16.00	57.49	4.35	22.87	4.40	25.16	2.23	18.14	5.51	29.32	3.45	30.91	0.71	8.93	0.53	24.65	1.41	17.74	8.16	20.89	0.25	24.51
G*Site (S)	7.06	12.95	1.69	6.07	1.64	8.62	3.28	18.75	0.62	5.04	1.47	7.82	2.22	19.89	0.14	1.76	0.05	2.32	0.63	7.92	4.59	11.75	0.00 [1]	0.00 [1]
G*Water regime (WR)	0.12	0.22	0.00 [1]	0.00 [1]	1.60	8.41	1.43	8.18	0.10	0.81	2.99	15.91	0.00 [1]	0.00 [1]	1.20	15.09	0.28	13.02	1.09	13.71	2.15	5.50	0.12	11.76
G*Nitrogen treatment (NT)	15.29	28.04	1.45	5.21	0.88	4.63	0.00 [1]	0.00 [1]	0.44	3.58	0.11	0.58	0.00 [1]	0.00 [1]	2.00	25.16	0.00 [1]	0.00 [1]	0.16	2.01	0.00 [1]	0.00 [1]	0.01	0.98
G*S*W	0.00 [1]	0.00 [1]	0.08	0.29	1.90	9.99	0.00 [1]	0.00 [1]	0.11	0.90	0.39	2.08	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.08	7.84
G*S*N	0.00 [1]	0.00 [1]	3.65	13.11	0.00 [1]	0.00 [1]	1.67	9.55	0.00 [1]	0.00 [1]	0.26	1.38	0.84	7.53	0.00 [1]	0.00 [1]	0.05	2.32	0.45	5.66	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]
G*W*N	0.50	0.92	0.30	1.08	0.00 [1]	0.00 [1]	1.79	10.23	0.00 [1]	0.00 [1]	0.38	2.02	0.22	1.97	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.98	12.33	0.00 [1]	0.00 [1]	0.09	8.82
G*S*W*N	0.09	0.16	0.00 [1]	0.00 [1]	0.05	0.26	0.00 [1]	0.00 [1]	0.12	0.98	0.42	2.23	0.00 [1]	0.00 [1]	0.00 [1]	0.00 [1]	0.34	15.81	0.00 [1]	0.00 [1]	0.11	0.25	0.00 [1]	0.00 [1]
Residual	12.38	22.71	7.50	26.95	8.60	45.22	4.92	28.13	8.67	70.54	7.26	38.64	4.43	39.70	3.90	49.06	0.90	41.86	3.23	40.63	24.05	61.57	0.47	46.08
Total variance	54.52	100	27.83	100	19.02	100	17.49	100	12.29	100	18.79	100	11.16	100	7.95	100	2.15	100	7.95	100	39.06	100	1.02	100
δ^2p	26.15		18.72		7.37		4.27		4.71		8.06		5.67		1.75		0.78		2.53		16.47		0.37	
H^2 (%)	74.67		85.47		59.70		60.52		47.37		68.36		60.87		40.46		67.95		75.68		49.55		68.03	
GAM (%)	20.71		26.44		2.85		2.21		1.78		13.38		22.54		10.93		1.05		21.56		3.55		10.72	

SE, number of seedlings emerged; DTH, days to 50% heading; DTM, days to maturity; PH, plant height (cm); TN, number of productive tillers; SL, spike length (cm); SPS, number of spikelets per spike; KPS, number of kernels per spike; TKW, thousand-kernel weight (g/1000 kernel); GY, gain yield (g/m^2); BM, biomass (g/m^2); HI, harvest index; Var, variance; 0[1] negative value; δ^2p, phenotypic variance; H^2, Broad sense heritability; GAM, genetic advance as percent of the mean, respectively.

