

# Variability and Traits Association Study of Durum Wheat Genotypes

## ABSTRACT

Twenty advanced line durum genotypes were tested to assess the presence of significant variability for grain yield and yield attributing traits by using randomized complete block design with three replications for two years at research farm of Agriculture and Forestry University, Chitwan, Nepal. Mean sum of squares revealed high significant differences among durum wheat genotypes for all traits investigated, suggesting the possibility of improving durum wheat for these traits. High heritability associated with high genetic gain was found on some traits namely; flag leaf area, 1000-kernel weight and days to heading indicates the presence of additive gene action in controlling these traits. Grain yield, harvest index, test weight, days to maturity, spike length and peduncle length showed low genetic gain associated with high heritability indicates the presence of non-additive gene action in controlling related traits. Grain filling rate, harvest index, grain number per spike, test weight, plant height and peduncle length were found significantly correlated with grain yield at both genotypic and phenotypic levels. Among these traits, grain filling rate, grain number per spike and test weight, had the maximum direct positive effect on grain yield, which can be used as effective traits for selection of superior genotypes.

## Keywords

(*Triticum turgidum* ssp. *durum* Desf.), heritability, genotypic-phenotypic correlation, path analysis, yield, genotype  $\times$  year interaction

## 1. INTRODUCTION

Durum (*Triticum turgidum* ssp. *durum* Desf), also commonly known as pasta or macaroni wheat, is originated and diversified from Mediterranean basin. It is a monocotyledonous tetraploid ( $2n = 4x=28$ ) plant of Poaceae family of *Triticeae* tribe and belongs to the genus *Triticum*. It is an exotic crop for Nepal. Due to food habit change and urbanization, demand of durum product and consumption in Nepal is soaring in alarming rate [1]. Wheat is the third most cultivated crop in Nepal. Almost all portion of wheat cultivation is represented by bread wheat. There is no production record of durum wheat at commercial scale till the date in Nepal due to lack of proper knowledge on it and suitable germplasm to be grown [2]. In 2007/08, Agriculture Botany Division (ABD) of Nepal Agricultural Research Council (NARC) has conducted feasibility and adaptive screening trial at Regional Agriculture and Research Station (RARS), Nepalgunj, Banke [3, 4]. Thereupon, Regional Agriculture Research Station-NARC, is carrying several "Durum Wheat Advanced Varietal Trial" for selection of genotypes in mid-western region of Nepal. In addition, many stakeholders are interested in durum grain production, processing and making end-use products, which are in fact important factors deciding success of this durum-based industry.

It is believed that durum performs better even under stress condition [5, 6]. In South-western part of Nepal, where low rainfall occurs, drought is the major problem in winter. Durum wheat can exploit the existing environment successfully (D. B. Thapa, personal communication, November 22, 2017) better than bread wheat. Durum is becoming the promising crop and an increasingly viable option to cultivate in near future. For better crop improvement, grain yield becomes the priority in breeding programs. Grain yield is the quantitative trait that is governed by polygenes. It is the function of several supporting other quantitative traits. Variation within the quantitative traits are mainly due to their complex inheritance and environmental effects. Thus, understanding the genetic variability and gene interaction of yield and yield associated traits are essential [5] which determines the success of crop improvement program. Only the characters governed by genetic constituents are transferred to the progenies. Thus, for successful breeding plan, study of heritability and genetic association of characters has paramount importance [5]. Genotypic correlation study provides the direction and

strength of association between the traits beyond the environmental effect. Direct selection of genotypes from few most seemingly important traits sometimes may not give effective results. Indirect selection for grain yield may give better result if the correlation between a yield component and yield is strong and the negative interrelationships of yield components are negligible. High correlated and heritable traits with yield can be selected in early generations. As correlation is affected by different genetic and environmental factors, sometimes correlation value may mislead research results due to over or under estimation of association. Thus, it is good to study the direct and indirect influence of traits to yield which can be studied through a standardized partial regression coefficient called path coefficient [7-9]. Therefore, the objective of the present study was to determine genetic variability, heritability, genetic association of traits and direct-indirect effects of important traits of yield components to yield in subtropical zone of Nepal.

## 2. MATERIALS AND METHODS

### 2.1 Materials Studied

Twenty advanced lines of durum wheat genotypes used as treatments (Table 1) were collected from RARS, Nepalgunj, Nepal which were originated from International Maize and Wheat Improvement Center (CIMMYT), Mexico.

