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Research Article

Evaluation of durum wheat (*Triticum turgidum*) genotypes for genetic variability, heritability, genetic advance and correlation studies

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ABSTRACT

The present investigation was undertaken to study the genetic variability, heritability and correlation coefficient analysis for 7 metric traits in 12 durum wheat genotypes at western Oromia during 2015-2018. Significant genotypic differences were observed for the majority traits studied, indicates considerable amount of variation among genotypes for each character. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for kernels per spikelet, thousand kernels weight, and number of kernels per spike and grain yield. The remaining traits were ranged from low to moderate estimates. High heritability estimates were recorded for the majority traits studied. The estimated broad – sense heritability (h2) has ranged from 31.6% for maturity to 80.8% for grain yield. High genetic advance combined with high heritability was recorded for plant height, thousand kernel weight, kernels per spike and grain yield, indicates that most likely selection based on phenotype of genotypes could be effective to improve these characters. Grain yield was positively and significantly correlated with spike length, kernels per spike and thousand kernels weight both at genotypic and phenotypic levels. The strong correlation of grain yield with the mentioned traits showed that grain yield could be indirectly improved through improving these traits. This information might be used in the genetics and breeding programmes for improvement of durum wheat.

Keywords: Genotypes, Genetic advance, Genetic variability, Heritability and Wheat

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INTRODUCTION

Ethiopia is one of the main centre of diversity for multiples plant species (Vavilov, 1951) which consists of more than 60,000 accessions of different crops maintained in its gene bank (IBC, 2008).Ethiopia is the center of diversity for durum wheat (Wolde et al., 2016). Durum wheat is one of the most diversified cereal crop species in Ethiopia and the ‘landraces’ are characterized a significant phenotypic variability (Mengistu et al., 2016).

Durum wheat (*Triticum durum* Desf.) is an economically important crop and producing in several parts of the country including western highland of Oromia. Durum wheat accounts roughly 20% of total wheat production (Negassa. et al., 2013). Recent estimates show that the national average yield is 27 quintals per hectare (Qha^{-1}) (CSA, 2018), which is by far below the experimental yield of 60 Qha^{-1} (Bako ARC, 2019; Kulumsa ARC, 2019).Durum wheat uses as the raw material of numerous foods such as pasta and semolina in the alimentation of world population. Wheat is the world's most favored staple food which is nutritious, easy to store and transport and can be processed into various types of food (Subedi et al., 2019). Moreover, it is considered a good source of protein, minerals, B-group of vitamins and dietary fiber (Kandel et al., 2018a). The development of high yielding varieties with desirable quality characteristics is the major objective in durum wheat breeding programme. Analysis of variability among the traits and the association of a particular character with other traits contributing to yield of a crop would be of great importance in planning a successful breeding programme (Mary & Gopalan, 2006).

The magnitude of genetic variability present in a population is of paramount importance for the success of any plant breeding program (Kandel et al., 2018b). The estimates of genetic parameters as variances, coefficients of variation, heritability, genotypic, phenotypic and environmental correlations, allow knowing the magnitude of the genetic variability of a population, and the selection gains (Bartaula et al., 2019). Genetic variability among durum wheat genotypes can be estimated based on qualitative and quantitative traits. For effective selection, information on nature and magnitude of variation in population, association of character with yield and among themselves and the extent of environmental influence on the expression of these characters are necessary (Yağdı, 2009).

Heritability is a parameter which is widely used in the establishment of breeding programs and formation of selection indexes (Falconer, 1985). However, Johnson et al. (1955) stated that heritability estimates together with genetic advance are more important than heritability alone to predict the resulting effect of selecting the best individuals. Genetic advance is also considerably important because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi et al., 2003). High genetic advance coupled with high heritability estimates offers the most effective condition for selection (Larik et al., 2000). Correlation coefficient analysis could be used as an important tool to bring information about appropriate relationship between yield and some yield components. Considering the importance of such information, this research was initiated with following objectives; i) to estimate the extent of both genotypic and phenotypic variance in durum wheat genotypes, ii) to estimate the heritability and genetic advance, iii) to study the extent of mutual association among yield and associated parameters.

MATERIALS AND METHODS

Experimental Materials and Design

The field experiment was conducted at two sub-station (Shambu and Gedo) of Bako Agricultural Research Center during 2015-2018 main cropping seasons. The Experiment was laid out in randomized complete block design (RCBD) with three replications. Each plot consisted of six rows spaced 20cm × 2.5m long. The spaces between replications and plots were 1.5 m and 50cm, respectively used for both sites. Urea and NPS fertilizers were applied at the recommended rate of 100 and 100 kg/ha, respectively. NPS is a compound fertilizer containing nitrogen, phosphorous and sulfur with the ratio of 19% N, 38% P_2O_5 and 7% S. The whole of the NPS was applied at sowing, while urea was applied in splits with the first half at sowing and the second top-dressed at full tillering stage. Planting was done at the rate of 125 kg/ha of seed. Seed and fertilizer was drilled uniformly by hand.