3.3. Correlation of Grain Yield and Yield-Related Traits

The genetic correlations (r_G) between various wheat traits are presented in Table 5, revealing significant pairwise associations among genotypic variance components. Under drought stress and low nitrogen (50 kg ha^{-1}), grain yield (GY) showed the strongest genetic correlation with days to heading (DTH) (r = 0.81, $p < 0.001$) and most correlations exceeded 0.40 (Table 5, above diagonal). GY exhibited weak genetic correlations (r < 0.05) with days to maturity (DTM), tillers per plant (TN), kernels per spike (KPS), thousand-kernel weight (TKW), and harvest index (HI) under drought stress and low-N (50 kg ha^{-1}) conditions. In contrast, non-stress and low-N (50 kg ha^{-1}) conditions revealed significant genetic correlations (0.32 < r < 0.72, $p < 0.001$) between GY and PH, TN, TKW, KPS, DTM, and BM (Table 5, below diagonal). DTH and KPS shifted from weak association under drought stress (r = 0.12, $p < 0.001$) to strong correlation under non-stress conditions (r = 0.71, $p < 0.001$) (Table 5, below diagonal).

Under drought-stressed and intermediate N (100 kg ha^{-1}) conditions, the degree of association between GY and TN was 0.73 (Table 5, above diagonal) compared to 0.78 observed under non-stressed and intermediate N (100 kg ha^{-1}) (Table 5, below diagonal) conditions. GY showed stronger correlations with TN (r = 0.73; $p < 0.001$) and DTH (r = 0.66; $p < 0.001$) under drought-stressed and intermediate N (100 kg ha^{-1}) conditions (Table 5, above diagonal), whereas, under non-stressed and intermediate N (100 kg ha^{-1}) condition, the GY revealed significant ($p < 0.001$) and stronger genetic associations with TN (r = 0.78) and SPS (r = 0.72). GY showed weak genetic associations below 0.08 with SE and DTM under both environmental conditions. The strongest genetic correlation under drought-stressed and intermediate N (100 kg ha^{-1}) was between SPS and DTM (r = 0.86; $p < 0.001$) (Table 5, above diagonal), and a high association was also measured between SPS and DTM (r = 0.79; $p < 0.001$) under non-stressed and intermediate N (100 kg ha^{-1}) (Table 5, below diagonal).

Genetic correlation coefficients exhibited consistently high and significant values for the majority of traits under drought-stressed and recommended N (200 kg ha^{-1}) and non-stressed and recommended N (200 kg ha^{-1}). The highest genetic association under drought-stressed and recommended N (200 kg ha^{-1}) condition was between SPS and TKW (r = 0.85; $p < 0.001$), followed by SPS and HI (r = 0.67; $p < 0.01$), and SL and GY (r = 0.66; $p < 0.01$), while other associations remained above 0.20 (Table 5, above diagonal). Under drought-stressed and recommended nitrogen (200 kg ha^{-1}) conditions, grain yield exhibited the weakest genetic correlations, with coefficients below 0.07 for SE, PH, and SPS. Under non-stressed and recommended N (200 kg ha^{-1}) conditions, GY showed highly significant ($p < 0.001$) genetic correlations, varying between 0.33 < r < 0.67 with TN, SPS, KPS, DTM, and SE (Table 5, below diagonal). GY and SPS were weakly associated (r = 0.04; $p < 0.05$) under drought-stressed and recommended N (200 kg ha^{-1}) conditions, yet they remained strongly associated (r = 0.45; $p < 0.001$) under non-stressed and recommended N (200 kg ha^{-1}) conditions (Table 5, below diagonal).

Table 5. Genetic correlation coefficients for 12 agronomic traits of 50 wheat genotypes evaluated in two sites under two water regimes and three nitrogen treatments with two replications. Note the top correlation matrix denotes trait correlations under drought stress (DS) and low N (50 kg ha^{-1}) (top diagonal) and non-stressed (NS) and low N (lower diagonal), while the middle displays DS and intermediate N (100 kg ha^{-1}) (top diagonal) and NS and intermediate N (lower diagonal), and the bottom refers DS and recommended N (200 kg ha^{-1}) (top diagonal) and NS and recommended N (lower diagonal) conditions.