**Table 1. Advanced line durum genotypes used as plant materials in this study**

| Treatment No | Name of genotypes |
|--------------|-------------------|
| 1            | ALTAR 84          |
| 2            | YAVAROS 79        |
| 3            | DWK26             |
| 4            | DWK38             |
| 5            | DWK46             |
| 6            | DWK72             |
| 7            | DWK82             |
| 8            | DWK94             |
| 9            | DWK102            |
| 10           | DWK109            |
| 11           | DWK101            |
| 12           | DWK110            |
| 13           | DWK126            |
| 14           | DWK116            |
| 15           | DWK117            |
| 16           | DWK121            |
| 17           | DWK122            |
| 18           | DWK125            |
| 19           | DWK124            |
| 20           | DWK118            |

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## 55 2.2 Description of experimental area, design and practices

56 The current research was carried out in research farm of Faculty of Agriculture, Agriculture and  
57 Forestry University, Chitwan, Nepal in 2015 and 2016. Geographic location is 27° 38' 50.92" N, 84° 20'  
58 49.43" E; 27° 38' 51.35" N, 84° 27' 51.62" E; 27° 38' 50.54" N, 84° 20' 51.99" E and 27° 38' 50.01" N,  
59 84° 20' 49.85". The elevation is 228 meters above sea level. The area is characterized as subtropical  
60 climate with unimodal rainfall pattern. The experimental design was randomized complete block  
61 (RCB) design with three replications and twenty treatments (20 durum genotypes). The unit plot was 4  
62 m<sup>2</sup> in 2015 and 6 m<sup>2</sup> in 2016 in area with 6 and 8 rows respectively at 25 cm spacing. The twenty  
63 genotypes used as treatments were grown under irrigated condition at normal sowing period in  
64 November. 120 kg/ha seed rate was used in the experiment. The dose of chemical fertilizer applied  
65 was 120:60:60 N:P:K kg/ha. Supplement irrigation was given at crown root initiation stage, anthesis  
66 stage and milking stage. All other agronomic management practices were done as recommended for  
67 wheat production in Nepal.

## 68 2.3 The traits recorded

69 The data were collected from each plot on 15 quantitative characters, namely grain yield (GYLD),  
70 biological yield (BYLD) flag leaf area (FLA), grain number per spike (GNPS), flag leaf duration (FLD),  
71 spike length (SPKL), plant height (HT), peduncle length (PDNL), 1000-kernel weight (TKW), test  
72 weight (TW), days to heading (DTH), days to maturity (DTM), harvest index (HI), grain filling rate  
73 (GFR) and chlorophyll content (SPAD).

74 Calculation of grain yield, 1000-kernel weight and test weight were done in 12% grain moisture basis.  
75 Biological yield was recorded by weighing the above-ground mass of the whole plant including spikes  
76 after drying in field for three days. Randomly selected ten plants were tagged for the observation of  
77 grain number per spike, plant height and peduncle length. Flag leaf area of plant was measured at the  
78 time of dough stage. It was measured by using Easy leaf area software that uses digital images  
79 scanned by camera [10]. Peduncle length was taken from the point of flag leaf blade extrusion to base  
80 of spike. Plant height was taken from the ground level to the top of spike without awn. Days to  
81 heading were recorded when 50% of the plants in a plot had spike emerged from boot. Similarly, for  
82 days to maturity, the date was recorded when more than 50% of peduncle color were changed to  
83 yellow straw color. Harvest index was estimated by dividing the grain yield of the plot by biological  
84 yield of that plot. Grain filling rate was calculated by dividing the grain weight with grain filling period.  
85 SPAD reading was taken at booting stage with a hand-held chlorophyll meter called Soil Plant  
86 Analysis and Development (SPAD) meter (model SPAD-502; Minolta Corp., Ramsey, N.J.).

## 87 2.4 Weather conditions

88 The field received 46.9 mm and 118 mm rainfall in 2015 and 2016 during the period of the  
89 experiment, respectively. Maximum temperature was recorded in April (37.36°C in 2015 and 33.3°C in  
90 2016) and minimum in January (8.77°C in 2015 and 3.6°C in 2016). Soil was sandy loam with pH  
91 6.11 and 5.73 in 2015 and 2016 respectively.

## 92 2.5 Statistical Procedure

93 All the data were collected and tabulated in Microsoft Excel. Analysis of variance was calculated by  
94 using R-studio software. Analysis of variance (Table 2) was used as suggested by Toker [11] and  
95 Rasmusson and Lambert [12].

96

97 **Table 2 Form of variance analysis for RCB design with genotype × year interaction**

| Source      | Degree of freedom | Mean square | F- ratio | p-value |
|-------------|-------------------|-------------|----------|---------|
| Replication | y(r-1)            |             |          |         |

|                 |             |       |           |
|-----------------|-------------|-------|-----------|
| Year            | (y-1)       |       |           |
| Genotype        | (g-1)       | $M_3$ | $M_3/M_1$ |
| Genotype × year | (g-1)(y-1)  | $M_2$ | $M_2/M_1$ |
| Error           | y(g-1)(r-1) | $M_1$ |           |

*y, r and g are the number of year, replications and genotypes.  $M_1$ ,  $M_2$ , and  $M_3$  are the observed value of various mean squares.*

### 2.5.1 Genetic variability and heritability

Phenotypic and genotypic variance were calculated as Toker [11] (Table 3):

**Table 3. Estimation of variance components and method of determination**

| Variance        | Components | Method of determination |
|-----------------|------------|-------------------------|
| Genotype        | Vg         | $(M_3 - M_2)/y$         |
| Genotype × year | Vgy        | $(M_2 - M_1)/r$         |
| Error           | Ve         | $M_1$                   |

*Vg, Vgy and Ve are components of variance for genotypes, genotype × year and error respectively*

Phenotypic variances ( $V_p$ ) was derived as follows:

$$V_p = V_g + V_{gy}/y + V_e/(yr) \quad (1)$$

where y, g and yr are number of year, genotype and replication.

