HSPI Inc. The Open Access Publisher
JPSP JOURNAL OF PLANT SCIENCE AND PHYTOPATHOLOGY
ISSN 2575-0135

Research Article

Genetic variability, divergence, and path coefficient analysis of yield and yield related traits of Durum wheat (*Triticum turgidum l. var. Durum*) genotypes at Jamma district, south wollo zone, amhara region, Ethiopia

Haile Tefera*

Department of Plant Science College of Agriculture and Natural Resource Mekdela Amba University, P.O. Box, 32, Tulu Awulia, Ethiopia

More Information

***Address for Correspondence:** Haile Tefera, Department of Plant Science College of Agriculture and Natural Resource Mekdela Amba University, P.O. Box, 32, Tulu Awulia, Ethiopia, Email: hailetikuye8@gmail.com

Submitted: June 08, 2022
Approved: July 01, 2022
Published: July 04, 2022

How to cite this article: Tefera H. Genetic variability, divergence, and path coefficient analysis of yield and yield related traits of Durum wheat (*Triticum turgidum l. var. Durum*) genotypes at Jamma district, south wollo zone, amhara region, Ethiopia. J Plant Sci Phytopathol. 2022; 6: 075-083.

DOI: 10.29328/journal.jpsp.1001078

Keywords: Divergence; Genotype; Phenotype; *Triticum durum*

Abstract

Durum wheat (Triticum turgidum L. var. durum) is a member of the Poaceae family and tetraploid (genomes of AABB) with 28 chromosomes (2n=4x=28). Narrow genetic variability was a problem to develop genotypes with better adaptation to different agro-ecologies. Therefore, the objective of this study was to investigate the genetic variability, divergence, and path coefficient analysis of durum wheat genotypes by using morphological traits and identifying essential yield-related traits of durum wheat, and to identify promising candidate genotypes to be used in future durum wheat breeding program. The study was carried out on 81 genotypes and the experiment was laid out in a triple lattice design with an arrangement of 9 x 9 x 3 treatment, which made 243 experimental units. Results obtained on genetic variability, path coefficient, and genetic divergent analysis among yield-related traits are presented here under the present study. Generally, the present study revealed the existence of significant genetic variability among the tested genotypes for different traits helpful for direct and indirect selection.

This study recommended that the potential durum wheat genotypes 214552, 208150, 238516, 5645, Mekuye, 236984, 7960, 7152, 231599, and 208242 could be used for durum wheat breeding programs for yield and yield component traits improvement under similar agro-ecologies.

Introduction

Durum wheat (*Triticum turgidum L. var. durum*) is the world's leading cereal grain and staple food of the population in the world [1]. Durum wheat is a member of the Poaceae family. It is tetraploid (genomes of AABB) with 28 chromosomes ($2n = 4x = 28$). In the World, durum wheat is cultivated on 218 million hectares of land with average yields have risen from 2.3 to 4.6 tons per ha [2]. In Ethiopia, Durum wheat is one of the major cereal crops. The first wheat was diploid einkorn and grown in the Near Eastern Fertile Crescent [3]. Wild einkorn was then cultivated and produced in domesticated form (*Triticum monococcum*). Emmer was domesticated from its wild progenitor (*Triticum dicoccoides*) and was derived from the hybridization between wild diploid wheat and relative of goat grass (*Aegilops speltoides*) occurring from 300,000 to 500,000 years ago [3]. In Ethiopia, durum wheat is cultivated over 2.5 million hectares of land with an annual production of 5.7 million tons [4]. Durum wheat requires 350-950 mm annual precipitation and the optimum temperature is 23-26^{o}c. Durum wheat can grow on fertile well-drained silt and clay loam soil with a soil pH of 5.2 - 8.5 [5]. Constraints of durum wheat production include lack of seeds of improved varieties and incidence of diseases. Besides in Ethiopia, production of durum wheat is restricted due to poor evaluation of the variability of durum wheat genotypes from major durum wheat-producing areas. Narrow genetic variability was a problem to develop genotypes with better adaptation to different agro-ecologies, resistant and tolerant to biotic and abiotic stresses. The targeted problem of durum wheat production was the use of poor yielder local durum wheat varieties. Similarly, there is no detailed information on the extent of genetic variability, the association between traits, genetic divergence, and path coefficient analysis among traits and their selection efficiency [6].

Identification of local genotypes adapted to different agro-ecologies that improve the productivity of durum wheat production is important. The experience of genetic variability in Ethiopian durum wheat genotypes is important for future breeding programs. Information on genetic divergence and path coefficient analysis of traits is essential for durum wheat improvement. The present study was important for the selection of promising candidate genotypes to be used in future durum wheat breeding programs. The objective of this study was to investigate the genetic diversity, divergence, and path coefficient analysis of Ethiopian durum wheat genotypes by using morphological traits and identify yield component traits of durum wheat, and further identify promising candidate genotypes to be used in future durum wheat breeding program.

Materials and methods

Description of experimental sit

The genotypes were evaluated at Jamma district South Wollo Zone, Amhara Region, Ethiopia. Jamma is one of the major durum wheat-producing areas of South Wollo Zone, Amhara Region, Ethiopia and it describes as follows (Table 1).

Experimental materials

Eighty-one genotypes of durum wheat were used and the seeds of the genotypes were obtained from the Biodiversity Institute of Ethiopia. The genotypes are listed in (Table 2).

