African Journal of Agricultural Research Vol. 6(17), pp. 3972-3979, 5 September, 2011
Available online at http://www.academicjournals.org/AJAR
DOI: 10.5897/AJAR10.880
ISSN 1991-637X ©2011 Academic Journals

Full Length Research Paper

Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum* L. var. *durum*) genotypes

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Accepted 18 January, 2011

Information on the extent of genetic variability and heritability as well as correlation among agronomically important traits is a requirement to design a suitable plant breeding method. The present research was conducted at Sinana, Southeastern Ethiopia during the 2009 main crop growing season. The experimental material consisted of 16 durum wheat genotypes tested in a randomized complete block design with three replications. Twelve agronomic traits were included in the investigation. Highly significant differences were revealed among durum wheat genotypes for all traits studied, suggesting the possibility of improving durum wheat for these traits. Plant height and number of kernels per spike showed the highest phenotypic and genotypic coefficients of variations and genetic advance, whereas, days to maturity and test weight had the lowest values. Plant height exhibited highest heritability value of 98.3% while number of spikelets per spike showed minimum value of 36.4%. The genotypic correlations estimated showed positive association of grain yield with days for heading (r=0.50), harvest index (r=0.69) and kernels number per spike (r=0.81). Harvest index (1.13) and biomass (0.81) exhibited the highest positive and significant direct effect on grain yield. Hence, these traits could be considered as suitable selection criteria for the development of high yielding durum wheat varieties.

Key words: Correlation coefficient, durum wheat, genetic advance, heritability, path coefficient.

INTRODUCTION

Wheat (*Triticum* spp.) is the most important cereal cultivated in Ethiopia. It ranks second in total grain production (2.31 million tones, 14.4%) next to maize (CSA, 2008). In area coverage, it is the fourth important cereal crop after 'tef', maize and sorghum. Tetraploid (2n = 4× = 28) wheats have been under cultivation in Ethiopia since ancient times. Among the tetraploid, durum wheat (*Triticum turgidum* L. var. *durum*) is the predominant species. Durum wheats serve as the raw material of numerous foods such as pasta and semolina in the alimentation of world population. Various researchers (Negassa, 1986; Belay et al., 1993; Messele, 2001) reported the uniqueness of the Ethiopian tetraploid wheat germplasm for different useful traits.

Historically, the yield level of durum wheat is about 80% of bread wheat, which has been attributed partly to less favorable crop growing environments and management practices (Srivastaval et al*.,* 1988). However, new high yielding semi-dwarf durums have been developed that have yield potential equal, or even superior to the highest yielding bread wheat in some areas (SARC, 2008). As the price of durum is often higher than that of bread wheat, it is a promising and viable alternative crop for farmers. Therefore, plant breeders should increase their efforts directed towards developing new varieties. It is of great importance for the wheat breeders to know the genetic variability and heritability of important agronomic traits to improve the yield effectively (Baker et al., 1971). However, these traits are influenced by the genotype and environment and

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because of the polygenic nature of the characteristics involved (Gaines et al., 1996; Novoselovic et al., 2004).

Broad-sense heritability is defined as the ratio of genotypic variance to the phenotypic one. It plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value (Rehman and Alam, 1994). Heritability is a parameter which is widely used in the establishment of breeding programs and formation of selection indexes (Falconer, 1985). There is a direct relationship between heritability and response to selection, which is referred to as genetic progress. The expected response to selection is also called genetic advance (GA). High genetic advance coupled with high heritability estimates offers the most effective condition for selection (Larik et al., 2000). The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program (Shukla et al., 2004). Phenotypic and genotypic coefficients of variations, heritability and genetic advance have been used to assess the magnitude of variance in wheat breeding material.