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Mean value of the trait}} * 100 \quad (2)$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Mean value of the trait}} * 100 \quad (3)$$

$$\text{Heritability (H}^2\text{)} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} * 100 \quad [13] \quad (4)$$

$$\text{Genetic advance as percentage of mean (GA\%)} = K * H^2 * \frac{\sqrt{\text{Phenotypic variance}}}{\text{Mean value of the trait}} * 100 \quad [13] \quad (5)$$

Where,

K = selection intensity (5% = 2.06)

$H^2$  = broad sense heritability

### 2.5.2 Phenotypic and Genotypic correlation study

Phenotypic and Genotypic correlation study were carried out as described by Sing and El-Bizri [14]

$$r_g = \frac{\text{Cov}_{g12}}{\sqrt{\sigma_g^2 1 * \sigma_g^2 2}} \quad (6)$$

$r_g$  = Genotypic correlation coefficient

$\text{Cov}_{g12}$  = Genotypic covariance of traits 1 & 2

$\sigma_g^2 1$  = Genotypic variance of trait 1.

$\sigma_g^2 2$  = Genotypic variance of traits 2.

$$r_p = \frac{\text{Cov}_{p12}}{\sqrt{\sigma_p^2 1 * \sigma_p^2 2}} \quad (7)$$

$r_p$  = Phenotypic correlation coefficient

$\text{Cov}_{p12}$  = Phenotypic covariance of traits 1 & 2

$\sigma_p^2 1$  = Phenotypic variance of trait 1.

$\sigma_p^2 2$  = Phenotypic variance of traits 2.

The significance of correlation of both phenotypic and genotypic was tested with the formula adopted by Sharma [15]

$$t = \frac{r}{\text{SE}(r)} \quad (8)$$

$$\text{where, SE}(r) = \frac{1-r^2}{\sqrt{n-2}} \quad (9)$$

where,  $r$  = correlation coefficient between the variables

$n$  = number of genotypes

Then calculated 't' – value was compared with standard t- value table at  $n-2$  degrees of freedom and  $\alpha$  levels of probability (where  $\alpha$  is 0.05 and 0.01).

### 2.5.3 Path coefficient analysis

Path coefficient analysis was carried out with the help of Microsoft Excel using genotypic correlation of traits [16]. Sixteen traits were entered as predictor for yield in path analysis that estimated their direct and indirect effect on dependent variable yield.

$$r_{10} = P_{10} + P_{20}r_{12} + P_{30}r_{13} + \dots + P_{01}r_{11} \quad (10)$$

$$r_{20} = P_{10}r_{21} + P_{20} + P_{30}r_{23} + \dots + P_{01}r_{21} \quad (11)$$

$$\vdots \quad \vdots \quad \vdots \quad \vdots$$

$$\vdots \quad \vdots \quad \vdots \quad \vdots$$

$$r_{i0} = P_{10}r_{i1} + P_{20}r_{i2} + P_{30}r_{i3} + \dots + P_{i0} \quad (12)$$

where,

$r_{10}, r_{20}, \dots, r_{i0}$  = genotypic correlation of independent variables (1, 2, .... i) with dependent variable (0)

$r_{11}, r_{12}, \dots, r_{ii}$  = genotypic correlation between independent variables (1-1, 1-2, .....i-i )

$P_{10}, P_{20}, \dots, P_{i0}$  = components of direct effects of the independent variable (0) on dependent variables (1, 2, .... i)

Residual was calculated as,

$$R = 1 - (P_{10}^2 + P_{20}^2 + \dots + P_{i0}^2) - 2[P_{10} * P_{20} * r_{12} + P_{10} * P_{30} * r_{13} + \dots + P_{(i-1)0} * P_{i0} * r_{(i-1)i}] \quad (13)$$

### 3. RESULTS

Significance of variance analysis of genotypes and genotype  $\times$  year interactions are presented in Tables 4 and 5. All the traits revealed high significant difference among the genotypes in the mean value. Variances due to genotype  $\times$  year interaction were found non-significant for grain yield, biological yield, harvest index, flag leaf area, test weight, spike length, plant height and peduncle length, and value of variance due to genotype  $\times$  year in these traits were found very small compared to genotypic variance (Table 6).

