Morphological characterization and genetic analysis in bread wheat germplasm: A combined study of heritability, genetic variance, genetic divergence and association of characters

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Abstract: The present study was conducted to assess the nature and magnitude of genetic variability and traits association of bread wheat genotypes for yield and related traits. A total of 180 genotypes were evaluated in alpha lattice design with three replications in 2017/18 cropping season. Data for 10 quantitative traits were collected and subjected to analysis of variance. The result from the analysis of variance revealed highly significant variability observed among genotypes for all traits studied. Phenotypic coefficient of variation (PCV) is superior over genotypic coefficient of variation (GCV) for most traits but narrow variations were found between PCV and GCV for most of the traits. Heritability in broad sense and genetic advance as percent of the mean (GA%) were relatively higher for Kernels per spike and grain filling period. Grain yield showed positive and highly significant (p≤0.01) association with number of tillers, kernel per spike and plant height both on genotypic and phenotypic levels. The path coefficient analysis showed that spike length, plant height and kernels per spike had positive direct effect on grain yield on both genotypic and phenotypic levels. Divergence analysis (D[2]) grouped the total test germplasm into 10 clusters. Among those, clusters IV and IX showed the highest genetic distance and thus the possibility to develop segregating populations upon the crossing of widely related genotypes in those clusters. The results could help researches to utilize the most promising wheat genotypes of this study in future breeding programmes for enhancing desirable traits.

Introduction

Bread wheat (*Triticum aestivum* L.) is a segmental hexaploid (6x) which has 21 pairs of chromosomes (2n=42) during meiosis, a self-pollinating annual plant in the true grass family Gramineae (Filiz, 2011; Baenziger, 2016). It is the most widely grown crop in the world and the main source of nutrients to most of the world's population.

Ethiopia is the largest wheat producer in Sub Saharan Africa followed by South Africa and fourth in Africa with harvested area of 1.7 million hectares with production of 4.6 million tons and an average yield of 2.7 t/ha, which was about 45% below the world average (Degewione and Alamerew, 2013; Demeke and Marcantonio, 2013; CSA, 2018).

Lack of broad genetic background has triggered improved crops varieties less tolerant to biotic and abiotic stresses. Narrow genetic variability in the crops increases vulnerability to pests and climatic variability. Genetic variability and heritability provide basic information for genetic improvement of the crops. Genetic variability is the measure of the tendency of individual genotypes in a population to vary from one to another for certain traits of interest, which is the base of crop improvement (Chimdesa et al., 2014). The existence of wide genetic variability in a population can be divided into transmitted and non-

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transmitted variation. The concept of heritability is associated with the relative influence of the heredity and environment. Genetic advance is an important and determinant parameter for selection of desirable traits (Boryana and Darina, 2014). Therefore, having good information on heritability and genetic advance existing in different yield parameters is a precondition for effective plant improvement.

Direct selection for yield could not be a grant because of the complex relationship between grain yield and its component (Ali et al., 2008; Dutamo et al., 2016). Correlation analysis provides information about inter-relations of plant traits that contribute for yield increment (Yusuf et al., 2018; Ullah et al., 2018). Correlation coefficient is a statistical method, which can help the plant breeder in selection for higher yield (Mohammad et al., 2002). Considering the importance of such information, this research was initiated with the objectives of: (1) to study the level of genetic variability of bread wheat genotypes for yield and other related traits; (2) to guesstimate heritability and genetic advance during selection; (3) to study the degree of mutual association among yield and associated characters.

Material and methods

Object of study

In the study 180 bread wheat (*Triticum aestivum* L.) genotypes consisting of improved varieties, candidate varieties and lines were collected from different Ethiopia Agricultural Research Centers and CIMMYT/ICARDA. The details of the genotypes are given in Tables 1 and 2. The genotypes were grown in alpha-lattice design with three replications at Gedo station of Bako Agricultural Research Center, during the main season of 2017/18. Each plot consisted of six rows of 2.5 m length with 20 cm and 50 cm spacing between rows and plots, respectively. The seed rate of 150 kg.ha^{-1} and fertilizer rate of 100 kg.ha^{-1} of DAP and 100 kg.ha^{-1} UREA were used. All other crop management and protection practices were undertaken following previous research recommendations for bread wheat production.

