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

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Abstract

Durum wheat (*Triticum turgidum* L. var. durum) is a member of the Poaceae family and tetraploid (genomes of AABB) with 28 chromosomes (*2n*=4*x*=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*=4*x*=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°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 site

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 925.6m² 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.

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.

Table 1: Description of the study area

| Description | Jamma (Location) |
|-------------|------------------|
| Longitude   | 15°E             |
| Latitude    | 11°N             |
| Altitude (m.a.s.l) | 2626           |
| Mean range of temperature (°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 | 20 | 203958    | Amhara |
| 2  | 236303     | Amhara | 21 | 208327    | Oromia |
| 3  | 208327     | Oromia | 22 | 203882    | Amhara |
| 4  | 203958     | Oromia | 23 | 203790    | Amhara |
| 5  | 203882     | Amhara | 24 | 226946    | Oromia |
| 6  | 208316     | Amhara | 25 | 208321    | Oromia |
| 7  | 208251     | Oromia | 26 | 208222    | Amhara |
| 8  | 236975     | Oromia | 27 | 236306    | Oromia |
| 9  | 5429       | Tigray | 28 | 208478    | Oromia |
| 10 | 208222     | Amhara | 29 | 208478    | Oromia |
| 11 | 203790     | Amhara | 30 | 8034      | Oromia |
| 12 | 226946     | Oromia | 31 | 208222    | Amhara |
| 13 | 208321     | Oromia | 32 | 203940    | Amhara |
| 14 | 208320     | Oromia | 33 | 236975    | Oromia |
| 15 | 8034       | Oromia | 34 | 208478    | Oromia |
| 16 | 7165       | Amhara | 35 | 203940    | Amhara |
| 17 | 208257     | Oromia | 36 | 208222    | Amhara |
| 18 | 208155     | Oromia | 37 | 236975    | Oromia |
| 19 | 208325     | Amhara | 38 | 236306    | Oromia |
| 20 | 231599     | Oromia | 39 | 203940    | Amhara |
| 21 | 208309     | Oromia | 40 | 7508      | Oromia |
| 22 | 7508       | Oromia | 41 | 208320    | Oromia |
| 23 | 236975     | Oromia | 42 | 236270    | Oromia |
| 24 | 236270     | Oromia | 43 | 208222    | Amhara |
| 25 | 208274     | Oromia | 44 | 203940    | Amhara |
| 26 | 208230     | Oromia | 45 | 208155    | Oromia |
| 27 | 208478     | Oromia | 46 | 208222    | Amhara |
| 28 | 208478     | Oromia | 47 | 208222    | Amhara |
| 29 | 208478     | Oromia | 48 | 208478    | Oromia |
| 30 | 6859       | Amhara | 49 | 208222    | Amhara |
| 31 | 208273     | Oromia | 50 | 208478    | Oromia |
| 32 | 236310     | Oromia | 51 | 208222    | Amhara |
| 33 | 7961       | Oromia | 52 | 208478    | Oromia |
| 34 | 214874     | Oromia | 53 | 208478    | Oromia |
| 35 | 208307     | Oromia | 54 | 208478    | Oromia |
| 36 | 7960       | Oromia | 55 | 208478    | Oromia |
| 37 | 204548     | Tigray | 56 | 208478    | Oromia |
| 38 | 203940     | Tigray | 57 | 208478    | Oromia |
| 39 | 236315     | Oromia | 58 | 208478    | Oromia |
| 40 | 8205       | Amhara | 59 | 208478    | Oromia |
| 41 | Felakit    | Oromia | 60 | 208478    | Oromia |

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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.

\[ Y_{ijl} = \mu + r_j + g_i + p(l_{(j)}) + \varepsilon_{ijl} \]

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

\( \mu \) = the general mean of trait Y

\( r_j \) = the effect of \( j^{th} \) replication

\( g_i \) = the effect of \( i^{th} \) genotypes

\( p(l_{(j)}) \) =block within replicate the effect

\( \varepsilon_{ijl} \) = 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 \( (PCV) = \frac{\sigma_p^2}{\bar{X}} \times 100 \)

Genotypic Coefficient of variation \( (GCV) = \frac{\sigma_g^2}{\bar{X}} \times 100 \)