**Table 4. Analysis of variance for studied traits of durum genotypes**

|                                     | Traits |       |       |       |       |       |       |       |
|-------------------------------------|--------|-------|-------|-------|-------|-------|-------|-------|
|                                     | GYLD   | BYLD  | GFR   | HI    | FLA   | GNPS  | TKW   | TW    |
| Genotype significance (P value)     | 0.000  | 0.003 | 0.016 | 0.000 | 0.000 | 0.000 | 0.001 | 0.001 |
| G $\times$ Y significance (P value) | 0.322  | 0.115 | 0.021 | 0.061 | 1.000 | 0.002 | 0.000 | 1.000 |
| CV%                                 | 24.25  | 13.48 | 24.34 | 22.14 | 13.15 | 22.78 | 7.44  | 5.19  |

*G = genotype, Y= year, CV= coefficient of variation, GYLD= grain yield, BYLD= biological yield, GFR= grain filling rate, HI= harvest index, FLA= flag leaf area, GNPS= grain number per spike, TKW= thousand kernels weight, TW= test weight*

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**Table 5. Analysis of variance for studied traits of durum genotypes**

|                                     | Traits |       |       |       |       |       |       |
|-------------------------------------|--------|-------|-------|-------|-------|-------|-------|
|                                     | DTH    | DTM   | FLD   | SPAD  | SPKL  | HT    | PDNL  |
| Genotype significance (P value)     | 0.000  | 0.000 | 0.003 | 0.000 | 0.000 | 0.000 | 0.000 |
| G $\times$ Y significance (P value) | 0.000  | 0.000 | 0.015 | 0.050 | 0.105 | 0.395 | 0.424 |
| CV%                                 | 2.11   | 1.52  | 5.57  | 6.82  | 4.41  | 5.00  | 5.12  |

*G = genotype, Y= year, CV= coefficient of variation, DTH= days to heading, DTM= days to maturity, FLD= flag leaf duration, SPAD= chlorophyll content of flag leaf, SPKL= spike length, HT= plant height, PDNL= peduncle length*

Coefficient of variation was found high in grain filling rate (24.34%), grain yield (24.25%), grain number per spike (22.78%) and harvest index (22.14%). Similar pattern was seen in genotypic and phenotypic coefficient of variation. Phenotypic coefficient of variations were found higher than genotypic coefficient of variations in all traits with narrow difference. Highest genotypic and phenotypic variance was obtained for grain yield that was followed by harvest index. Lowest genotypic and phenotypic variance was obtained for days to maturity. All the investigated traits showed more than 50% of variation because of genetic variation due to which heritability were found high in all traits. Highest heritability was obtained for flag leaf area (0.93) which was followed by peduncle length (0.92), grain yield (0.90), days to heading (0.87), harvest index (0.86), days to maturity (0.85), spike length (0.82) and 1000 kernel weight (0.81). Grain yield, harvest index and flag leaf area showed high heritability with high genetic advance. Similarly, grain number per spike, grain filling rate, 1000 kernels weight and biological yield had moderate heritability associated with high genetic advance. On the other hand, test weight, days to heading, days to maturity, spike length,

174 peduncle length, chlorophyll content, flag leaf duration and plant height revealed the high heritability  
175 with low genetic advance.

176

177 **Table 6 Estimates of genetic parameters for 15 traits of durum genotypes**

| Traits | Adj. Mean | Range           | Vg    | Vp    | Vgy   | GCV   | PCV   | H    | GA%   |
|--------|-----------|-----------------|-------|-------|-------|-------|-------|------|-------|
| GYLD   | 1.56      | 0.13 - 3.33     | 0.29  | 0.33  | 0.02  | 34.85 | 36.73 | 0.90 | 68.14 |
| BYLD   | 4.48      | 1.50 - 7.08     | 0.32  | 0.42  | 0.09  | 12.68 | 14.52 | 0.76 | 22.79 |
| GFR    | 0.03      | 0.00 - 0.06     | 0.00  | 0.00  | 0.00  | 21.53 | 26.09 | 0.68 | 36.59 |
| HI     | 0.27      | 0.03 - 0.57     | 0.01  | 0.01  | 0.00  | 30.65 | 33.08 | 0.86 | 58.50 |
| FLA    | 29.70     | 16.81 - 57.24   | 28.37 | 30.46 | 0.00  | 17.93 | 18.58 | 0.93 | 35.65 |
| GNPS   | 27.15     | 3.00 - 51.10    | 43.56 | 60.00 | 20.12 | 24.30 | 28.53 | 0.73 | 42.66 |
| TKW    | 44.51     | 26.74 - 60.84   | 25.23 | 31.32 | 8.68  | 11.28 | 12.57 | 0.81 | 20.87 |
| TW     | 76.26     | 53.50 - 85.30   | 9.51  | 11.91 | 0.00  | 4.04  | 4.53  | 0.80 | 7.44  |
| DTH    | 78.41     | 62.00 - 90.00   | 22.67 | 26.18 | 6.17  | 6.07  | 6.53  | 0.87 | 11.64 |
| DTM    | 123.40    | 109.00 - 133.00 | 13.32 | 15.67 | 3.59  | 2.96  | 3.21  | 0.85 | 5.62  |
| FLD    | 48.48     | 31.00 - 69.00   | 8.37  | 11.12 | 3.08  | 5.97  | 6.88  | 0.75 | 10.66 |
| SPAD   | 44.52     | 32.08 - 54.90   | 8.60  | 11.28 | 2.45  | 6.59  | 7.54  | 0.76 | 11.85 |
| SPKL   | 6.47      | 5.35 - 7.81     | 0.11  | 0.13  | 0.02  | 5.11  | 5.63  | 0.82 | 9.53  |
| HT     | 73.88     | 62.96 - 87.22   | 6.71  | 9.14  | 0.61  | 3.51  | 4.09  | 0.73 | 6.19  |
| PDNL   | 18.67     | 14.96 - 23.08   | 2.18  | 2.39  | 0.10  | 7.92  | 8.27  | 0.92 | 15.60 |