Experimental design

The experiment was prepared in a triple lattice design with the arrangement of 9 x 9 blocks with three replications. The total experimental units were 243. Area of the experimental field covered 925.6m^2 with 26m in width and 35.6m in length. Each treatment was assigned randomly to the experimental units within a block. Data were collected from three central rows for most of the variables and from randomly sampled plants for some of the traits. All experimental factors were applied uniformly to the entire plot except genotypes of durum wheat in the experiment.

Table 1: Description of the study area

Description	Jamma (Location)
Longitude	15^{0}E
Latitude	11 ^{0}N
Altitude (m.a.s.l)	2626
Mean range of temperature (^{0}c)	16 to 22
Mean annual rainfall (mm)	360 to 970
Soil type	Vertisol

Source: (Jamma Agricultural Sector Office, 2017)

Table 2: List of durum wheat genotypes used in the study and their origin

No	Genotypes	Origin	No	Genotypes	Origin
1	208168	Tigray	42	228768	Tigray
2	236303	Amhara	43	238120	Tigray
3	208327	Oromia	44	208319	Amhara
4	203958	Oromia	45	208170	Oromia
5	203882	Amhara	46	208482	Oromia
6	208316	Amhara	47	208281	Amhara
7	208251	Oromia	48	208127	Amhara
8	236975	Oromia	49	228763	Oromia
9	5429	Tigray	50	208141	Oromia
10	208220	Amhara	51	208531	Oromia
11	203790	Amhara	52	208484	Oromia
12	226946	Oromia	53	214861	Amhara
13	208321	Oromia	54	236984	Amhara
14	208320	Oromia	55	208142	Oromia
15	8034	Oromia	56	238133	Oromia
16	7165	Amhara	57	Mekuye	Tigray
17	208257	Oromia	58	231597	Tigray
18	208155	Oromia	59	238555	Oromia
19	208325	Amhara	60	208198	Oromia
20	231599	Oromia	61	238516	Amhara
21	208309	Oromia	62	208471	Amhara
22	5454	Amhara	63	214552	Tigray
23	203940	Amhara	64	236279	Amhara
24	7508	Oromia	65	208173	Oromia
25	236270	Oromia	66	208150	Oromia
26	208274	Oromia	67	208309	Oromia
27	208230	Oromia	68	8034	Oromia
28	236306	Oromia	69	5645	Oromia
29	208478	Oromia	70	7148	Oromia
30	6859	Amhara	71	214555	Oromia
31	208273	Oromia	72	203966	Oromia
32	236310	Oromia	73	208254	Amhara
33	7961	Oromia	74	208242	Amhara
34	214874	Oromia	75	228862	Oromia
35	208307	Oromia	76	5503	Oromia
36	7960	Oromia	77	213310	Oromia
37	204548	Tigray	78	236982	Tigray
38	208314	Tigray	79	214887	Amhara
39	236315	Oromia	80	7152	Amhara
40	8205	Amhara	81	208319	Amhara
41	Felakit	Oromia			

Data collected

Data collection was done on a pilot basis and a sample plant basis. Besides the data were collected from the net plot that includes days to heading, days to maturity, above-ground biomass per hectare, grain yield in kg per hectare, thousand kernels weight, and harvest index.

On the other hand, the data were collected from randomly selected ten plants from the three middle rows of each plot that include plant height, number of tillers per plant, number of tillers per unit area, and number of spikelets per spike and spike length.

Statistical analysis

The data were analyzed as per the design used in the experiment using an R-Software computer. The data obtained for different traits were statistically analyzed using appropriate ways for analysis of variance, coefficient of variance, genetic advance, path coefficient, and genetic divergent analysis of traits for durum wheat genotypes.

Analysis of variance (ANOVA)

The analysis of variance (ANOVA) was performed using an R-Software computer for Triple-Lattice Design. The analyses of variances were done using the mean of ten sample plants for plant height, tillers per plant, tillers per unit area, spikelet per spike, and spike length on a plant basis. However, a plot basis was used for characters such as days to heading and maturity, grain yield per hectare, above-ground biomass yield, and harvest index for analysis of variance. Mean separation was performed with Duncan's Multiple Range Test (DMRT) at ($p < 0.05$) 5% level of significance.

$$Y_{ijl} = \mu + r_j + g_i + pl_{(j)} + \varepsilon_{ijl}$$

Where, Y_{ijl} = the observed value of the trait Y for the i^{th} genotype in j^{th} replication

μ = the general mean of trait Y

r_j = the effect of j^{th} replication

g_i = the effect of i^{th} genotypes

$pl_{(j)}$ =block within replicate the effect

ε_{ijl} = the experimental error associated with the trait y for the i^{th} genotype in l^{th} block within replication and j^{th} replication [7].

Estimation of phenotypic and genotypic parameters

Environmental, genotypic, and phenotypic variance components and their coefficients of variation were estimated based on the methods detailed as follows (Sharma, 1998).