Estimation of Variance Components

Environmental variance or error variance (**δ^2_e**), genotypic variance (**δ^2_g**) and phenotypic variance (**δ^2_p**) components and their coefficients of variation was estimated as suggested by Sharma, (1998).

$$Genotypicvariance(\delta^2 g) = \frac{MSG - MSE}{r}$$

Where; MSG=mean square of genotypes
MSE=mean square of error,
r= Number of replication

$$Phenotypicvariance(\delta^2 p) = \delta^2 g + \ \delta^2 e$$

Where: **δ^2_p=**phenotypic variance, **δ^2_g** = genotypic variance, δ2e =Environmental variance or error variance

The phenotypic (PCV) and genotypic (GCV) coefficients of variations were estimated as percentage of the corresponding phenotypic (σ^2p) and genotypic (σ^2g) standard deviations of the grand mean of the trait. Hence,

$$Genotypic\ cofficientvariation(\mathrm{GCV}) = \frac{\sqrt{\delta^2 g}}{x}\ X100$$

$$Phenotypic\ cofficientvariation(\mathrm{GCV}) = \frac{\sqrt{\delta^2 p}}{x}\ X100$$

Where x= population mean

Estimate of Heritability

Heritability (H^2): Heritability in broad sense for all characters was computed as per the formula adopted from Allard (1960).

$$\mathrm{H}^2 = \frac{\delta^2 g}{\delta^2 p}$$

Where: **δ^2_p=**phenotypic variance, **δ^2_g** = genotypic variance, H^2= broad sense heritability

Estimation of Expected Genetic Advance

Expected genetic advance under selection assuming a selection intensity of 5% was computed following the formula developed by (Allard, 1960):
GA = (K) (δ_p) (H^2), where GA = expected genetic advance, K= selection differential that varies depending up on the selection intensity and stands at 2.056 for selecting 5% of the genotypes, δ_p = phenotypic standard deviation and H^2= heritability (in broad sense)
Genetic advance as percent of mean was obtained as;

$$GA(\%\ of\ mean) = \frac{GA}{\mathrm{x}}\ X100$$

where GA=Expected genetic advance mean percentage, $\bar{x}$ = population mean for the trait considered

Phenotypic and Genotypic Correlation coefficients

The character associations represented by correlation coefficient between different pairs of characters at the genotypic and phenotypic levels were calculated from the genotypic, phenotypic and environmental covariance obtained by covariance analysis

Phenotypic and genotypic correlations between yield and yield related traits were estimated using the method described by (Miller et al., 1958).

$$rpxy = \frac{copxy}{\sqrt{\delta^2 px.\delta^2 py}}$$

Where: rpxy= phenotypic correlation coefficient between character x and y

COVpxy= phenotypic covariance between character x and y $\boldsymbol{\sigma}^2$px= phenotypic variance for character x

$\boldsymbol{\sigma}^2$pxy= phenotypic variance for character y

$$rgxy = \frac{cogxy}{\sqrt{\delta^2 gx.\delta^2 gy}}$$

Where; rgxy = genotypic correlation coefficient between character x and y

COVgxy = genotypic covariance between character x and y

$\boldsymbol{\sigma}^2$gx = genotypic variance for character x

$\boldsymbol{\sigma}^2$gxy = genotypic variance for character y

Statistical analysis

The mean values of the recorded data were subjected to analysis of variance as per Gomez and Gomez (1984). The mean squares were used to estimate genotypic and phenotypic variance according to Sharma, (1998). Phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV) and genotypic coefficient of variation (GCV) were estimated according to the method suggested by Burton and De Vane, (1953). Broad sense heritability was calculated as the ratio the genotypic variance to the phenotypic variance according to Falconer and Mackay (1996). Expected genetic advance as part of the mean (GA) for each character at 5% selection intensity (K=2.056) was computed using the method illustrated by Allard, (1960). Expected genetic advance as percent of mean (GAM) was calculated to compare the extent of predicted advance of different traits under selection, using the formula described by Comstock and Robinson (1952). Phenotypic and genotypic correlations coefficients for different characters in possible combination were estimated using variances and covariance as the method described by Sharma (1998).