Study of yield contributing components in respect of their genetic mechanism is very important for improvement in grain yield. Information regarding interrelationships between quantitatively inherited plant traits and their direct and indirect effects on grain yield is of great importance for success in selections to be conducted in breeding programs (Khan et al., 2010). The analysis of correlation coefficient is the one among numerous methods that can be used for this purpose but it cannot provide reasons of association. Path coefficient analysis is simply a standardized partial regression coefficient and as such measures the direct and indirect effect for one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effect (Dewey and Lu, 1959). Using path coefficient analysis, it is easy to determine which yield component is influencing the yield substantially. Having this information, selection can then be based on that criterion thus making possible great progress through selection. Path coefficient analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Garcia et al., 2003; Khaliq et al., 2004).

The present study is therefore, aimed at assessing genetic variation, broad sense heritability and expected genetic advance as well as relationship among agronomic traits in durum wheat.

MATERIALS AND METHODS

Experimental materials and design

Sixteen durum wheat (*Triticum turgidum* L.var. *durum*) genotypes consisting of thirteen released varieties and three elite breeding lines were included in the study (Table 1). They were selected based on their agronomic performances and suitability to the growing conditions. The genotypes were grown under rainfed during 2009 main (bona) cropping season with uniform conditions at Sinana, Southeastern Ethiopia (7°N latitude and 40°E longitude and 2400 m.a.s.l., 867.7 mm mean annual rainfall during the crop growing season). The average annual maximum and minimum temperatures are 21°C and 9°C, respectively. The soil is clay in textural type with slightly acidic pH (Mengistu et al., 2008).

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each experimental plot was 2.5 m long and 2.4 m wide, with twelve rows 20 cm apart, giving a gross plot area of 6 m^2 and net plot area of 5 m^2. Adjacent blocks were 1 m apart. Sowing was done by hand drilling and covered lightly with soil. The seed rate and fertilizer rate was 150 $kgha^{-1}$ and 41/46 N/P_2O_5 kg ha^{-1}respectively (MoARD, 2004). All other agronomic practices are done as recommended for wheat production in the area.

The following agronomic traits were included the investigation:

(1) Days for heading.
(2) Days to maturity.
(3) Number of productive tillers per m^2.
(4) Plant height.
(5) Spike length (cm).
(6) Spikelets number of per spike.
(7) Kernels number of per spike.
(8) Biomass.
(9) Harvest index.
(10) 1000- kernel weight.
(11) Test weight.
(12) Grain yield on 12.5% moisture basis.

Statistical analysis

The SAS GLM procedure (SAS Institute, Inc. 2002) was employed for the analysis of variance. Fisher's protected least significant difference (LSD) test at 5% level of significance was used for mean comparisons, whenever genotype differences were significant. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated following the method of Burton (1952). Broad-sense heritability (h^2) was calculated as the ratio of the genotypic variance to the phenotypic variance according to Singh and Ceccarelli (1996). Genetic advance as percentage of the mean assuming selection of the superior 5% of the genotypes was also estimated following the procedure elaborated by Singh and Chaudhary (2004):

$$Phenotypic\ coefficient\ of\ \text{var}iation\ (PCV) = \frac{\sqrt{phenotypic\ \text{var}iance}}{Mean\ value\ of\ the\ trait} \times 100$$

$$Genotypic\ coefficient\ of\ \text{var}iation\ (GCV) = \frac{\sqrt{Genotypic\ \text{var}iance}}{Mean\ value\ of\ the\ trait} \times 100$$

$$Heritability\ (h^2{}_B) = \frac{Genotypic\ \text{var}iance}{Phenotypic\ \text{var}iance} \times 100$$

$$Genetic\ advance\ (\%\,mean) = K \times h^2{}_B \times \frac{\sqrt{phenotypic\ \text{var}iance}}{Mean\ value\ of\ the\ trait} \times 100$$

K= selection intensity (5% = 2.06), $h^2{}_B$= broad- sense heritability Genotypic correlations between traits were calculated using

Table 1. Description of durum wheat genotypes used in the experiment.