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 \( (\sigma_g^2) \) to the phenotypic variance \( (\sigma_p^2) \) as described by [5]:

\[ (H^2) = \frac{\sigma_g^2}{\sigma_p^2} \times 100 \]

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

\[ GA = K \cdot \sigma_p \cdot H^2 \]

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].

\[ GAM = \frac{GA \cdot 100}{X} \]

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 \( r_{xy} = \frac{\text{Cov}_{xy}}{\sigma_x \cdot \sigma_y} \)

Genotypic correlation coefficient \( r_{xy} = \frac{\text{COV}_{xy}}{\sigma_x \cdot \sigma_y} \)

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

\[ t = \frac{r_{xy}}{SE(r_{xy})} \]

\[ SE(r_{xy}) = \sqrt{\frac{1-r_{xy}^2}{n-2}} \]

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

\[ t_{cal} = \frac{r_{xy}}{SE(r_{xy})} \]

\[ SE(r_{xy}) = \sqrt{\frac{1-r_{xy}^2}{2H^2 \cdot H^2}} \]

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].

\[ r_{xy} = p_y + \varepsilon_{xy} \cdot p_x \]
Where, $r_{ij}^2$ = mutual relation between independent trait (i) and dependent trait (j) as measured by genotypic correlation coefficient.

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

\[ \varepsilon_{ij} = \text{Residual factor,} \]

\[ e_{ij} = \text{Summation of components of the indirect effect of a given independent trait (i) on a given dependent trait (j) and vice versa for all other independent traits (k).} \]

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

\[ 1 = p^T R + \sum p_{ij} \cdot r_{ij} \]

Where, $p^T R$ = the residual factor,

\[ p_{ij} = \text{the direct effect of yield by } j^{th} \text{ trait, and} \]

\[ r_{ij} = \text{the correlation of yield with the } j^{th} \text{ trait.} \]

The contribution of the remaining unknown factor was measured as the residual factor ($P_2$), which is calculated as [12].

\[ P_2 = \sqrt{1 - e_{ij}^2 p_{ij}} \]

The magnitude of $P_2$ indicates how best the causal factors determine the variability of the dependent factor. If $P_2$ value is small for instance, nearly zero, and the yield is explained by the variability in the independent traits. However, higher $P_2$ the value indicates that other factors which have not been considered in the analysis to determine the variation in the yield.

Genetic divergence 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].

\[ D_{ij}^2 = (X_i - X_j)^T \text{cov}^{-1} (X_i - X_j) \]

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

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

\[ \text{cov}^{-1} = \text{the pooled within-group variance-covariance matrix.} \]

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. Scicca, 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.
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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 biomass and grain yield.

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**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       | 26663     | 30.7                | 278**             | 15.7         | 262**           | 3.2|
| PH       | 17486     | 64                  | 624**             | 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**           | 8.6|
| 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      | 8668      | 15.4                | 109**             | 5**          | 94**            | 5.7|
| GY       | 8210245   | 644650              | 4742321**         | 435267       | 4336769**       | 13.7|
| H%       | 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, SPS=spikelet per spike, BM = above-ground biomass, TKW=1000kernel weight, GY=grain yield, SE= Standard Error, and H=Harvest index

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

| Trait | Range   | Mean + SE | $\sigma_P^2$ | $\sigma_G^2$ |
|-------|---------|-----------|---------------|--------------|
| 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    | 8909-1518| 10923 ± 180| 3017744       | 2438945     |
| TKW   | 28-53.4 | 39 ± 0.62 | 34.7          | 29.7         |
| GY    | 1876-6476| 3360 ± 133| 1813614       | 1378347     |
| H%    | 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 H=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 | $\sigma_G^2$ | 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|
| H%    | 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
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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). Tillers per plant (0.689) followed by thousand kernels weight (0.643), days to maturity (0.565), plant height (0.02), tillers 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, days to maturity, 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. 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 6: Phenotypic correlation coefficients (*r*) 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 | 0.4** | 0.7** | 0.4* | 0.3 | 0.3 | 0.3** | 0.4** |
| **DM** | 0.5** | 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** | 0.4** | 0.3** | 0.5** | 0.3 | 0.3** | 0.4** |
| **SL** | 0.5** | 0.7** | 0.5** | 0.1 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 |
| **SPS** | 0.2 | 0.7** | 0.3** | 0.4** | 0.3 | 0.3** |
| **PH** | -0.3* | 0.3 | 0.2 | 0.3 | 0.2 | 0.3 |
| **SKW** | 0.1 | 0.6** | 0.5** |
| **BM** | -0.1 | -0.3 | 0.5** |
| **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), TPA = 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*) 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 | 0.3 | 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* | 0.9** | 0.8* | 0.9** | 0.8* |
| **TPUA** | 0.9** | 0.7 | 0.8* | 0.9** | 0.9** | 0.7 | 0.9** | 0.7 |
| **SL** | 0.9** | 0.8* | 0.9** | 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* |
| **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 at 5% probability level, respectively.
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 (D²)**