Quantitative data were collected both from plot and plant basis. The four central rows were used for data collection based on plots, such as days to 50% heading, days to physiological maturity, grain yield, and kernels thousand weight. Ten randomly selected plants from the four central rows of each plot were used for data collection on plant basis and the averages of the 10 plants in each experimental plot were used for statistical analysis for traits such as plant height, productive tillers per plant, number of kernels per spike, number of spikelets per spike and spike length.

Statistical analysis

All data were subjected to analysis of variance using general linear model (GLM) procedure of SAS statistical version 9.3 software (SAS, 2009). Least significant difference (LSD) was used to separate differences in parameters means of genotypes where significant variation was observed at 5%

probability level. The analysis of variance was conducted according to alpha lattice design using the mean of 10 sampled plants for plant based data recorded and plot basis. Similarly, correlation analysis was performed using SAS PROC CORR (SAS system version 9.3) to determine the relationship among yield and related parameter components. Path analysis was done through Excel to distinguish parameters that cause a direct and indirect effect on grain yield. Cluster analysis was conducted using R studio and SAS (9.3 ver) software.

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 were estimated as suggested by Singh and Chaudhary (2004):

GV(δ^2_g) = (MSG - MSE) / r,

Where; GV(δ^2_g)= genotypic variance (δ^2_g), MSG= mean square of genotypes, MSE= mean square of error, r= Number of replication.

PhV(δ^2_p) = δ^2_g + δ^2_e ,

Where: PhV(δ^2_p)= phenotypic variance, δ^2_g= genotypic variance, δ^2_e= environmental variance or error variance.

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

GCV(%) = ($\sqrt{\delta^2_g}$ / X).100,

PCV(%) = ($\sqrt{\delta^2_p}$ / X). 100,

Where X= population mean.

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

H^2(%) = [(δ^2_g) / (δ^2_p)].100,

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

Estimation of expected genetic advance: Expected genetic advance (GA) 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 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 (GA) as percentage of mean was obtained as;

GA(% of mean) = (GA / $\bar{x}$). 100,

Where: GA(% of mean)= Expected genetic advance mean percentage, $\bar{x}$ = population mean for the trait considered.

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

rpxy = COVpxy / $\sqrt{\delta^2px . \delta^2py}$,

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

COVpxy= phenotypic covariance between character x and y;

δ^2px= phenotypic variance for character x;

δ^2py= phenotypic variance for character y.

rgxy = COVgxy / $\sqrt{\delta^2 gx . \delta^2 gy}$

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

COVgxy= genotypic covariance between character x and y;

δ^2gx= genotypic variance for character x;

δ^2gy= genotypic variance for character y.

Path coefficient analysis: The direct and indirect effect of yield related traits on grain yield per plot was analyzed through path coefficient analysis. This analysis computed as suggested by Dewey and Lu (1959) with the following formula:

$$\sqrt{1 - R^2},$$

Where: $R^2 = \sum Pij rij$, where: Pij= component of direct effects of the independent character (i) and dependent character (j) as measured by the path coefficient; rij= mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficient.