No.	Genotypes	Pedigree	Year of release
1.	Leliso	Cocorit71/3/Gerardo//61- 30/G//"S"/4/Boohai//Hora// Gerardo/3/ Boohai	2002
2.	Oda	DZ046881/imlo//cit71/3/RCHI/LD357//imlo/4/Yemen/ cit'5'/Plc's'/3/Taganroy	2004
3.	Ilani	Ilumilo/Rahum/A4#72/3/Gerardo	2004
4.	Bakkalcha	98-OFN-Gedilfa/Guerou/ 15patho	2005
5.	Ejersa	LABUD/NIGRIS-3//Gan-CD98206	2005
6.	Obsa	ALTAR84//ALTAR84/SERI/3/6* ALTAR84	2006
7.	Tate	DACK/KIWI/OSTE/3/CHEN 84//4/MEXI/5/5…	2009
8.	Cocorit-71	-	1976
9.	Yerer	CHEN/TEZ/GVIL//C11	2002
10.	Ude	CHEN/ALTAR84//JO69	2002
11.	Denbi	AJAIA/BAUSHEN…CSS98IY00025-0MXI-3QK-4DZR	2009
12.	Hitosa	CHEN/ALTAR 84...CDS-97-B00265…IQX…6DZR	2009
13.	CDSS94	CANGRUS/POHO-1//SUGU-14CDSS94Y00597T-A-1M-0Y-0B-1Y-0B	Advanced line
14.	CD86772	Cit-71/DUKEM/DON87 CD86772-DZ491	Advanced line
15.	CD1B2620	KUCK CD1B2620-G-8M-030Y-030M-2Y-0-2Y-0B	Advanced line
16.	Gerardo	VZ466/61-130xLdsxGII's'CM9605	1976

variances and covariances according to Singh and Chaudhary (1996). Path analysis was carried out using GENRES3 for windows version 7.01 (Pascal Intl Software Solutions, 1994) to study the direct and indirect contributions of the traits to the associations. Spike length, spikelets number per spike, kernels number per spike, biomass, harvest index, thousand kernel weight and test weight were entered as predictor variables in a path analysis (Dewey and Lu, 1959; Li, 1975; Williams et al., 1990) that estimated their direct effects (path coefficients) and indirect effects on grain yield which is the response (dependent) variable.

$$r_{ij} = p_{ij} + \sum r_{ik}\ p_{kj}$$

r_{ij} = Mutual association between the independent variable 'i' and the dependent variable 'j' as measured by correlation coefficient.

p_{ij} = Components of direct effects of the independent variable (i) on dependent variable (j) as measured by the path coefficients.

$\sum r_{ik}\ p_{kj}$ = Summation of components of indirect effects of independent trait (i) on the given dependent trait (j) via all other independent variables (k).

The contribution of the remaining unknown factor was measured as the residual factor. This was calculated as:

$$residual\ effect = \sqrt{1 - R^2} \quad \text{, where} \quad R^2 = \sum p_{ij}\ r_{ij}$$

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant difference among genotypes for all traits studied (Table 2). The significant difference among genotypes for the traits implies the presence of substantial variation among genotypes which is central to the study of both quantitative and qualitative traits and gives an opportunity to plant breeders for improvement of these characters through breeding. The amount of genotypic and phenotypic variability that exist in a species is of utmost importance in breeding better varieties and in initiating a breeding program. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population. Estimated genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), broad sense heritability (h^2_B) and genetic advance as percent of mean (GA) of the traits studied are presented in Table 2.

Genetic variability

Among all traits, higher GCV and PCV values (>10%) were observed for plant height and number of kernels per spike. Days to maturity, number of spikelets per spike and test weight showed low PCV and GCV (<5%) suggesting the difficulty of manipulating these traits through plant breeding. In general, the PCV values were greater than GCV values although the differences were small. This indicated that the environmental effect was small for the expression of most characters which also supports the findings of Sabhashchandra et al. (2009).

Table 2. Mean squares, means, genotypic and phenotypic coefficient of variability, heritability and genetic advance of the 12 agronomic traits of the sixteen durum wheat genotypes tested.