Genotypic variance $(\sigma_g^2) = \frac{MS_g - MS_e}{r}$

Phenotypic variance on a mean basis $(\sigma_p^2) = \sigma_g^2 + \sigma_e^2$

Phenotypic coefficient of variation $(\mathrm{PCV}) = \frac{\sqrt{\sigma_p^2}}{\bar{x}} * 100$

Genotypic Coefficient of variation $(\mathrm{GCV}) = \frac{\sqrt{\sigma_g^2}}{\bar{x}} * 100$

Estimation of heritability in a broad sense and genetic advance under selection

Broad sense heritability (H^2) was expressed as the percentage of the ratio of the genotypic variance (σ_g^2) to the phenotypic variance (σ_g^2) as described by [5]:

$$(H^2) = \frac{\acute{o}_g^2}{\acute{o}_p^2} * 100$$

Genetic advance under selection (GA): expected genetic advance for each character at 5% selection intensity was computed using the methodology described [3].

$$\mathrm{GA} = \mathrm{K} * \sigma_p * H^2$$

Genetic advance as percent of the mean calculated to compare the extent of the predicted advance of different traits under selection, using the following formula [3].

$$\mathrm{GAM} = \frac{GA}{\bar{X}} * 100$$

Estimation of phenotypic and genotypic correlations

Phenotypic and genotypic correlations coefficients between yield and yield-related traits would estimate using the standard method as described [8].

Phenotypic correlation coefficient $= \frac{Cov_{p_{xy}}}{\sqrt{(\sigma_{p_x}^2)(\sigma_{p_y}^2)}}$

Genotypic correlation coefficient $(r_{g_{xy}}) = \frac{COV_{g_{xy}}}{\sqrt{(\sigma_{g_x}^2)(\sigma_{g_y}^2)}}$

The phenotypic correlation coefficient was tested their significance using the formula suggested by [9].

$$\mathrm{t} = \frac{r_p}{SE(r_p)}$$

$$SE_{(r_p)} = \sqrt{\frac{1 - r_p^2}{n - 2}}$$

The genotypic correlation coefficient was tested with the following formula as suggested by [9].

$$t_{cal} = \frac{r_g}{SE(r_g)}$$

$$SE_{r_g} = \sqrt{\frac{1 - r_g^2}{2H_x^2 * H_y^2}}$$

The calculated absolute *t*-value was tested against the tabulated t-value at n-2 degree of freedom for both phenotypic and genotypic correlations.

Path coefficient analysis

Path coefficient analysis was involved using the genotypic and phenotypic correlation coefficients to determine the indirect and direct effect of yield-related traits of durum wheat on grain yield of durum wheat by considering grain yield per hectare as the dependent variable. Path coefficients were obtained by solving the following simultaneous equations, which express the basic relationship between correlation and path coefficient by using the formula as follows [10].

$$r_{ij} = p_{ij} + \varepsilon r_{ik} * p_{kj}$$

Where, r_{ij} = mutual relation between independent trait (i) and dependent trait (j) as measured by genotypic correlation coefficient.

p_{ij} = Components of direct effects of the independent trait (i) on the dependent variable (j) as measured by genotypic path coefficient and

$\varepsilon r_{ik} * p_{kj}$ = Summation of components of the indirect effect of a given independent trait (i) on a given dependent trait (j) and vice versa for all other independent traits (k)

The residual effect, which determines how best causal factors account for the variability of the dependent factor, was calculated using the following formula [11].

$$1 = p^2 r + \sum p_{iy} * r_{iy}$$

Where, p^2r = the residual factor,

p_{iy} = the direct effect of yield by i^{th} trait, and

r_{iy} = the correlation of yield with the i^{th} trait.

The contribution of the remaining unknown factor was measured as the residual factor (P_R), which is calculated as [12].

$$P_R = \sqrt{(1 - \varepsilon r_{ij} p_{ij})}$$

The magnitude of P_R indicates how best the causal factors determine the variability of the dependent factor. If P_R value is small for instance, nearly zero, and the yield is explained by the variability in the independent traits. However, higher P_R the value indicates that other factors which have not been considered in the analysis to determine the variation in the yield.

Genetic divergent of genotypes

Error variance and covariance matrix were used to get the standardized uncorrelated means (Y) from the original mean values (X) through the pivotal condensation method. The D^2 value of a pair of varieties was obtained as the sum square of differences between the corresponding Y values. In matrix notation, the distance between two groups was estimated from the following relationship [12].

$$D_{ij}^2 = (X_i X_j) cov^{-1} (X_{i-} X_j)$$

Where, D_{ij}^2 = distance between class i and j,

X_i and X_j = the vector means of the traits for the i^{th} and j^{th} groups,

cov^{-1} = the pooled within-group variance-covariance matrix.

Genetic divergence is the statistical distance between the genotypes. It is determined by using cluster analysis, which assigns genotypes to different groups.

Results and discussion

Variability of traits

The analysis of variance showed significant variation among genotypes ($p < 0.01$) for days to maturity, tillers per plant, and tillers per unit area, plant height, spike length above-ground biomass, 1000 kernels weight, grain yield, and harvest index. Sciacca, et al. [13] also reported considerable genetic variability for days to heading, days to maturity, plant height, spike length, tillers per plant, and grain yield except for above-ground biomass, 1000 kernel weight, and harvest index among durum wheat genotypes. Tsegaye, et al. [5] also reported highly significant differences among durum wheat genotypes for days to heading, plant height, tillers per plant, spikelet per spike, and spike length (Tables 3-5).

Estimates of phenotypic and genetic coefficient of variation

Phenotypic and genetic coefficients of variation of days to heading, days to maturity, plant height, spike length, tillers per plant and tillers per unit area, spikelet per spike, above-ground biomass, 1000 kernel weight, grain yield, and harvest index were shown (Table 5). The PCV values were slightly greater than GCV values in the present study although the difference was very small. This indicated that the environmental effect was very small for the expression of all traits.