	DS, Low N (50 kg ha^{-1})												
	Traits	SE	DTH	DTM	PH	TN	SL	SPS	KPS	TSW	GY	BM	HI
NS, Low N (50 kgha^{-1})	SE		0.084 *	−0.064	−0.142 **	0.112 **	−0.013	−0.050	−0.049	−0.018	0.057	−0.047	−0.004
	DTH	0.014		0.241 **	0.615 *	0.471 *	−0.005	0.573 **	0.121 ***	0.058 **	0.811 ***	0.081 *	0.789 *
	DTM	−0.038	0.636 **		0.029 *	−0.025	−0.003	−0.056	−0.006	0.868 **	−0.009	0.022	0.023
	PH	0.555 *	0.044	0.655 *		−0.066	0.558 **	0.473 **	0.789 *	0.067 **	0.674 ***	0.579 **	0.030 *
	TN	−0.007	−0.010	0.030 *	0.652 **		0.008	−0.012	−0.004	0.051	0.019 *	0.057	0.567 **
	SL	0.006	−0.009	−0.045	0.054	0.526 **		0.557 **	0.468 **	0.624 **	0.558 ***	0.125 **	0.064
	SPS	−0.098 *	0.723 **	−0.023	0.649 **	0.058	0.613 **		0.543 **	0.781 *	0.426 **	0.591 **	0.684 *
	KPS	−0.100 *	0.708 ***	−0.021	−0.001	−0.154 **	0.584 *	0.451 **		0.061	0.042	0.649 **	0.034
	TSW	−0.021	0.018 *	0.002	−0.135 **	−0.110 **	0.006	−0.040	0.057		0.038 **	0.219 **	0.092 *
	GY	−0.012	−0.008	0.715 ***	0.518 **	0.323 ***	0.622 **	0.007 **	0.646 ***	0.638 ***		0.722 ***	0.532 ***
	BM	0.629 **	0.737 **	0.005	0.532 **	0.557 **	0.476 *	0.589 *	−0.140 **	−0.021	0.714 ***		−0.171 **
	HI	0.012 *	−0.047	0.526 **	−0.047	−0.308 **	−0.064	−0.096 *	0.573 **	0.048	0.022 **	−0.634 **	
	DS, Intermediate N (100 kg ha^{-1})												
	Traits	SE	DTH	DTM	PH	TN	SL	SPS	KPS	TSW	GY	BM	HI
NS, Intermediate N (100 kgha^{-1})	SE		0.424 *	0.423 **	0.065	−0.031	−0.346	0.380 *	0.546 ***	0.667	0.065	0.084	0.008
	DTH	0.545 ***		0.251	0.609 **	0.294 **	0.205	0.529	0.604 ***	−0.074	0.661 ***	−0.072	0.354 *
	DTM	0.194 **	−0.103		−0.243 *	0.661 *	0.752 ***	0.858 **	0.411	0.564 *	0.019 **	0.536 *	0.114
	PH	0.305 *	−0.082	0.380 *		0.424	0.436 *	0.471	0.008	0.039 *	0.367 *	0.544 *	0.664 **
	TN	−0.035	0.295 ***	0.033	−0.021		−0.597	0.063	0.291	−0.144	0.731 ***	0.641 **	0.047
	SL	0.423 *	0.527 **	−0.103 **	0.163 *	0.780 **		−0.244 *	−0.137	0.007	0.507 ***	0.432	−0.116
	SPS	0.458 **	0.076	0.793 ***	0.315	−0.031	0.640 **		0.340 ***	0.098 *	0.441 **	−0.268 *	0.022
	KPS	0.627	−0.038	0.423 **	−0.011	0.124 *	0.045	−0.074		−0.014	0.044	0.071	−0.271
	TSW	0.236 *	0.305 *	0.751 ***	0.621 *	0.505	−0.334	0.317	0.021		0.535 *	−0.103	0.011
	GY	0.074	0.190 ***	−0.074	0.507 **	0.778 ***	−0.354 **	0.722 ***	0.069 **	0.338 *		0.195 **	0.603 **
	BM	0.529 **	0.551 **	−0.081	0.156	0.251	0.071	0.532 **	−0.061	−0.122	0.067		0.551 *
	HI	0.122	0.127	0.551 ***	−0.071	0.627 *	0.022	0.004	0.446	0.569 **	0.628 ***	0.075	