Table 1. List of bread wheat genotypes used in the study

No	Acc no	Pedigree	No	Acc no	Pedigree
1	1092	MXI12-13\M47IBWSN/194	82	85	AON
2	6223	MXI12-13\M24ISEPTON\56	83	2122	MXI12-13\M25HRWSN\1148
3	6201	MXI12-13\M24ISEPTON\25	84	86	AON
4	61	AON	85	6220	MXI12-13\M24ISEPTON\36
5	2042	MXI12-13\M25HRWSN\1053	86	2014	MXI12-13\M25HRWSN\1012
6	6208	MXI12-13\M24ISEPTON\96	87	94	AON
7	1108	MXI12-13\M47IBWSN/247	88	1279	MXI12-13\M47IBWSN\779
8	20	Adap	89	6207	MXI12-13\M24ISEPTON\102
9	6239	MXI12-13\M24ISEPTON\26	90	6218	MXI12-13\M24ISEPTON\13
10	1102	MXI12-13\M47IBWSN/222	91	6203	MXI12-13\M24ISEPTON\63
11	6229	MXI12-13\M24ISEPTON\95	92	1299	MXI12-13\M47IBWSN\847
12	2	Adap	93	6241	MXI12-13\M24ISEPTON\66
13	2132	MXI12-13\M25HRWSN\1166	94	63	AON
14	6221	\\0	95	1179	MXI12-13\M47IBWSN\496
15	2034	MXI12-13\M25HRWSN\1041	96	9217	MXI12-13\M24ISEPTON\97
16	2083	MXI12-13\M25HRWSN\1100	97	2010	MXI12-13\M25HRWSN\1007
17	1096	MXI12-13\M47IBWSN/208	98	6219	MXI12-13\M24ISEPTON\44
18	80	AON	99	40	AON
19	1242	MXI12-13\M47IBWSN/655	100	1295	MXI12-13\M47IBWSN\830
20	1161	MXI12-13\M47IBWSN/415	101	2105	MXI12-13\M25HRWSN\1124
21	5	Adap	102	1034	MXI12-13\M47IBWSN\74
22	1141	MXI12-13\M47IBWSN/335	103	1097	MXI12-13\M47IBWSN\217
23	73	AON	104	6235	MXI12-13\M24ISEPTON\62
24	1087	MXI12-13\M47IBWSN/185	105	6242	MXI12-13\M24ISEPTON\73
25	1089	MXI12-13\M47IBWSN/188	106	51	AON
26	2106	MXI12-13\M25HRWSN\1127	107	6216	MXI12-13\M24ISEPTON\42
27	67	AON	108	2135	MXI12-13\M25HRWSN\1174
28	6205	MXI12-13\M24ISEPTON\89	109	6211	MXI12-13\M24ISEPTON\74
29	1265	MXI12-13\M47IBWSN\722	110	2131	MXI12-13\M25HRWSN\1162
30	2114	MXI12-13\M25HRWSN\1138	111	71	AON
31	6230	MXI12-13\M24ISEPTON\32	112	87	AON
32	1178	MXI12-13\M47IBWSN/492	113	6228	MXI12-13\M24ISEPTON\20
33	2082	MXI12-13\M25HRWSN\1099	114	2104	MXI12-13\M25HRWSN\1123
34	6240	MXI12-13\M24ISEPTON\85	115	6214	MXI12-13\M24ISEPTON\51
35	2123	MXI12-13\M25HRWSN\1150	116	52	AON
36	58	AON	117	2136	MXI12-13\M25HRWSN\1175
37	1103	MXI12-13\M47IBWSN\224	118	1294	MXI12-13\M47IBWSN\823
38	1293	MXI12-13\M47IBWSN\811	119	6210	MXI12-13\M24ISEPTON\71