Estimates of heritability

Broad sense heritability (H^2) of traits ranged from 57.9% to 89.7% (Table 5). Pramoda and Gangaprasad (2007) categorized heritability estimates as low (< 40%), medium (40% - 59%), moderately high (60% - 80%), and very high (> 80). Higher heritability estimates (> 80%) were recorded for traits days to heading (89.7%), spikes length (88.9%), spikelet per spike (88.2%), plant height (87.1%), 1000 kernels weight (85.6%), days to maturity (83.9%) and tillers per unit area (82.1%).

Estimates of expected genetic advance

Genetic advance as percent of mean was categorized as low (0% - 10%), moderate (10% - 20%), and high (20%) and above [3]. Accordingly, the expected genetic advance as the percent of means expressed ranged from 13.9% for days to maturity to 67.2% for grain yield (Table 5). GAM indicates that selecting the top 5% of the base population could result in an advance of 13.9% to 67.2% over the respective population mean. High GAM was observed in grain yield (67.2%), days to heading (24.5%), 1000 kernel weight (26.6%), above-ground biomass yield (26.5%), tillers per plant (38%), tillers per unit area (24.3), spike length (28.2%), spikelet per spike (28.5%), plant height (34.4) and harvest index (30%). This suggested that selection could be effective in genotypes for these traits and the possibility of improving durum wheat yield through a direct selection of grain yield-related traits.

Table 3: The mean square of traits of 81-durum wheat genotypes tested

Traits	Rep(df=2)	Block(adj.) (df=24)	Tr(unadj.) (df=80)	Inbe (df=136)	Tr(adj.) (df=80)	CV
DH	4075	61	259**	8.6	234**	4.2
DM	26683	30.7	278**	15.7	262**	3.2
PH	17486	64	824**	35	744**	6.8
SL	169	0.4	5.2**	0.2	4.7**	6.3
TPP	117	0.7	2.6**	0.2	2.3**	9.6
TPUA	41753	340	1998**	113	1973**	6.0
SPS	4309	4.7	37.9**	1.4	33**	5.3
BM	34973599	1740097	8785515**	578799	7895636**	6.9
TKW	8868	15.4	109**	5	94**	5.7
GY	8210245	644650	4742321**	435267	4336769**	13.7
HI%	143	29	141**	24	123**	16.4

DF=Degree of freedom, DH=days to heading, DM=days to maturity, PH=plant height, SL=spike length, TPP=tillers per plant, TPUA=tillers per unit area, SV=source of variation, Rep= Replication, Tr (unadj.)= Treatment (Unadjusted), Inbe = Intra block error and Tr (adj.) = Treatment (adjusted)

Table 4: Range, mean, phenotypic, and genotypic variance for 11 traits of durum wheat genotypes tested.

Trait	Range	Mean ± SE	σ_p^2	σ_g^2
DH	48-80	69 ± 0.98	83.7	75.1
DM	102-138	124 ± 1.04	97.8	82.1
PH	63-128	86 ± 1.78	271.3	236.3
SL	6.4-11.3	8 ± 0.14	1.8	1.6
TPP	3.4-7.0	5 ± 0.1	0.9	0.7
TPUA	131-232	176 ± 2.62	631	518
SPS	17-30	22 ± 0.37	11.9	10.5
BM	8909-15188	10923 ± 180	3017744	2438945
TKW	28-53.4	39 ± 0.62	34.7	29.7
GY	1876-6476	3360 ± 133	1813614	1378347
HI%	16-43	30 ± 0.71	57	33

DF=Degree of freedom, DH=days to heading, TPP=tillers per plant, TPUA=tillers per unit area, SL=spike length, SPS=spikelet per spike, PH=plant height, DM=days to maturity, BM = above-ground biomass, TKW=1000kernel weight, GY=grain yield, SE= Standard Error, and HI=Harvest index

Table 5: Environmental variance, phenotypic and genotypic coefficient of variability, broad-sense heritability, genetic advance, and genetic advance as percent of the mean for the 11 characters of durum wheat genotypes tested

Trait	σ_g^2	PCV	GCV	H^2	GA	GAM
DH	8.6	13.3	12.6	89.7	16.9	24.5
DM	15.7	8.0	7.4	83.9	17.1	13.9
PH	35	19.2	17.9	87.1	29.6	34.4
SL	0.2	16.8	15.2	88.9	2.3	28.2
TPP	0.2	23.7	20.9	77.8	1.5	38
TPUA	113	14.4	13.0	82.1	42.5	24.3
SPS	1.4	15.7	14.7	88.2	6.3	28.5
BM	578799	15.9	14.3	80	2891	26.5
TKW	5	15.1	14.0	85.6	10.4	26.6
GY	435267	37.4	35	76	2259	67.2
HI%	24	25.2	19.1	57.9	9.0	30.0

DF=Degree of freedom, DH=days to heading, TPP=tillers per plant, TPUA=tillers per unit area, SL=spike length, SPS=spikelet per spike, PH=plant height, DM=days to maturity, BM = above-ground biomass, TKW=1000kernel weight, GY=grain yield, HI= harvest index

Estimates of correlation coefficients of traits

Estimates of the phenotypic and genotypic correlation coefficient between each pair of traits presented are (Tables 6,7), respectively. In the present study, the phenotypic correlation coefficients were less in magnitude than the genotypic correlation coefficients revealing the presence of inherent genetic relationships among various traits and less dependent on environmental effects (Tables 6,7).