Table 5. *Cont.*

		DS, Recommended N (200 kg ha^{-1})											
	Traits	SE	DTH	DTM	PH	TN	SL	SPS	KPS	TSW	GY	BM	HI
NS, Recommended N (200 kgha^{-1})	SE		0.384 ***	−0.012	0.542 ***	0.424 **	0.514 **	0.127	0.118	0.465 **	0.062 *	0.354 *	0.044
	DTH	0.056		0.607 ***	0.033	0.056	0.148	0.445 **	−0.265	−0.042	0.462 *	0.622 ***	0.390
	DTM	0.456 **	0.072		−0.282 *	0.158 **	0.241 ***	0.006	0.615 **	0.031	0.225	−0.201	0.647 ***
	PH	−0.034	−0.271 *	0.061		−0.094	−0.228	0.314 *	0.268	0.548 ***	−0.064	−0.254	0.551 **
	TN	0.648 ***	0.581	0.264	0.369 *		0.647 ***	0.158 *	0.418 *	−0.224	0.575 **	0.070	0.413 *
	SL	0.559 ***	0.187	0.712 ***	0.510 ***	0.257 *		0.591 ***	0.587 ***	0.418 **	0.665 **	0.546 ***	0.321
	SPS	0.008	0.710 ***	0.040	0.117	−0.084	0.021		0.328	0.850 ***	0.044 *	0.287 *	0.667 **
	KPS	0.310 *	0.667	0.308 *	0.004	0.571 ***	0.714 ***	0.714 **		0.364	0.670 ***	0.115	−0.103
	TSW	0.010	−0.041	−0.220	0.212 **	0.459	0.032	−0.315	−0.265		0.411	0.681 ***	0.423 *
	GY	0.667 ***	0.326 *	0.610 ***	−0.372	0.328 ***	0.612 *	0.447 ***	0.552 ***	0.417 *		0.008	0.152 **
	BM	0.426	0.114	0.442 *	0.094	0.051	0.374	−0.546	0.320 **	0.640 ***	0.521 **		0.065
	HI	−0.025 *	0.655 ***	0.014	0.636 **	0.337 *	0.285	0.307	0.081	0.148	0.238	0.421 **	

SE, number of seedlings emerged; DTH, days to 50% heading; DTM, days to maturity; PH, plant height (cm); TN, number of productive tillers; SL, spike length (cm); SPS, number of spikelets per spike; KPS, number of kernels per spike; TKW, thousand-kernel weight (g/1000 seed); GY, grain yield (g/m^2); BM, biomass (g/m^2); HI, harvest index; *, ** and *** denote significant at $p < 0.05$; $p < 0.01$ and $p < 0.001$ probability levels, respectively.

4. Discussion

4.1. Data Analysis

The combined analysis of variance found significant ($p < 0.001$) genetic differences for all assessed agronomic and phenological traits across two water regimes and three nitrogen treatment combinations, except for days to 50% seedling emergence and harvest index (Table 3). This indicates the availability of significant genetic heterogeneity within the tested wheat genotypes, which can be exploited in wheat breeding. Significant genetic variations were observed for the assessed traits among the tested genotypes under varying water regimes and nitrogen treatments (Supplementary Table S1). Mwadzingeni, Shimelis [28] and Mathew, Shimelis [44] documented comparable findings on yield and associated traits under drought and non-stressed conditions. The genotype performance varied with the changes in the environmental conditions. For instance, genotypes exposed to drought and low-N stressed conditions revealed a high reduction in grain yield, number of tillers, spike length, number of kernels per spike, and plant biomass. This indicates the significance of evaluating genotypes across various locations and the opportunities for selecting and developing wheat varieties with drought and low-nitrogen tolerance.