39	2115	MXI12-13\M25HRWSN\1141	120	2133	MXI12-13\M25HRWSN\1169
40	2108	MXI12-13\M25HRWSN\1129	121	2113	MXI12-13\M25HRWSN\1137
41	1015	MXI12-13\M47IBWSN/25	122	1033	MXI12-13\M47IBWSN\73
42	1185	MXI12-13\M47IBWSN\517	123	70	AON
43	2058	MXI12-13\M25HRWSN\1074	124	1029	MXI12-13\M47IBWSN\64
44	6237	MXI12-13\M24ISEPTON\2	125	2121	MXI12-13\M25HRWSN\1147
45	4	AON	126	2011	MXI12-13\M25HRWSN\1008
46	1099	MXI12-13\M47IBWSN/220	127	1041	MXI12-13\M47IBWSN\95
47	6215	MXI12-13\M24ISEPTON\4	128	60	AON
48	1101	MXI12-13\M47IBWSN/221	129	6206	MXI12-13\M24ISEPTON\55
49	3	AON	130	1035	MXI12-13\M47IBWSN\78
50	6209	MXI12-13\M24ISEPTON\31	131	1236	MXI12-13\M47IBWSN\644
51	7	Adap	132	6202	MXI12-13\M24ISEPTON\12
52	82	AON	133	6246	MXI12-13\M24ISEPTON\16
53	1143	MXI12-13\M47IBWSN\345	134	2126	MXI12-13\M25HRWSN\1154
54	1030	MXI12-13\M47IBWSN\69	135	2125	MXI12-13\M25HRWSN\1152
55	95	AON	136	39	K6295-4A
56	62	AON	137	2117	MXI12-13\M25HRWSN\1144
57	6226	MXI12-13\M24ISEPTON\34	138	77	AON
58	6245	MXI12-13\M24ISEPTON\88	139	84	AON
59	66	AON	140	6238	MXI12-13\M24ISEPTON\58
60	1093	MXI12-13\M47IBWSN\196	141	2023	MXI12-13\M25HRWSN\1023
61	6213	MXI12-13\M24ISEPTON\18	142	72	AON
62	6224	MXI12-13\M24ISEPTON\99	143	2059	MXI12-13\M25HRWSN\1075
63	2107	MXI12-13\M25HRWSN\1128	144	55	AON
64	6227	MXI12-13\M24ISEPTON\65	145	12	AON
65	69	AON	146	31	AON
66	2033	MXI12-13\M25HRWSN\1040	147	1042	MXI12-13\M47IBWSN\96
67	6234	MXI12-13\M24ISEPTON\92	148	1172	MXI12-13\M47IBWSN\470
68	1162	MXI12-13\M47IBWSN\418	149	6222	\\0
69	2012	MXI12-13\M25HRWSN\1009	150	4	Adap
70	1241	MXI12-13\M47IBWSN\653	151	1037	MXI12-13\M47IBWSN\82
71	6243	MXI12-13\M24ISEPTON\69	152	2103	MXI12-13\M25HRWSN\1122
72	16	AON	153	79	AON
73	2134	MXI12-13\M25HRWSN\1170	154	6232	MXI12-13\M24ISEPTON\33
74	6225	MXI12-13\M24ISEPTON\83	155	44	K6290-Bulk
75	2013	MXI12-13\M25HRWSN\1011	156	89	AON
76	6204	MXI12-13\M24ISEPTON\86	157	83	AON
77	6244	MXI12-13\M24ISEPTON\70	158	1104	MXI12-13\M47IBWSN\225
78	6212	MXI12-13\M24ISEPTON\101	159	6236	MXI12-13\M24ISEPTON\50
79	74	AON	160	1032	MXI12-13\M47IBWSN\72
80	6231	MXI12-13\M24ISEPTON\23	161	6233	MXI12-13\M24ISEPTON\78
81	1036	MXI12-13\M47IBWSN\81			

Source: CIMMYT – The International Maize and Wheat Improvement Center

Table 2. List and description of bread wheat genotypes (released and candidate varieties) used in the experiment

Sr No	Genotypes	Breeding Center	Year of release	Adaptation area (altitude, m asl)
1	Danda'a	EAIR/KARC	2010	2000-2600
2	ET-13A2	EAIR/KARC	1981	2200-2900
3	Alidoro	EAIR/HARC	2007	2200-2900
4	Huluka	EAIR/KARC	2011	2200-2600
5	Hoggana	EAIR/KARC	2011	2200-2800
6	Sofumar	OARI/SARC	1999/00	2300-2800
7	King bird	EAIR/KARC	2015	_
8	Maddawalabu	OARI/SARC	1999/00	1900-2800
9	Merero	OARI/SARC	-	-
10	Bika	EAIR/KARC	2014	_
11	Pavon-76	EAIR/KARC	1982	750-2500
12	Acc//23	EAIR/KARC	NR	
13	Acc//24	EAIR/KARC	NR	
14	Acc//15	EAIR/KARC	NR	
15	Acc//25	EAIR/KARC	NR	
16	Acc//27	EAIR/KARC	NR	
17	Acc//255	OARI/SARC	NR	
18	Acc//9	OARI/SARC	NR	
19	Acc//12	EAIR/KARC	NR	

N.t: Acc= Accession, HARC= Holeta Agricultural Research Center, KARC= Kulumsa Agricultural Research Center, NR= Not released, SARC= Sinana Agricultural Research Center.