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA)

The mean squares of analysis of variance (ANOVA) among 12 Durum wheat genotypes for 8 characters are presented in Table 1. Highly significant differences (P<0.01) were observed among genotypes for grain yield and thousand kernels, and significant difference (P<0.05) was observed for days to heading and, while non-significant variability was observed for days to maturity (Table 1). This indicating the presence of variability, which can be exploited through selection for further breeding programs. Similar finding was reported by Abinasa, (2011); Tilahun et al. (2020)

Table 1: Analysis of Variance (Mean Squares) for the 7 Characters of 12 Durum Wheat genotypes.

Parameters	Rep(DF=2)	Genotype(DF=11)	Error(DF=22)	CV (%)
Days to maturity	51.7	23.9	30.0	4.8
Days to heading	31.5	27*	43.5	13.5
Plant height	66.7	118.9	84.2	11.8
Panicle length	0.5	1.5**	0.9	19.4
Grain per Head	11.5	23.5*	17.4	13.0
1000 grain weight	38.9	71.2**	27.1	13.4
Grain yield (Kg/ha	45.1	134.3**	238.0	17.7

Genetic variability, heritability and genetic advance

The estimation of genotypic variance (σ^2 g) and phenotypic variance (σ^2 p) were obtained for different characters showing that a wide range of variance was observed for all the characters. High genotypic variability (σ^2 g) and Phenotypic variability (σ^2 p) was recorded for number of kernels per spikelet with the value of 146 and 177.3, respectively, while lower values were observed for spike length (1.3 and 2.2) (Table 2) .Phenotypic variance was higher than genotypic variance for all the yield and yield contributing characters, which indicates the influence of environmental factors on these traits. Tilahun et al. (2020) and Alemu et al. (2020) also reported that phenotypic variance was higher than genotypic variance for all the yield and yield contributing characters.

Estimates of phenotypic coefficients (PCV) value was ranged from 5.9% (for days to maturity) to 92.20% (for kernels per spikelet) and genotypic coefficient of variation was ranged from 3.3% for days to maturity and 71.6% for kernels per spike (Table 2). The higher PCV and GCV (>20) values was recorded for number of kernels per spikelet, thousand kernels weight, kernels per spike and grain yield (Table 2). Alemu et al. (2020) reported similar findings for grain yield and thousand kernels weight and Hassan and Hamlet (2017) for kernels per spike. This indicated that selection may be effective based on these characters and their phenotypic expression would be good indication of the genotypic potential. Moderate PCV and GCV (10-20) value was recorded for plant height and spike length but the lower PCV and GCV (<10) value was recorded for days to maturity (Table 2). The characters grouped under low phenotypic and genotypic coefficients of variation, indicates the environmental factors had more influence on the expression of these characters than the genetic factors. Therefore, improvements through selection cannot be effective on the basis of these characters

Although the genotypic coefficient of variation revealed the extent of genetic variability present in the genotypes for various traits, it does not give full information to assess heritability of the variation. The genotypic coefficient of variation along with heritability estimates give reliable estimates of the amount of genetic advance to be expected through phenotypic selection (Burton, 1952). Heritability, genetic advance (GA) and genetic advance as percent of mean (GAM) can provide full information about heritability of the variation. Robinson et al. (1949) classified heritability values as high (>60%), moderate (30-60%) and low (<30%). Accordingly, the results of the present study indicated that high >60% heritability values were observed in plant height, spike length, thousand kernels weight, kernels per spike and in grain yield. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. The rest of the characters grouped under moderate heritability (30-60), indicating moderate scope of selection as they were under the partial influence of environment.

The expected genetic advance expressed as a percentage of the mean by selecting the top 5% (high grain yielder) of the durum wheat advanced genotypes. Expected genetic advance was ranged from 2.3% for Kernels per spikelet to 22.5% for kernels per spike(Table 3), indicating that selecting the top 5% of the base population could result in an advance of 2.3 to 22.5% over the respective population mean. Falconer and Mackay, (1996) classified genetic advance as percent of mean as low (0-10%), moderate (10-20%) and high (20% and above). High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action, (Singh & Narayanan, 1999).

Johnson and Hernandez (1980) reported that high heritability and high genetic advance as percentage of mean provide better information than each parameter alone. High heritability and genetic advance as percent of mean were found in plant height, thousand kernel weight, kernels per spike and grain yield, indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. This finding was agreed with the result of Tilahun et al. (2020).

Table 2. Estimate of different parameters of variability7 characters of durum wheat.