Path coefficient analysis

Phenotypic and genotypic path coefficient analyses were used to determine essential yield attributes by estimating the direct effects of traits contributing to grain yield. Path coefficient analysis was separating direct effects from the indirect effects through other related traits by partitioning the correlation coefficient and searching out the relative essential traits as selection criteria. Grain yield is the complex outcome of various traits that are considered resultant traits. The other traits indicating significant relations with grain yield were considered causal traits. In the study area, the residual effects were not highly significant that indicates all traits that influenced grain yield were considered. Soriano, et al. [14] reported a negative association between above-ground

Table 6: Phenotypic correlation coefficients (r_p) of yield and yield-related traits of durum wheat genotypes tested.

	DM	TPP	TPUA	SL	SPS	PH	SKW	BM	GY	HI
DH	0.6**	0.1	0.1	0.4**	0.7**	0.4*	0.3*	0.3*	0.5**	0.4**
DM		0.1	0.2	0.1	0.1	0.2	0.1	0.1	0.1	0.1
TPP			0.6**	0.4**	0.5**	0.1	-0.1	0.4*	0.6**	0.4*
TPUA				0.5**	0.1	0.4**	0.3*	0.5**	0.3*	0.4**
SL					0.5**	0.7**	0.5**	0.1	0.2*	0.1
SPS						0.2	0.7**	0.3**	0.4**	0.3*
PH							-0.3*	0.3*	0.2*	0.3*
SKW								-0.1	0.6**	0.5**
BM									-0.1	-0.3*
GY										0.5**

Note, ** and * indicates highly significant at 1% and significant at 5% probability levels, respectively. DH = Days to heading, DM = Days to maturity, TPP = Tillers per plant, PH = Plant height (cm), TPUA = Tillers per unit area, SL = Spike Length, SPS = Spike per spikelet, BM = above ground biomass (kg/ha), SKW = 100 seed weight (g), GY = Grain yield (kg/ha).

Table 7: Genotypic correlation coefficients (r_g) of yield and yield-related traits of durum wheat genotypes tested.

	DM	TPP	TPUA	SL	SPS	PH	SKW	BM	GY	HI
DH	0.9**	0.1	0.6	0.9**	0.8*	0.7	0.7	0.3	0.9**	0.8*
DM		0.7	0.8*	0.8*	0.8*	0.9**	0.6	0.9**	0.7	0.7
TPP			0.9**	0.8*	0.9**	0.8*	-0.6	0.9**	0.9**	0.8*
TPUA				0.9**	0.7	0.8*	0.9**	0.9**	0.8*	0.8*
SL					0.9**	0.8*	0.9**	0.7	0.9**	0.7
SPS						0.8*	0.9**	0.9**	0.9**	0.8*
PH							-0.9**	0.9**	0.8*	0.8*
SKW								-0.4	0.9**	0.9**
BM									-0.6	-0.8*
GY										0.9**

DH = Days to heading, DM = Days to maturity, TPP = Tillers per plant, PH = Plant height (cm), TPA = Tillers per unit area, SL = Spike Length, SPS = Spike per spikelet, BM = Biomass (kg/ha), SKW = 100 kernel weight (g), GY = Grain yield (kg/ha),*, ** = Significant a 5% and 1% probability level, respectively.

biomass and harvest index similar to the present finding. This indicated that an increase in the above-ground biomass reduces the harvest index ratio.

Phenotypic direct and indirect effects of traits on grain yield

In the study area, tillers per plant (0.508) and tillers per unit area (0.736) had a high phenotypic direct effect on the grain yield of durum wheat indicating the association between these traits as good contributors to grain yield (Table 8). Tillers per plant and tillers per unit area could be considered as the main components of selection in a breeding program for obtaining a higher grain yield of durum wheat. A highly significant positive correlation and considerable direct effects of tillers per plant and tillers per unit area on grain yield justified the need to identify the nature of relationships between yield and yield-related traits by using path coefficient analysis.

Genotypic direct and indirect effects of traits on grain yield

In the study area, the genotypic direct and indirect effects of traits on grain yield were presented in (Table 9). Tilers per plant (0.689) followed by thousand kernels weight (0.643), days to maturity (0.565), plant height (0.02), tilers per unit area (0.08); spike length (0.056), spikelets per spike (0.065), above-ground biomass (0.087) and harvest index (0.025) were exerted a positive direct effect on grain yield. In agreement with the present study, Qureshi, et al. [12] reported thousand kernels weight, days to maturity, plant height, tillers per unit area, spike length, spikelets per spike, and harvest index. However, plant height (-0.05) had a negative direct effect on grain yield. But, its negative direct effect was counterbalanced by its considerable positive indirect effect. Biomass yield and harvest index which showed a positive genotypic correlation with grain yield exerted a considerable direct effect on grain yield. 1000 kernels weight showed highly significant positive genotypic correlations and a considerable positive direct effect on grain yield. Johnson, [15] reported that 1000-kernels weight exerted the highest direct positive effect on grain yield similar to the present study.