Agronmic traits	Mean squares	Mean ±SE	GCV	PCV	h^2_B	GA(%mean)
Days for heading (days)	37.15**	66.1±0.81	5.18	5.59	85.5	9.86
Days to maturity (days)	14.61**	134.6±0.74	1.55	1.81	72.1	2.69
Number of productive tiller/m^2	1277.99**	223±4.33	9.05	9.65	87.9	17.48
Plant height (cm)	513.47**	84.8±1.00	15.38	15.52	98.3	31.42
Spike length (cm)	0.81**	5.3±0.14	4.62	6.80	46.2	6.47
Spikelets number per spike	1.04**	16±0.32	3.09	4.63	36.4	3.48
Kernels number per spike	97.25**	49±1.88	10.91	12.75	73.2	19.33
Biomass(kg/5m^2)	0.35**	4.3±0.20	6.58	10.40	40.0	8.57
Harvest index (%)	47.73**	40.9±1.24	9.28	10.66	75.8	16.62
Thousand kernel weight(g)	44.32**	42.9±0.68	8.83	9.25	91.1	17.33
Test weight ($kghl^{-1}$)	5.55**	81.7±0.30	1.62	1.74	88.7	3.19
Grain yield($kgha^{-1}$)	285762.00**	3509.4±167.33	7.39	11.08	44.5	10.16

**, *= significant at ($p \le 0.01$) and ($p \le 0.05$) levels respectively, SE: standard error, GCV: genotypic coefficient of variation (%), PCV: phenotypic coefficient of variation (%), h^2_B: broad sense heritability (%), GA: genetic advance.

Table 3. Estimates of genotypic correlation coefficients among 12 traits of durum wheat genotypes.

Traits	DH	DM	NPTm^2	Plh	SL	SNPS	KNPS	BM	HI	TKW	TW	GY
DH	1.0	0.02	-0.06	-0.23	-0.29	0.36	0.48	0.16	0.31	-0.14	0.39	0.50*
DM		1.0	-0.19	0.53*	-0.06	0.15	-0.43	0.33	-0.53*	0.69**	0.42	-0.36
NPTm^2			1.0	-0.23	-0.09	-0.47	-0.26	-0.06	0.07	-0.20	-0.28	0.03
Plh				1.0	-0.16	0.15	-0.32	0.58*	-0.71**	0.45	0.09	-0.32
SL					1.0	0.07	-0.17	0.06	-0.28	0.30	-0.45	-0.23
SNPS						1.0	0.37	0.49*	-0.16	-0.10	0.44	0.26
KNPS							1.0	0.20	0.54*	-0.59*	0.42	0.81**
BM								1.0	-0.54*	0.19	0.18	0.23
HI									1.0	-0.57*	0.19	0.69**
TKW										1.0	-0.13	-0.49
TW											1.0	0.36
GY												1.0

, *: significant at 0.05 and 0.01 probability levels respectively, DH: days for heading, DM: days to maturity, NPTm^2:number of productive tiller per m^2, Plh: plant height (cm), SL: spike length (cm), SNPS: spikelets number per spike, KNPS: kernels number per spike, BM: biomass ($kg5m^{-2}$), HI: harvest index (%), TKW: thousand kernel weight (g), TW: test weight ($kghl^{-1}$), GY: grain yield ($kgha^{-1}$).

Heritability and genetic advance

Heritability is a significant parameter for the selection of an efficient population improvement method. Single plant selection and that in the earlier generations may be much effective for a character that is highly heritable as compared to that a character which is less heritable. Furthermore, environment may also interact with the genotypic constitution to influence heritability (Raiz, 2003). In the present study days for heading, plant height, thousand kernel weights, test weight, number of productive tiller per m^2 and harvest index exhibited relatively higher broad sense heritability values (Table 3). High expected genetic advance estimates were obtained for plant height, kernels number per spike, productive tiller per m^2 and thousand kernel weights.

The intermediate to high estimates of heritability and relatively high estimates of genetic advance (as percentage of mean) was observed in the present study for grain yield and yield related traits like number of productive tiller per m^2, plant height, thousand kernel weight, kernels number per spike and harvest index. This suggested most likely that heritability is due to the additive genetic effects and selection could be effective in early segregating generations for these traits and the possibility of improving durum wheat grain yield through direct selection for grain yield related traits. Similar findings have been reported by Dwived et al. (2002) and Yousaf at al. (2008). However, high heritability for test weight and relatively lower estimates for genetic advance

Table 4. Estimates of genotypic path coefficients of direct (bold diagonal) and indirect effects of 7 traits on grain yield in durum wheat genotypes.