Parameters	Mean	SE	$\delta^2 g$	$\delta^2 p$	GCV	PCV	Her (%)	GA (%)	GAM
Days to maturity	113.0	6.6	13.8	43.8	3.3	5.9	31.6	4.3	3.8
Plant height (cm)	77.9	10.7	90.8	115.0	12.2	13.8	79.0	17.4	22.3
Spike length(cm)	6.5	1.5	1.3	2.2	17.7	12.7	60.4	1.8	28.2
Grain per spikelet	4.8	10.7	11.8	113.9	71.6	92.2	33.4	2.3	47.5
1000 kernels weight	38.8	9.4	62.1	89.3	20.3	24.3	69.6	13.5	34.8
Kernels per spike	58.4	13.3	146.0	177.3	20.7	22.8	82.3	22.5	38.6
Grain yield Qha^{-1}	41.0	8.2	54.9	67.9	21.1	23.1	80.8	13.7	33.4

$\delta^2 g$ = Genotypic variance, GCV = Genotypic coefficient of variation, H=Broad sense heritability, GA= genetic advance, GA(%) = Genetic advance as percent of mean, PCV = phenotypic coefficient of variance, $\delta^2 p$ =Phenotypic variance, SE=Standard error of mean,Qha^{-1}=quintals per hectare

Correlation coefficients

Phenotypic correlation coefficients of grain yield with other characters are presented in Table 3. Grain yield had positive and highly significant phenotypic correlation with kernels per spike, spike length and thousand kernels, and negative non-significant associated with days to heading and maturity. This findings was similar to the findings reported by Adhikari et al. (2018).

Arega et al. (2010) also reported significant positive associations of grain yield with number of kernels spike and thousand kernels weight and negative non-significant associated with days to maturity. Thousand seed weight had positive and significant correlation with spike length and non-significantly correlated with days to maturity and kernels per spike. Alemu et al. (2020) reported similar findings for days to maturity and kernels per spike and Ayer et al.

(2017) for spike length. It had negative and significant correlation with plant height. Day to maturity had significant and negative correlation with plant height and kernels per spike but spike length and kernels per spike had positive correlation. Plant height had positive and significant correlation with spike length and kernels per spike, and positive and non-significant correlation with grain yield

Table 3. Correlation coefficient between yield component trait and grain yield in durum wheat at phenotypic levels

Traits	DTM	PHT	SL	KPS	TKW	GY/ha
DTM	1					
PHT	-0.171**	1				
SL	0.101	0.689**	1			
NKPS	-0.219**	0.205**	0.722**	1		
TKW	0.447	-0.143*	0.611**	0.21602	1	
Gy/ha	-0.463	0.343	0.561**	0.560**	0.88**	1

*DTM = Days to maturity, PHT=plant height, KPS=Kernels per spike, SL= Spike length, TSW=Thousand seed weight ,** = highly siginificance difference, *=siginificance difference*

Genotypic correlation coefficients of grain yield with other characters are presented in Table 4. Significant and positive correlation of grain yield with spike length, kernels per spike and thousand grain weight. Arega et al. (2010) reported significant positive phenotypic correlation of grain yield with spike length and thousand kernels weight. Thousand kernels weight showed positive and no significant correlation with plant height but negative and non-significant with spike length and kernels per spike. Similarly, Alemu et al. (2020) reported that Thousand kernels weight positive and no significant association with plant height but negative and non-significant with spike length and kernels per spike. The positive association of days to maturity with plant height, kernels per spike, thousand kernels weight and grain yield but negative and non-significant correlation with spike length. Plant height was showed positive and significant correlation with spike length and positive and non-significant correlation with kernels per spike, 1000 seed weight and grain yield.

Table 4. Correlation coefficient between yield component trait and grain yield in Durum wheat at genotypic levels

Traits	DTM	PHT	SL	NKPS	TKW	GY/ha
DTM	1					
PHT	0.18	1				
SL	-0.213	0.108*	1			
NKPS	0.139	0.214	-0.04	1		
TKW	0.222	0.213	-0.197	-0.569	1	
Gy/ha	0.328	0.402	0.521*	0.548**	0.524*	1

*DTM = Days to maturity, PHT=plant height, KPS=Kernels per spike, SL= Spike length, TSW=Thousand seed weight ,** = highly siginificance difference at 0.01 level, *=siginificance difference at 0.05 level*

CONCLUSION

The present study illustrated the existence of wide ranges of variations for most of the traits among durum wheat genotypes and opportunities of the genetic gain through selection or hybridization. High heritability accompanied with high genetic advance as per cent means were observed in the characters like grain yield and kernels per spike, indicating that most likely the heritability is due to additive gene effects and selection may be effective for these traits. The correlation coefficients were determined to find out the inter relationship among the 7 most responsive traits in relation to grain yield. Grain yield had positive and significant association with spike length, kernels per spike and thousand kernels weight at both genotypic and phenotypic levels. The information obtained from the study is useful for plant breeders in construction their breeding materials and implementing breeding strategies at the aim of further improving the yield and associated traits.

Conflict of interest

The author declares no conflicts of interest regarding publication of this manuscript.

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