Genetic divergence

The qualitative and quantitative description of genotype collection for agronomical useful traits is an essential prerequisite for effective utilization of germplasm collection in the durum wheat breeding program. In the present study, divergence analysis helps to group the genotypes based on their similarity and differences that are similar into one group and others into different groups as well as analysis of D^2 revealed the presence of significant differences among the tested genotypes for all the traits that justify the need to estimate squared distance values for genotypes of durum wheat. Genetic improvement through hybridization and selection depends upon the extent of genetic diversity between parents. Based on the D-square value genotypes were grouped into six clusters. The number of clusters indicates that the

Table 8: Estimate of indirect effects (off-diagonal) and direct effects (boldface and diagonal) at a phenotypic level in 81 durum wheat genotypes tested in the study area

	DH	DM	TPP	TPUA	SL	SPS	PH	SKW	BM	HI	GY
DH	**0.08**	0.05	0.02	0.01	-0.04	0.03	0.02	0.02	0.02	0.03	**0.61****
DM	0.04	**0.05**	0.06	0.04	0.02	0.04	0.04	-0.08	0.02	0.03	**0.53****
TPP	0.02	-0.06	**0.51**	0.07	0.01	0.02	0.03	0.031	0.04	0.03	**0.75****
TPUA	0.07	0.04	0.07	**0.74**	0.02	-0.07	0.03	0.04	-0.06	0.03	**0.86****
SL	0.06	-0.03	0.03	0.04	**0.03**	0.02	0.04	0.06	0.06	-0.04	**0.35***
SPS	0.04	0.04	-0.05	-0.03	0.04	**-0.07**	0.02	0.04	0.02	0.03	**0.24***
PH	0.07	0.06	0.05	0.04	0.03	0.07	**0.02**	0.06	0.05	0.04	**0.24***
SKW	0.04	0.08	-0.06	0.02	0.04	0.04	0.05	**-0.05**	0.04	-0.05	**0.57****
BM	0.08	0.04	0.04	0.05	0.05	0.04	0.03	0.04	**0.05**	0.07	**0.51****
HI	0.03	0.03	0.05	0.02	0.02	0.03	0.05	0.02	0.04	**0.01**	**0.23***

Residual value =0.11

Note, * and ** indicates significant at 5% and highly significant at 1% probability levels, respectively. DH = Days to heading, DM = Days to maturity, TPP = Tillers per plant, TPUA = Tillers per unit area, SL = Spike Length, SPS = Spikelet per spike, PH = Plant height (cm), SKW = 1000 seed weight (g), BM = Above ground biomass (kg/ha), HI= Harvest index and GY = Grain yield (kg/ha).

Table 9: Estimate of indirect effects (off-diagonal) and direct effects (boldface and diagonal) at a genotypic level in 81 durum wheat genotypes tested in the study area

	DH	DM	TPP	TPUA	SL	SPS	PH	SKW	BM	HI	GY
DH	**0.02**	0.08	0.75	-0.09	0.08	0.68	0.08	0.08	0.76	0.08	**0.39***
DM	0.16	**0.59**	0.06	0.09	0.07	0.08	0.08	0.09	0.07	0.47	**0.79****
TPP	0.07	0.08	**0.69**	-0.07	0.07	0.07	0.05	-0.08	0.05	0.07	**0.93****
TPUA	0.14	0.21	0.06	**0.08**	0.76	0.08	0.69	0.09	0.65	0.09	**0.65****
SL	0.07	0.07	0.03	0.06	**0.06**	0.08	0.09	0.77	0.08	0.04	**0.47***
SPS	0.06	0.03	0.09	0.08	0.09	**0.07**	0.58	0.67	0.08	0.44	**0.58****
PH	0.05	0.18	0.09	0.26	0.08	0.07	**-0.05**	-0.07	0.76	0.08	**0.46***
SKW	0.07	0.07	0.09	0.13	0.09	0.04	0.09	**0.64**	0.74	0.74	**0.87****
BM	0.08	0.08	0.25	0.05	0.07	0.08	0.13	0.04	**0.09**	0.32	**0.52****
HI	0.07	0.07	0.43	0.08	0.54	0.05	0.07	0.09	0.09	**0.03**	**0.41***

Residual value = 0.03

Note, ** and * indicates highly significant at 1% and significant at 5% probability levels, respectively. DH = Days to heading, DM = Days to maturity, TPP = Tillers per plant, TPUA = Tillers per unit area, SL = Spike Length, SPS = Spike per spikelet, PH = Plant height (cm), SKW = 1000 seed weight (g), BM = Above ground biomass (kg/ha), HI= Harvest index and GY = Grain yield (kg/ha).

tested genotypes were divergent, due to the composition of the genotypes that were collected from different sources of germplasm in the biodiversity of Ethiopia.

Squared distance (D^2)

In the present study, tested genotypes had average D-square values ranging from 88.95-354.72 (Table 10). This indicated the presence of genetic divergence among the 81durum wheat genotypes. As per average D-square values of genotypes 236315 (354.72), 228768 (321.91), 214552 (320), 208316 (305.84) and 204548 (302.76) were on an average maximum divergent from all the tested durum wheat genotypes (Table 9). However, genotypes of 203958 (98.86), 213310 (98.82), 226946 (97.86), and 5503 (88.95) were the least on average genetic divergent from all the tested durum wheat genotypes (Table 10).

Intra and inter-cluster square distances

In the presented study, average intra and inter-cluster D^2 values were presented in (Table 11). Maximum average intra cluster D^2 value was obtained in cluster III (143.76) while moderate average intra cluster D^2 value was obtained in cluster I (98.76), cluster IV (97.94), and cluster II (94.86). However, the lowest intra-cluster was recorded in cluster V (47.83) and cluster VI (49.12), which shows the presence of less genetic diversity within the cluster (Table 11). Maximum average inter-cluster D^2 value was obtained between cluster V and cluster VI (286.97) while moderate average inter-cluster D^2 value was obtained among cluster IV and cluster VI (276.86) as well as cluster III and cluster VI (254.75). However, the lowest inter clusters were recorded between cluster I and cluster III (103.65) which indicated the presence of less genetic diversity among this cluster.