Traits	SL	SNPS	KNPS	BM	HI	TKW	TW	r_g
SL	0.03	0.00	-0.01	0.05	-0.32	0.01	0.01	-0.23
SNPS	0.00	0.03	0.02	0.40	-0.18	0.00	-0.01	0.26
KNPS	0.00	0.01	0.05	0.16	0.61	-0.01	-0.01	0.81**
BM	0.00	0.02	0.01	0.81	-0.61	0.00	0.00	0.23
HI	-0.01	-0.01	0.03	-0.44	1.13	-0.01	0.00	0.69**
TKW	0.01	0.00	-0.03	0.15	-0.64	0.02	0.00	-0.49
TW	-0.01	0.02	0.02	0.15	0.21	0.00	-0.02	0.36

Residual=0.089 **: significant at 0.01 probability level, r_g= genotypic correlation coefficient of traits with grain yield.

indicates non additive genetic sources of variation and improvement of the trait through selection may not be effective in this population.

Correlation coefficient

Correlation between different traits is generally due to the presence of linkage disequilibrium, pleiotropic gene actions and epistatic effect of different genes (Falconer, 1985). Environment also plays an important role in the correlation. In some cases, environment affects both the traits simultaneously in the same direction or some time in different directions. Genetic and environmental causes of correlation combine together and give phenotypic correlation. The dual nature of phenotypic correlation makes it clear that the magnitude of genetic correlation cannot be determined from phenotypic correlation. Therefore, estimation of degree of genotypic and phenotypic correlation of grain yield with yield components is very important to utilize the available genetic variability through selection (Singh et al., 1998).

The genetic correlation coefficients showed significant association among some traits (Table 3). Significant positive association was observed for grain yield with days for heading, kernels number per spike and harvest index. This partially agrees with the results of Akram et al. (2008) who reported significant positive correlation between number of kernel per spike, number of spikelet per spike and grain yield in wheat.

Plant height had significant and positive correlation with biomass and significant negative correlation with harvest index. However, negative but non significant correlation was observed for plant height with kernels number per spike and grain yield. These results are in accordance with the findings of Dogan (2009). The negative correlation of some important characters with yield may lead to some undesirable selection depending on whether negative association is due to linkage or pleiotropic effect. To improve yield components with negative association with other, suitable recombination may be obtained through biparental mating, mutation breeding or diallele selective mating by breaking undesirable linkages.

Biomass was positively and moderately related with spikelets number per spike and negatively correlated with harvest index. Harvest index showed negative and significant relation with days to maturity and positive and moderately significant correlation with kernels number per spike. Negative and significant relation was observed between biomass and harvest index.

Path coefficient

The path coefficient analysis appeared to provide a clue to the contribution of various components of yield to over all grain yields in the genotypes under study. This analysis is used to partition the relative contribution of yield components via standardized partial regression coefficients (Li, 1975; Williams et al., 1990). It provides an effective way of finding out direct and indirect sources of correlation. Direct and indirect effects of these components determined on grain yield are presented in Table 4.

The results of path coefficient analysis of important yield components with yield revealed that harvest index exerted the highest positive and significant direct effect (+ 1.13) on grain yield followed by biomass (+0.81). These traits showed positive correlations with grain yield. This agrees with the findings of Izzat et al. (2000). As a result, these characters could be considered as main components for selection in a breeding program for higher grain yield. This implies that these traits were the major contributors for the improvement of grain yield.

The indirect effect of harvest index through spike length (-0.01), number of spikelets per spike (-0.01), thousand kernel weight (-0.01) and biomass (-0.44) counter balanced the direct effect of harvest index on grain yield and reduced the correlation coefficient to (+0.69). Similarly, the indirect effect of biomass through harvest

Table 5. Mean performance of sixteen durum wheat genotypes for different agronomic traits.