*Adj= adjusted, Vg= genotypic variance, Vp= phenotypic variance, Vgy= genotype × year variance, GCV= genotypic coefficient of variation, PCV= phenotypic coefficient of variation, H= broad sense heritability, GA%= genetic advance as % of mean*

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179 The results of genotypic and phenotypic correlation among studied traits are shown in Table 7.  
180 Among fourteen studied yield components, nine traits showed positive significant genotypic and  
181 seven traits showed phenotypic correlation with grain yield. Harvest index, grain filling rate and grain  
182 number per spike showed highest genotypic correlation with grain yield that were followed by test  
183 weight, biological yield, chlorophyll content of flag leaf, plant height, flag leaf area and peduncle  
184 length. Flag leaf area and chlorophyll content of flag leaf though had significant correlation with grain  
185 yield in genotypic level had non-significant association with yield in phenotypic level. Days to maturity  
186 and flag leaf duration had positive and significant correlation with biological yield but non-significant  
187 correlation with grain yield. Similarly, grain filling rate and grain number per spike were found highly  
188 correlated with chlorophyll content of the flag leaf, plant height and flag leaf area at both levels.

189

190 **Table 7 Genotypic (above the diagonal) and phenotypic (below the diagonal) correlation coefficients among grain yield and yield attributing traits**  
191 **of durum wheat**

| Traits | GYLD     | BYLD     | GFR      | HI       | FLA      | GNPS     | TKW      | TW       | DTH      | DTM      | FLD      | SPAD     | SPKL     | HT       | PDNL     |
|--------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| GYLD   | <b>1</b> | 0.63**   | 0.94**   | 1.00**   | 0.50*    | 0.81**   | -0.06    | 0.68**   | -0.03    | 0.04     | 0.14     | 0.53*    | 0.23     | 0.51*    | 0.45*    |
| BYLD   | 0.51*    | <b>1</b> | 0.82**   | 0.42     | 0.76**   | 0.46*    | 0.43     | 0.38     | 0.60**   | 0.65**   | 0.82**   | 0.66**   | 0.63**   | 0.57**   | 0.20     |
| GFR    | 0.84**   | 0.55*    | <b>1</b> | 0.91**   | 0.78**   | 0.95**   | 0.02     | 0.47*    | 0.00     | 0.05     | 0.14     | 0.91**   | 0.54*    | 0.77**   | 0.59**   |
| HI     | 0.94**   | 0.26     | 0.79**   | <b>1</b> | 0.40     | 0.90**   | -0.17    | 0.63**   | -0.30    | -0.16    | -0.04    | 0.50*    | 0.12     | 0.61**   | 0.55*    |
| FLA    | 0.43     | 0.59**   | 0.60**   | 0.32     | <b>1</b> | 0.66**   | -0.17    | -0.01    | 0.55*    | 0.31     | 0.15     | 0.49*    | 0.71**   | 0.88**   | 0.32     |
| GNPS   | 0.80**   | 0.38     | 0.92**   | 0.78**   | 0.54*    | <b>1</b> | -0.40    | 0.52*    | 0.06     | 0.01     | -0.01    | 0.85**   | 0.27     | 0.66**   | 0.49*    |
| TKW    | -0.06    | 0.36     | -0.05    | -0.12    | -0.13    | -0.39    | <b>1</b> | -0.20    | -0.22    | 0.17     | 0.60**   | -0.03    | 0.29     | 0.15     | 0.18     |
| TW     | 0.56**   | 0.20     | 0.39     | 0.57**   | 0.06     | 0.43     | -0.08    | <b>1</b> | -0.37    | -0.16    | -0.08    | 0.19     | 0.01     | 0.33     | 0.39     |
| DTH    | -0.05    | 0.41     | 0.00     | -0.27    | 0.46*    | 0.05     | -0.27    | -0.29    | <b>1</b> | 0.90**   | 0.15     | 0.18     | 0.46*    | 0.21     | -0.41    |
| DTM    | 0.03     | 0.59**   | 0.00     | -0.22    | 0.30     | 0.01     | 0.10     | -0.16    | 0.81**   | <b>1</b> | 0.72**   | 0.18     | 0.33     | 0.02     | -0.30    |
| FLD    | 0.16     | 0.69**   | 0.18     | 0.03     | 0.13     | 0.04     | 0.60**   | -0.04    | 0.05     | 0.50*    | <b>1</b> | 0.57**   | 0.25     | 0.25     | 0.19     |
| SPAD   | 0.38     | 0.50*    | 0.61**   | 0.31     | 0.42     | 0.61**   | -0.11    | 0.10     | 0.18     | 0.26     | 0.32     | <b>1</b> | 0.54*    | 0.51*    | 0.63**   |
| SPKL   | 0.22     | 0.54*    | 0.42     | 0.04     | 0.64**   | 0.31     | 0.11     | -0.03    | 0.43     | 0.35     | 0.16     | 0.43     | <b>1</b> | 0.70**   | 0.18     |
| HT     | 0.49*    | 0.49*    | 0.60**   | 0.41     | 0.74**   | 0.54*    | 0.04     | 0.22     | 0.22     | 0.17     | 0.14     | 0.50*    | 0.71**   | <b>1</b> | 0.60**   |
| PDNL   | 0.47*    | 0.22     | 0.45*    | 0.52*    | 0.28     | 0.36     | 0.22     | 0.34     | -0.40    | -0.28    | 0.15     | 0.44     | 0.15     | 0.46*    | <b>1</b> |