The mean value of 11 quantitative traits in each cluster is presented in (Table 11). Cluster I consisted of 22 genotypes having the characteristic of late flowering (58), a medium number of days to mature (128), and a relatively high number of spikelets per spike (27) next to cluster VI (31). Cluster VI could be characterized by a low number of days to heading (46) and days to maturity. However, relatively high number of tilers per unit area (12), spikelets per spike (31), longest spike length (9 cm), plant height (129), heaviest 1000 kernels weight (57.5 gram per plot), above-ground biomass (14820kg per ha), grain yield (6281 kg per ha) and high harvest index (42.2) in (Table 12).

The distribution of the evaluated durum wheat genotypes was presented in (Table 13). According to the present experiment, 22 (27.16%) of genotypes in cluster I, 14 (17.28%) of genotypes in cluster II, 15 (18.52%) of genotypes in cluster III, 12 (14.81%) of genotypes in cluster IV, 8 (9.88%) of genotypes in cluster V and 10 (12.35%) of

Table 10: Average D^2 values for each durum wheat genotype.

Entry No	Genotype	Average D^2 value	Entry No	Genotype	Average D^2 value
1	208168	235.12	42	228768	321.91
2	236303	125.52	43	238120	132.65
3	208327	231.63	44	208319	236.84
4	203958	98.86	45	208170	163.62
5	203882	213.21	46	208482	163.63
6	208316	305.84	47	208281	236.91
7	208251	134.83	48	208127	152.83
8	236975	126.93	49	228763	125.70
9	5429	243.16	50	208141	297.54
10	208220	147.43	51	208531	129.52
11	203790	187.64	52	208484	238.31
12	226946	97.86	53	214861	161.92
13	208321	128.94	54	236984	162.87
14	208320	215.76	55	208142	192.85
15	8034	147.94	56	238133	231.64
16	7165	182.87	57	Mekuye	238.13
17	208257	125.54	58	231597	123.64
18	208155	129.93	59	238555	213.65
19	208325	231.67	60	208198	172.73
20	231599	195.87	61	238516	186.27
21	208309	194.83	62	208471	272.23
22	5454	142.43	63	214552	320.00
23	203940	132.62	64	236279	217.82
24	7508	143.21	65	208173	154.90
25	236270	231.91	66	208150	132.43
26	208274	217.21	67	208309	142.96
27	208230	153.32	68	8034	216.12
28	236306	163.83	69	5645	231.54
29	208478	129.84	70	7148	127.42
30	6859	231.73	71	214555	287.32
31	208273	123.64	72	203966	164.32
32	236310	142.83	73	208254	182.74
33	7961	152.76	74	208242	147.92
34	214874	236.81	75	228862	124.65
35	208307	132.79	76	5503	88.95
36	7960	143.76	77	213310	98.82
37	204548	302.76	78	236982	127.84
38	208314	221.53	79	214887	187.98
39	236315	354.72	80	7152	183.72
40	8205	231.57	81	208319	142.87
41	Felakit	298.64			

Table 11: Average intra and inter-cluster divergence D^2 value in 81 durum wheat genotypes.

Cluster	I	II	III	IV	V	VI
I	**98.76**	121.32	103.65	185.72	205.21	243.32
II		**94.86**	112.21	207.83	210.51	260.82
III			**143.76**	215.14	217.71	254.75
IV				**97.94**	206.93	276.86
V					**47.83**	286.97
VI						**49.12**

Table 13: Distribution of 81 durum wheat genotypes in different clusters.

	No of genotype	Genotypes					
Cluster I	22	208168	208251	208327	7961	208307	214555
		236303	236975	7960	214874	208316	203966
		228768	208142	208531	214887	208198	238516
		238120	208127	208484	7152		
Cluster II	14	213310	228763	214861	Mekuye	208471	5503
		236982	208141	236984	228862	214552	208531
		208319	238133				
Cluster III	15	203958	208254	208150	204548	5454	208257
		203882	208242	208309	208314	203940	236306
		5645	Felakit	7148			
Cluster IV	12	236279	208321	231599	7508	208478	208482
		208173	208320	208309	236270	6859	208281
Cluster V	8	203790	8034	208273	231597	238555	236310
		226946	7165				
Cluster VI	10	236315	5429	208155	208274	208319	208170
		8205	208220	208325	208230		

genotypes in cluster VI were presented from the total number of durum wheat genotypes in (Table 13). Generally, moderate genetic divergence among the genotypes was because they were developed at different times with repeated crossing and selection from genetically different parents for similar purposes.

Summary and conclusion

Results obtained from genetic variability assessment, phenotypic, and genotypic correlation coefficients of ten traits with grain yield were partitioned into direct and indirect effects. Genetic divergence distance is essential for a hybridization program to get better yield and the best recombinant parents. The maximum and minimum average intra-cluster distance D^2 was obtained in cluster III (143.76) and in cluster V (47.83), respectively. On the other hand the minimum and maximum average inter-cluster distance D^2 was obtained between cluster I and cluster III (103.65) and between cluster V and cluster VI (286.97), respectively. Generally, this study recommended that the potential durum wheat genotypes could be used for durum wheat breeding programs for yield and yield component traits improvement under similar agro-ecologies. The founding potential durum wheat genotypes should be tested for the future in a different location for yield and yield component traits improvement under different agro-ecologies.