Genotypes	DH‡	DM‡	NPTm^{2}‡	Plh‡	SL‡	SNPS‡	KNPS‡	BM‡	HI‡	TKW‡	TW‡	GY‡
Leliso	62.0^{ef}	137.3^{ab}	215.7^{de}	118.3^{a}	4.8^{ef}	16.3^{abc}	46.3^{def}	5.2^{a}	31.3^{e}	45.7^{b}	82.0^{cde}	3286.3^{def}
Oda	68.3^{bc}	137.7^{a}	209.0^{ef}	116.7^{a}	5.0^{def}	16.3^{abc}	43.7^{ef}	4.5^{bcd}	36.3^{d}	47.3^{ab}	82.3^{cd}	3259.7^{ef}
Ilani	60.3^{f}	132.3^{ef}	211.7^{ef}	87.7^{b}	6.1^{b}	15.3^{de}	46.3^{def}	4.1^{cd}	38.0^{d}	47.7^{a}	78.9^{f}	3142.7^{ef}
Bakkalcha	64.0^{de}	136.7^{abc}	239.0^{bc}	81.0^{d}	5.3^{cd}	15.7^{cde}	44.7^{ef}	4.2^{cd}	42.7^{ab}	47.9^{a}	82.4^{cd}	3577.3^{abcde}
Ejersa	68.0^{c}	136.0^{abcd}	201.7^{f}	79.3^{de}	5.1^{cde}	16.0^{bcd}	51.3^{cd}	4.0^{cd}	42.3^{ab}	43.5^{cd}	82.5^{bc}	3353.3^{def}
Obsa	70.3^{ab}	132.0^{ef}	257.3^{a}	79.0^{def}	5.2^{cde}	16.0^{bcd}	56.0^{abc}	4.7^{bc}	44.0^{ab}	38.5^{gh}	81.6^{de}	4006.3^{a}
Tate	65.7^{d}	134.0^{de}	243.0^{b}	81.0^{d}	5.3^{cd}	15.3^{de}	53.7^{bc}	4.5^{bcd}	43.0^{ab}	38.4^{gh}	81.3^{e}	3758.3^{abcd}
Cocorit-71	63.3^{e}	132.0^{ef}	265.0^{a}	76.3^{f}	4.8^{ef}	15.3^{de}	42.3^{ef}	3.9^{d}	42.0^{bc}	40.0^{fg}	79.1^{f}	3296.7^{def}
Yerer	71.0^{a}	136.3^{abc}	235.0^{bc}	79.3^{de}	5.9^{b}	17.0^{a}	47.3^{de}	4.8^{ab}	36.0^{d}	46.1^{ab}	81.9^{cde}	3434.7^{cdef}
Ude	69.0^{abc}	136.7^{abc}	227.3^{cd}	81.3^{d}	4.6^{f}	15.0^{e}	44.7^{ef}	4.1^{cd}	43.7^{ab}	46.6^{ab}	82.4^{cd}	3495.7^{abcdef}
Denbi	62.7^{e}	134.0^{de}	211.3^{ef}	84.7^{c}	5.2^{cde}	16.7^{ab}	54.0^{abc}	4.3^{bcd}	45.7^{a}	38.9^{fg}	83.5^{a}	3912.0^{abc}
Hitosa	63.7^{de}	135.3^{bcd}	229.7^{c}	78.7^{def}	5.1^{cde}	16.0^{bcd}	47.0^{def}	4.0^{cd}	38.7^{cd}	39.8^{fg}	83.3^{ab}	3040.7^{f}
CDSS94	71.0^{a}	134.7^{cd}	188.7^{g}	77.3^{ef}	4.9^{def}	17.0^{a}	59.3^{a}	4.5^{bcd}	44.0^{ab}	42.3^{de}	82.5^{bc}	3946.0^{ab}
CD86772	68.0^{c}	130.7^{f}	206.0^{ef}	76.3^{f}	4.9^{def}	16.3^{abc}	51.7^{cd}	4.0^{cd}	44.7^{ab}	36.9^{h}	81.3^{e}	$3580.7a^{bcde}$
CD1B2620	68.3^{bc}	132.0^{ef}	216.7^{de}	79.0^{def}	5.4^{c}	16.0^{bcd}	58.3^{ab}	4.5^{bcd}	43.3^{ab}	40.6^{ef}	82.4^{cd}	3857.7^{abc}
Gerardo	62.3^{ef}	135.3^{bcd}	212.7^{ef}	81.0^{d}	6.6^{a}	16.0^{bcd}	41.7^{f}	4.3^{bcd}	38.0^{d}	45.4^{bc}	79.7^{f}	3202.0^{ef}
Mean	66.1	134.6	223	84.8	5.3	16.0	49.0	4.3	40.9	42.9	81.7	3509.4
SE	0.81	0.74	4.33	1.00	0.14	0.32	1.88	0.20	1.24	0.68	0.30	167.33
LSD (5%)	2.33	2.13	12.5	2.9	0.42	0.93	5.42	0.58	3.57	1.96	0.87	483.27
CV (%)	2.1	1.0	3.4	2.0	4.7	3.5	6.6	8.1	5.2	2.7	0.6	8.3