\* Significant at  $P \leq 0.05$ ; \*\* significant  $P \leq 0.01$

193 The direct and indirect effect of the yield component on grain yield is presented in Table 8. The  
194 residual effect was found 0.0117. In the results of path coefficient analysis, days to maturity (0.84)  
195 followed by flag leaf area (0.58), grain filling rate (0.53) and grain number per spike (0.46) had highest  
196 direct effect on grain yield. Among which, days to maturity had non-significant correlation with grain  
197 yield. The maximum positive direct effect of days to maturity on grain yield was counter balanced by  
198 the indirect effects via days to heading and flag leaf duration rendering weak genotypic correlation  
199 with grain yield. The direct effect of grain filling rate was not found collaborated with the genotypic  
200 correlation value. The contribution of indirect effect via flag leaf area and grain number per spike to  
201 grain filling rate caused the high genotypic correlation of it with grain yield. Similarly, positive and  
202 strong genotypic correlation of grain number per spike with grain yield was found due to positive  
203 indirect effects of grain filling rate and flag leaf area. On the other hand, days to heading (-0.75), plant  
204 height (-0.52), flag leaf duration (-0.37) and chlorophyll content of flag leaf (-0.33) showed the  
205 considerable negative direct effect on grain yield. Chlorophyll content of flag leaf and plant height had  
206 significant positive genotypic correlation with grain yield but their direct effect on grain yield revealed  
207 considerable negative effect. It was found that grain number per spike, grain filling rate and flag leaf  
208 area had contributed significant indirect effect to plant height which resulted in positive significant  
209 genotypic correlation with grain yield. A similar condition was found in case of chlorophyll content of  
210 flag leaf trait. The indirect effects of days to maturity and flag leaf area counter balanced the negative  
211 direct effect of days to heading making its genotypic correlation coefficient insignificant. Harvest index  
212 and biological yield, having the high positive genotypic correlation, showed the lowest positive direct  
213 effect in path analysis. The significant and positive genotypic correlation of harvest index and  
214 biological yield with grain yield was found due to the positive indirect effects via grain filling rate, flag  
215 leaf area and grain number per spike

216 **Table 8 Estimates of genotypic path coefficient (direct effect - bolded diagonal and indirect effect- off diagonal) of different characters on grain**  
217 **yield of durum wheat**