4.2. Genetic Parameters

The water regime and nitrogen treatment had substantial contributions to total phenotypic variation. This agrees with Sedri, Amini [45], who reported high heritability and substantial genetic gain for most traits, wide genetic variation, and lower environmental influence under drought stress, revealing the effects of additive genes. The significant influences of water and nitrogen treatments on most traits highlight the necessity of tailored agronomic practices and site selection for efficient wheat production. Selected genotypes could be used in breeding the local germplasm adapted to various environmental conditions in semi-arid and arid areas with minimal nitrogen availability. Abid, Tian [15] pinpointed that water stress and low nitrogen availability caused stunted plant growth and seed deformation or abortion during grain filling. Significant differences caused by water regime were noticeable in all agronomic traits, especially under marginal irrigation, which is well known to negatively impact grain yield by influencing tissue elongation necessary for plant biomass, plant height, and spike length. The combined effects of drought and nitrogen deficiency in wheat truncate the grain-filling period, inducing premature maturity, reduced plant growth, and compromised seed development, culminating in yield loss [45]. The present study revealed that drought stress and low nitrogen levels significantly reduced days to heading and maturity, plant biomass, and seed size, resulting in diminished grain quality. Drought stress limits nutrient mobility, impacting the photosynthetic capacity, leading to reduced growth, early senescence, shorter grain filling period, and reduced grain weight, lowering wheat productivity [15].

Under drought and low N stress conditions, the highest genetic variance was recorded for SE (96.48%), DTH (83.75%), TKW (74.23%), SPS (63.53%), DTM (63.22%), KPS (57.49%), GY (55.08%), and HI (51.22%). High genetic advance values were computed for KPS (28.10%), followed by DTH (15.89%) and SE (14.28%) under both water regimes. These findings suggest that environmental factors have a negligible impact on the phenotypic manifestation of these characteristics, implying that direct selection can effectively improve these traits. The high heritability estimates (H > 60%) recorded for SE, DTH, SL, and SPS under both water regimes and recommended N (200 kg ha^{-1}), implied that the environment less influenced these traits. Mathew (2018) reported comparable results, revealing high heritability estimates (H > 75%) for days to heading (DH) under both drought and optimal conditions, and noted that water availability had a relatively minor effect on flowering compared to grain yield, which exhibited low heritability. The heritability estimates ranged from low (30%) to high (78%) under drought and recommended N (200 kg ha^{-1}). DTH (78.05%), HI (69.70%), SL (65.46%), and SE (65.52%) recorded high heritability values, implicating that these traits were genetically controlled and their selection could bring significant variation within the population. Okechukwu, Agbo [46], and Mwadzingeni, Shimelis [28] reported heritability ranging between 30 and 95% for agronomic traits in wheat. Kandić, Dodig [47] also reported high heritability for DH (75%). The present study revealed high heritability estimates (H > 50%) for DTM, SPS, KPS, TKW, GY, and HI under drought and non-stress conditions at low N (50 kg ha^{-1}), indicating the successive contribution of genetic components in determining the variation in these traits (Table 4). Tian, Wen [48] reported that DTH had a high heritability estimate above 65% and was controlled by major QTLs such as the *Rht* allele, which influenced the stability of heritability under contrasting environments.

Several studies identified important genetic components encoding for functional genes that regulate key agronomic characteristics in wheat under drought-stressed conditions [49–51]. A higher genetic advance was recorded for PH (GAM = 22.49), TKW (GAM= 20.64), and HI (GAM = 20.18) under drought and intermediate N (100 kg ha^{-1}). Heritability estimates and genetic advances varied with treatment combinations in this study. High heritability and genetic gain were observed for SE, DTH, SL, and BM under non-stress and recommended N (200 kg ha^{-1}), suggesting that these traits were genetically controlled by additive and dominant genes which promote improvement through direct selection under stressed conditions [52,53]. High heritability estimates coupled with significant genetic advance values for grain yield were observed across water regimes, supporting the efficacy of direct selection in both drought-stressed and non-stressed conditions.

Previous research has consistently demonstrated high heritability and substantial genetic gain for DH, DTM, PH, SL, and TKW [54–56]. Low to moderate heritability estimates between 32.06 and 55.08% were recorded for most traits across water regimes and nitrogen treatments, suggesting a substantial proportion of variation attributed to the environment compared to the genotypic variance. Rattey, Shorter [57] reported that environmental effects accounted for a larger proportion of variation than genotypic differences in grain yield, plant height, plant biomass, and harvest index. These results indicate that the environmental effects may hinder the breeding progress for improving grain yield in wheat, even when there is adequate genetic variation within the population. Agronomic traits with low heritability and genetic advancement pose challenges in selection programs. In this regard, indirect selection for traits with high heritability and genetic advance, which are positively correlated with the target trait, can be utilized to enhance genotypic response under varied environmental conditions [28]. Further, marker-assisted selection can be used to improve agronomic selection response.