Where: SE, LSD, CV(%), DH, DM, NPT, Plh(cm), SL(cm),NSPS, NKPS, BM(kg/5 m^{2}), HI(%), TKW(g),TW($kghl^{-1}$), GY(kg ha^{-1}) are as described in Table 3. ‡ Means within each column followed by the same letter are not significantly different from each other based on the 0.05 probability level of LSD.

index (-0.61) counter balanced the direct effect of biomass on grain yield (0.81) and reduced the correlation coefficient to (+0.23). This is partially in agreement with the findings of Berhanu (2004).

The lower residual effect (0.089) indicated that most of the variability in grain yield for the genotypes under the present has been explained by the independent variables included in the analysis (Singh and Chaudhary, 1999).

Correlation and path coefficient analysis can be used as an important tool to bring information about appropriate cause and effects relationship between yield and some yield components (Khan et al., 2003).

Agronomic performance of durum wheat genotypes

Mean values of genotypes for different agronomic traits are given in Table 5. The studied genotypes showed grain yield variation ranging from 3004.7 $kgha^{-1}$(Hitosa) to 4006.3 $kgha^{-1}$(Obsa). The genotypes also showed thousand kernel weights ranging from 36.9g to 47.9g and test weight from $79.7kghl^{-1}$ to $83.5kghl^{-1}$. This was within the range reported by (Efrem et al., 2000; Bemnet et al., 2003) from 33 to 50 g for thousand kernel weight and 76 to 86 $kghl^{-1}$ for test weight on Ethiopian released durum wheat varieties. Accordingly, Denbi, Hitosa, Bakkalcha and CDSS94 showed the highest values, whereas; Ilani, Cocorit-71 and Gerardo had significantly lower test weight values ($p<0.05$) than other genotypes. The acceptable thousand kernel weight for durum wheat is 30 to 35 g db (dry basis) (Petrova, 2007) and that of test weight is 81 kgh^{-1}(Sisson, 2004; Petrova, 2007; Workneh et al., 2008).

Conclusions

The present study showed the presence of considerable variations among durum wheat genotypes for all traits tested which gives an opportunity to plant breeders for the improvement of these traits. Genetic correlation coefficient analysis indicated that important agronomic traits are positively correlated with grain yield. This suggests a common genetic/physiological basis among these traits. Hence, simultaneous improvement of these traits would be possible. Biomass and harvest index showed significant positive direct effect along with positive correlation with grain yield and can be considered as suitable selection criteria for the development of high yielding durum wheat varieties.

ACKNOWLEDGMENTS

The authors acknowledge Oromia Agricultural Research Institute and Sinana Agricultural Research Center for financial support and Debre Zeit Agricultural Research Center for the provision of samples of durum wheat varieties. The residual IFS-OPCW (E/3173-2) fund, a grant to Dr. Geremew Bultosa at Haramaya University is acknowledged for covering this publication cost..

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