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 81 durum wheat genotypes. As per average D-square values of genotypes 236315 (354.72), 228768 (321.91), 214552 (283.81) and 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 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 tillers 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

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**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  |
|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|
| 0.08| 0.05| 0.02| 0.01 | -0.04| 0.03| 0.02| 0.02| 0.03| 0.03| 0.61**|
| 0.04| 0.05| 0.04| 0.02 | 0.04 | 0.04| 0.04| 0.08| 0.02| 0.03| 0.53**|
| 0.02| 0.06| 0.51 | 0.07 | 0.01 | 0.02| 0.03| 0.03| 0.04| 0.03| 0.75**|
| 0.07| 0.04| 0.74 | 0.02 | -0.07| 0.03| 0.04| 0.06| 0.06| 0.04| 0.35**|
| 0.04| 0.04| 0.05 | 0.03 | 0.04 | 0.07| 0.02| 0.04| 0.02| 0.03| 0.24* |
| 0.07| 0.06| 0.05 | 0.04 | 0.03 | 0.07| 0.02| 0.06| 0.05| 0.04| 0.24* |
| 0.04| 0.08| 0.06 | 0.02 | 0.04 | 0.05| 0.04| 0.05| 0.04| 0.05| 0.24**|
| 0.08| 0.04| 0.04 | 0.05 | 0.05 | 0.04| 0.03| 0.04| 0.05| 0.07| 0.51**|
| 0.03| 0.03| 0.05 | 0.02 | 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  |
|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|
| 0.02| 0.08| 0.75 | -0.09| 0.08| 0.68| 0.08| 0.08| 0.76| 0.08| 0.39* |
| 0.16| 0.59| 0.06 | 0.09 | 0.07| 0.08| 0.08| 0.09| 0.07| 0.47| 0.79**|
| 0.07| 0.08| 0.69 | -0.07| 0.07| 0.07| 0.05| -0.08| 0.06| 0.07| 0.93**|
| 0.14| 0.21| 0.06 | 0.08 | 0.76| 0.06| 0.09| 0.09| 0.08| 0.04| 0.65**|
| 0.07| 0.07| 0.03 | 0.06 | 0.06| 0.08| 0.09| 0.07| 0.58| 0.67| 0.08| 0.44| 0.58**|
| 0.06| 0.03| 0.09 | 0.08 | 0.09| 0.07| 0.05| -0.05| 0.07| 0.76| 0.08| 0.46|
| 0.05| 0.18| 0.09 | 0.26| 0.08| 0.07| -0.05| -0.07| 0.76| 0.08| 0.87**|
| 0.07| 0.07| 0.09 | 0.13| 0.09| 0.04| 0.09| 0.64| 0.74| 0.74| 0.87**|
| 0.08| 0.08| 0.25 | 0.05| 0.07| 0.08| 0.13| 0.04| 0.09| 0.32| 0.52**|
| 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 = 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 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   | 163.83              |
| 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   | 126.94              | 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       | 231597   | 238.13              |
| 17       | 208257   | 255.12              | 58       | 231599   | 123.64              |
| 18       | 208155   | 129.93              | 59       | 238555   | 213.65              |
| 19       | 208325   | 231.67              | 60       | 208198   | 172.73              |
| 20       | 231599   | 196.87              | 61       | 238165   | 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       | 7966     | 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 | 287.32 |
| III| 143.76| 215.14 | 217.81 | 254.75 |        |        |
| IV | 97.94 | 206.93 | 276.86 |        |        |        |
| V  | 47.83 | 286.97 |        |        |        |        |
| VI | 49.12 |        |        |        |        |        |

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 | 8 | 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 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).
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

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