4.3. Agronomic Trait Associations

Breeding programs focused on improving early maturity in wheat must be undertaken with caution to avoid compromising the plant biomass and number of kernels per spike that are more favorably correlated to grain yield. Analysis showed that days to maturity exhibited significant negative correlations with key agronomic characteristics (Table 5). The positive correlation between PH and BM across water regimes under low N (50 kg ha^{-1}) (Table 5) suggests that the size of the root system was a pivot to control optimal water and N nutrient absorption in the soil. Subota, Rotureau [58] reported a strong and positive correlation (r > 0.55) between plant height and total plant biomass in tall and semi-dwarf wheat genotypes. Enhancing root system development is crucial for optimized soil resource (water and nutrients) utilization, facilitating increased plant height, biomass production, and grain yield. The positive relationship between plant height and biomass suggests that PH is a key factor in optimizing plant biomass production (r > 0.50; $p < 0.01$) under non-stress and low N (50 kg ha^{-1}) and drought stress and low N (50 kg ha^{-1}). These correlations were higher than r = 0.46 for PH and shoot dry matter in wheat, as reported by Bai, Liang [59]. Such genetic correlations play a significant role in formulating a selection strategy for developing genotypes with drought and low N tolerance mechanisms.

The substantial positive correlations observed between grain yield (GY) and associated traits suggest enhanced resilience to drought and low-nitrogen conditions (Table 5). Grain yield was significant and positively correlated to TN (r = 0.78; $p < 0.001$) and SPS (r = 0.72; $p < 0.001$) under non-stress and intermediate N (100 kg ha^{-1}) and under non-stress and intermediate N (100 kg ha^{-1}) condition for DTH (r = 0.66; $p < 0.001$) and TN [r = 0.73; $p < 0.001$ (Table 5)]. These findings agree with Lopes, El-Basyoni [60] and Okechukwu, Agbo [46], who reported a strong positive direct association between GY and PH (r > 0.65). Mathew, Shimelis [44] asserted that tall plants with increased seed weight are susceptible to lodging under unfavorable environmental conditions. This could reduce crop yield drastically. However, the significant positive correlations found between GY and DTH and DTM under non-stress and recommended N [200 kg ha^{-1} (Table 5)] and drought-stressed and recommended N [200 kg ha^{-1} (Table 5)] provide better insight as this association promotes accelerated flowering and maturity in crops, potentially due to reduced vegetative growth and grain-filling duration [61,62]. The selection of early heading and maturing genotypes for drought-prone areas could potentially take yield penalties when not monitored accordingly. Both early flowering and maturity traits are advantageous for escaping environmental effects including drought stress, poor soil fertility, frost damage, and disease abundance.

5. Conclusions

This study revealed substantial genetic diversity among tested genotypes for all evaluated traits, offering valuable genetic materials and identifying beneficial correlations between key agronomic features crucial for enhancing wheat yield resilience to drought and nitrogen deficiency. High heritability and genetic advance values were recorded for DTH, DTM, TN, SPS, KPS, and TKW, indicating that these traits were genetically conditioned, which facilitates genetic gain through targeted selection for enhanced grain yield under drought stress. Agronomic traits with low heritability and substantial genetic gain are complex to improve, but their genetic composition can be enhanced using indirect selection through related traits. PH, DTH, DTM, SL, and SPS exhibited low heritability and genetic advance, but they are positively correlated to grain yield. These traits could be used to enhance drought and low N tolerance and increase grain yield in wheat. The study identified three wheat genotypes: SBO 19, SBO 16, and SBO 36 as best-performing lines, combining high yields with impressive drought and low nitrogen tolerance. These genotypes are ideal candidates for advanced breeding programs focused on developing climate-resilient varieties. Future research should concentrate on uncovering the genomic regions underlying their tolerance mechanisms, enabling the selection of complementary genotypes with enhanced stress resilience.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/nitrogen5040076/s1, Table S1: Mean squares and significant tests among 50 wheat genotypes evaluated for 12 phenotypic traits under two water regime and three nitrogen levels.

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