Table 12: Mean values of six clusters for 11 traits

Group	DH	DM	TPP	TPA	SL	SPS	PH	SKW	BM	GY	HI
Cluster I	58	128	5	8	6	27	78	37.8	9074	2376	29.3
Cluster II	79	139	4	9	5	22	74	39.5	9089	3276	36.2
Cluster III	88	127	5	7	6	19	79	38.3	10790	2326	21.9
Cluster IV	79	126	5	6	5	23	90	49.6	12828	3877	32.9
Cluster V	77	138	5	8	6	19	78	39.7	10192	3452	31.7
Cluster VI	46	116	4	12	9	31	129	57.5	14820	6281	42.2

Note, ** and * indicates highly significant at 1% and significant at 5% probability levels, respectively. DH = Days to heading, DM = Days to maturity, TPP = Tillers per plant, TPA = Tillers per unit area, SL = Spike Length, SPS = Spikelet per spike, PH = Plant height (cm), SKW = 1000 seed weight (g), BM = Above ground biomass (kg/ha), HI= Harvest index and GY = Grain yield (kg/ha).

References

1. Zecevic V, Boskovic J, Dimitrijevic M, Petrovic S. Genetic and phenotypic variability of yield components in wheat (triticum aestivum l). Bulgarian Journal of Agricultural Science, 2010; 16(4), 422–428. https://doi.org/10.2298/gensr0402151z
2. Sahri A, Chentoufi L, Arbaoui M, Ardisson M, Belqadi L, Birouk A, Roumet P, Muller MH. Towards a comprehensive characterization of durum wheat landraces in Moroccan traditional agrosystems: analysing genetic diversity in the light of geography, farmers' taxonomy and tetraploid wheat domestication history. BMC Evol Biol. 2014 Dec 21;14:264. doi: 10.1186/s12862-014-0264-2. PMID: 25528060; PMCID: PMC4300848.
3. Ahmadizadeh M, Shahbaz H, Valizadeh M, Zaefizadeh M. Genetic diversity of durum wheat landraces using multivariate analysis under normal irrigation and drought stress conditions. African Journal of Agricultural Research, 2011; 6(10), 2294–2302.
4. Mehdiabadi S, Mohammadi R, Etminan AR, Shooshtari L. Evaluation of Genetic Diversity in Durum Wheat Advanced Lines. 2015; 7(1), 236–240.
5. Tsegaye D, Dessalegn T, Dessalegn Y, Share G. Genetic variability, correlation and path analysis in durum wheat germplasm (Triticum durum Desf). Agricultural Research and Reviews, 1(May), 2012; 107–112.
6. Jaradat AA. Ecogeography, genetic diversity, and breeding value of wild emmer wheat (Triticum dicoccoides Körn ex Asch. & Graebn) Thell. Australian Journal of Crop Science, 5(9 SPEC. ISSUE), 2011; 1072–1086.
7. Habash DZ, Kehel Z, Nachit M. Genomic approaches for designing durum wheat ready for climate change with a focus on drought. J Exp Bot. 2009;60(10):2805-15. doi: 10.1093/jxb/erp211. Erratum in: J Exp Bot. 2010 Feb;61(4):1249. PMID: 19584119.
8. Zaeifizadeh M, Khayatnezhad M, Ghasemi M, Azimi J, Vahabzadeh M. Path analysis of yield and yield components in synthetic bread wheat (Triticum aestivum L) genotypes. Advances in Environmental Biology, 2011; 5(1), 98–103.
9. Singh AK, Singh D. Genetic variability, heritability and genetic advance in marigold. Indian Journal of Horticulture, 2010; 67(1), 132–136.
10. Berhanu M, Wassu M, Yemane T. Genetic variability, correlation and path analysis of yield and grain quality traits in bread wheat (Tritium aestivum L) genotypes at Axum, Northern Ethiopia. Journal of Plant Breeding and Crop Science, 2017; 9(10), 175–185. https://doi.org/10.5897/jpbcs2017.0671
11. Medouri A, Bellil I, Khelifi D. Genetic diversity of high and low molecular weight glutenin subunits in algerian aegilops geniculata. Notulae Botanicae Horti Agrobotanici Cluj-Napoca, 2014; 42(2), 453–459. https://doi.org/10.1583/nbha4229511
12. Qureshi N, Bariana H, Kolmer JA, Miah H, Bansal U. Genetic and Molecular Characterization of Leaf Rust Resistance in Two Durum Wheat Landraces. Phytopathology. 2017 Nov;107(11):1381-1387. doi: 10.1094/PHYTO-01-17-0005-R. Epub 2017 Aug 16. PMID: 28812937.
13. Sciacca F, Fichera C, Di Silvestro S, Conte E, Palumbo M. Genetic diversity of durum wheat as determined by AFLP in fluorescence. Biologia Plantarum, 2010; 54(1), 198–200. https://doi.org/10.1007/s10535-010-0035-x
14. Soriano JM, Villegas D, Aranzana MJ, García Del Moral LF, Royo C. Genetic Structure of Modern Durum Wheat Cultivars and Mediterranean Landraces Matches with Their Agronomic Performance. PLoS One. 2016 Aug 11;11(8):e0160983. doi: 10.1371/journal.pone.0160983. PMID: 27513751; PMCID: PMC4981446.
15. Johnson M, Johnson M. Association Mapping and Genetic Diversity Studies of Agronomic and Quality Traits in Durum Wheat [Triticum turgidum L. var. durum (Desf.)]. November. 2017. https://library.ndsu.edu/ir/handle/10365/27462