| Traits                   | BYLD        | GFR         | HI          | FLA         | GNPS        | TKW         | TW          | DTH          | DTM         | FLD          | SPAD         | SPKL         | HT           | PDNL        |
|--------------------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|--------------|-------------|--------------|--------------|--------------|--------------|-------------|
| BYLD                     | <b>0.08</b> | 0.43        | 0.02        | 0.44        | 0.21        | 0.08        | 0.09        | -0.45        | 0.55        | -0.30        | -0.22        | 0.00         | -0.30        | 0.02        |
| GFR                      | 0.07        | <b>0.53</b> | 0.03        | 0.45        | 0.44        | 0.00        | 0.11        | 0.00         | 0.04        | -0.05        | -0.30        | 0.00         | -0.40        | 0.06        |
| HI                       | 0.03        | 0.48        | <b>0.04</b> | 0.23        | 0.41        | -0.03       | 0.15        | 0.22         | -0.13       | 0.01         | -0.17        | 0.00         | -0.32        | 0.06        |
| FLA                      | 0.06        | 0.41        | 0.02        | <b>0.58</b> | 0.30        | -0.03       | 0.00        | -0.41        | 0.26        | -0.06        | -0.16        | 0.00         | -0.46        | 0.03        |
| GNPS                     | 0.04        | 0.50        | 0.03        | 0.38        | <b>0.46</b> | -0.07       | 0.13        | -0.05        | 0.01        | 0.00         | -0.28        | 0.00         | -0.35        | 0.05        |
| TKW                      | 0.03        | 0.01        | -0.01       | -0.10       | -0.18       | <b>0.19</b> | -0.05       | 0.16         | 0.14        | -0.22        | 0.01         | 0.00         | -0.08        | 0.02        |
| TW                       | 0.03        | 0.25        | 0.02        | -0.01       | 0.24        | -0.04       | <b>0.24</b> | 0.27         | -0.14       | 0.03         | -0.06        | 0.00         | -0.17        | 0.04        |
| DTH                      | 0.05        | 0.00        | -0.01       | 0.32        | 0.03        | -0.04       | -0.09       | <b>-0.75</b> | 0.75        | -0.06        | -0.06        | 0.00         | -0.11        | -0.05       |
| DTM                      | 0.05        | 0.02        | -0.01       | 0.18        | 0.01        | 0.03        | -0.04       | -0.67        | <b>0.84</b> | -0.26        | -0.06        | 0.00         | -0.01        | -0.03       |
| FLD                      | 0.07        | 0.07        | 0.00        | 0.09        | 0.00        | 0.11        | -0.02       | -0.11        | 0.60        | <b>-0.37</b> | -0.19        | 0.00         | -0.13        | 0.02        |
| SPAD                     | 0.05        | 0.48        | 0.02        | 0.28        | 0.39        | -0.01       | 0.05        | -0.13        | 0.15        | -0.21        | <b>-0.33</b> | 0.00         | -0.27        | 0.06        |
| SPKL                     | 0.05        | 0.29        | 0.00        | 0.41        | 0.13        | 0.06        | 0.00        | -0.34        | 0.27        | -0.09        | -0.18        | <b>-0.01</b> | -0.36        | 0.02        |
| HT                       | 0.05        | 0.41        | 0.02        | 0.51        | 0.30        | 0.03        | 0.08        | -0.16        | 0.01        | -0.09        | -0.17        | 0.00         | <b>-0.52</b> | 0.06        |
| PDNL                     | 0.02        | 0.31        | 0.02        | 0.19        | 0.22        | 0.04        | 0.10        | 0.32         | -0.27       | -0.06        | -0.20        | 0.00         | -0.31        | <b>0.11</b> |
| <i>Residual: 0.01167</i> |             |             |             |             |             |             |             |              |             |              |              |              |              |             |

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## 4. DISCUSSION

For the crop improvement, it is desired to have high variation in the crop resources that enables plant breeders to create novel plant gene combinations which help to select more suited crop varieties to the needs of diverse agricultural systems [17]. All the traits, in this study, revealed large variation. Variation due to genotype was found very high as compare to variance due to genotype  $\times$  year effect in most of the traits. For adaptability and stability of traits over a period of time, assessment of genotypic and genotype  $\times$  year variance is suitable [18]. In present investigation, grain yield, biological yield, harvest index, flag leaf area, test weight, spike length, plant height and peduncle length revealed significantly no differences in genotype  $\times$  year interaction and very low variation due to it. This implies that, these traits were consistence in performance for both year which is of great importance in breeding program. For other traits, it seems that further study is required to ascertain the stability of performances.

The coefficient of phenotypic variation was found slightly higher than coefficient of genotypic variation. The narrow difference between coefficient of genotypic and phenotypic variation was also found in other studies [18-20]. This indicates the less influence of environmental effect in expression of phenotype of traits. This means that these traits have immense inherent variability that remains unaltered by environmental conditions, which is of great value for exploitation in selection and hybridization programs [21]. Although these coefficients of variation revealed the extent of genetic and phenotypic variability present in the traits, these do not provide the full scope to assess the variation that is heritable. Thus, selection efficiency is related to magnitude of heritability and genetic advance [22]. In this study, high heritability ( $>80\%$ ) were obtained for grain yield, harvest index, 1000 kernels weight, test weight, flag leaf area, days to heading, days to maturity, spike length and peduncle length. Abinasa, Ayana [19] also found high heritability in days to heading, test weight and thousand kernels weight. Başçıftçı, Kınacı [18] found high heritability in spike length. Gashaw, Mohammed [23] also obtained the similar results for spike length and 1000 kernels weight. High broad sense heritability gives an idea of total variation ascribable to genotypic effects, which are exploitable portion of variation. This means that selection of these characters would be more effective as compare to others.

However, heritability along doesn't indicate high genetic gain. Knowledge of heritability together with genetic advance is necessary to consider the selection of traits [18]. High heritability associated with high genetic advance of traits indicates the influence of additive gene [24]. Grain yield, harvest index, flag leaf area, grain number per spike, grain filling rate, 1000 kernels weight and biological yield had considerably high heritability coupled with high genetic advance. Transgressive segregants may be looked for these traits while selecting for high yielding genotypes in early segregating generations. On the other hand, traits with high heritability and low genetic advance indicate the effect of dominance and epistatic gene action [18]. Therefore, for test weight, days to heading, days to maturity, spike length, peduncle length, chlorophyll content, flag leaf duration and plant height early selection is not judicious. Similar results for grain number per spike and spike length was found in study of Başçıftçı, Kınacı [18]. Gupta and Verma [24] also reported the similar results for plant height, grain number per spike and 1000 kernel weight.

Pleiotropic gene actions, linkage disequilibrium and epistatic effect of different genes result in the association of different traits in plants which are genetic causes of correlation [25]. Similarly, environmental effect also sometimes affects the traits simultaneously in the same or different directions beyond the effect of genetic constituents. Correlations among traits are, therefore, observed due to genetic or/and environmental causes. Study of genetic and environmental effect on traits association is necessary. The correlation due to combine effect is known as phenotypic correlation [25]. This is true that, effect of environment in trait association is non-heritable. Therefore, estimation of degree of phenotypic and genotypic correlation of grain yield with yield attributing traits is very important to exploit the available genetic variability through selection [26]. In this study, harvest index, grain filling rate and grain number per spike were found highly correlated with grain yield. Abinasa, Ayana [19] also found similar results for harvest index and grain number per spike. Similarly, finding of Gashaw, Mohammed [27] was also corroborated with this study of correlation in plant height, grain number per spike and biological yield. Wolde, Eticha [28] in their study found non-significant correlation at both levels for days to maturity and days to heading and significant positive correlation at both level for harvest index, grain number per spike and biological yield in durum which are in accordance with the findings of this study. Azimi, Marker [29] in bread wheat found positive and significant correlation of peduncle length with grain yield and Gelalcha and Hanchinal [30] in bread

wheat found non-significant but positive correlation at both levels which also supported the finding of this study. Days to maturity and flag leaf duration had positive and significant correlation with biological yield but the non-significant correlation with grain yield. This indicates that late maturity genotypes with long stay green at normal condition only increases the biomass of plant but not to the grain yield. Similarly, grain filling rate and grain number per spike were found highly correlated with chlorophyll content of the flag leaf, plant height and flag leaf area at both levels. It was surprising that 1000 kernels weight was found non-significantly correlated with grain yield in durum which was also found in some other studies [19, 31, 32]. This could be because of source-sink balance. The crops might have passed through source limited condition at late grain filling period due to which spike with low grain number might have high grain weight and vice-versa. To ascertain the causes further study is required.

The path coefficient analysis provides information about the contribution of various yield components to grain yield in the genotypes under study. It is an effective way to partition the relative contribution of components of yield via standardized partial regression coefficients [33, 34]. This provides an effective way of finding out direct and indirect effect on correlation of the traits. In the results, days to maturity revealed highest path coefficient though had non-significant correlation with grain yield. This agrees with the findings of Gashaw, Mohammed [23] and Joshi, Mudwari [35]. Days to heading and flag leaf duration were the cause to render weak correlation of days to maturity with grain yield. Behind days to maturity, flag leaf area, grain filling rate and grain number per spike showed high direct effect with high genetic correlation on grain yield. In path coefficient study, it was found that grain filling rate, flag leaf area and grain number per spike had indirect support for each other to provide high direct effect on and genotypic correlation with grain yield. For other traits which were found significant and positively correlated at genotypic level with negative or small direct effects like chlorophyll content of flag leaf, plant height, harvest index and biological yield were also indirectly influenced by flag leaf area, grain filling rate and grain number per spike. So, it is better to select these three important traits which had high positive correlation with grain yield that indirectly exert the performance of harvest index, biological yield, chlorophyll content of flag leaf and plant height.

## 5. CONCLUSION

All the traits observed in the study revealed the existence of considerable variations among durum wheat genotypes that can be utilized in effective selection for breeding plan. Variation due to genotype  $\times$  year was found considerably very small as compared to genotypic variation. Therefore, heritability estimates of traits were found high. The high heritability with low variation due to genotype  $\times$  year interaction in most of the important traits implies that traits are inherited quantitatively. In this study, grain filling rate, grain number per spike and flag leaf area showed high heritability coupled with high genetic advance as percentage of mean, significant positive genotypic correlation and high positive direct effect. These traits are, therefore, the key contributors to grain yield and should be focused on crop improvement program for increasing grain yield.

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