Results and discussion

Analysis of variance

The results of analysis of variance of 13 characters for 180 genotypes studied are presented in Table 3. The analysis result of the mean squares of the traits in the present study revealed that there is highly significant difference ($p \le 0.01$) among the tested genotypes. It indicates the presence of adequate variability among the genotypes for all the traits studied. Similarly, Kifle et al. (2016), Mesele et al. (2016), Birahanu et al. (2016) and Obsa et al. (2016) also reported the existence of an enormous amount of genetic variability for phonological, yield and associated characters. On the contrary to the present finding, Khan (2013) established non-significant differences among bread wheat genotypes for phonological, yield and associated characters. This disparity may be due to the differences in genotype and environments used by the authors. The significant differences among bread wheat genotypes under investigation indicate the presence of genetic variability in the material used and provide a good opportunity for yield improvement.

Table 3. Mean square from analysis of variance for 12 quantitative traits of 180 bread wheat genotypes evaluated at Gedo

Traits	Rep	Block	Msg	Erorr (A.lattice)	Error (RCBD)	CV (A.lattic)	CV (RCBD)	Efficiency (A. lattice over RCBD, %)
Days to heading	0.7	1.1	41.5**	1.2	1.2	1.6	3.5	108.9
Days to flowering	4.6	1.2	31**	0.9	1.2	12.5	25.0	136.0
Grain filling period	0.5	1.0	25.75	1.0	0.9	1.9	2.5	128.6
Days to maturity	9.4	0.4	4.8**	0.7	0.6	0.6	0.6	99.9
Plant height	28.8	44.3	83.5**	31.9	33.9	6.6	6.8	106.3
Spike length	1.1	0.4	1.4**	0.4	0.4	7.3	7.4	101.6
No of effective tillers	2.1	0.4	0.8**	0.4	0.4	18.0	18.1	101.6
No of spikelets/spike	5.3	1.6	2.7**	1.4	1.4	6.7	6.8	102.6
Thousand seed weight	51.8	120.1	95.4*	69.6	77.9	12.0	12.7	111.8
Harvest index	0.03	0.1	0.02**	0.0	0.0	24.7	25.1	103.2
No of kernels/ spike	4.8	3.6	81.3**	8.4	7.6	4.4	4.2	90.6
No of kernels /spikelet	2.4	0.1	0.2**	0.1	0.1	8.9	8.9	100.7
Grain yield	79767.5	276054.6	170082.1**	59744.0	66549.8	18.9	19.9	111.6

N.t: *= significance difference, **= highly significance difference, Msg= mean of square for genotypes, A. lat= alpha lattice

Estimation of variance components

Estimation of phenotypic and genotypic parameters: The present study revealed that phenotypic coefficient of variability (PCV) values ranged from 1.6 (days to maturity) to 34.53% (grain yield), whereas the genotypic coefficient of variability (GCV) ranged from 1.5 (days to maturity) to 28.92% (grain yield) (Table 4). The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for grain yield and number of productive tillers. Similarly, high PCV and GCV values for

grain yield and number of tillers were also found by Kifle et al. (2016) and Dergicho et al. (2016). Relatively moderate PCV and GCV values were recorded for spike length, kernels per spike, kernels per spikelet and thousnad kernel weight, whereas traits with low PVC and GCV values were obtained for days to heading, days to maturity and days to flowering. Similarly, Abdul et al. (2017) reported low PVC and GCV values for the characters of days to flowering, days to heading and days to maturity. This implied that selection is not efficient for such traits.

Table 4. Variance parameters, heritability and genetic advance for 12 major quantitative traits of 180 bread wheat genotypes evaluated at Gedo, Western Oromia

Characters	Mean	Range	δ2e	δ2g	δ2p	GCV	PCV	H, %	GA%	GA
Days to heading	68.8	59.5-96	1.2	40.9	42.2	9.3	9.4	97.1	13.0	18.8
Days to flowering	76.3	65-87	0.9	30.6	31.4	7.4	7.5	97.2	11.2	14.7
Grain filling period	64.6	52-74	1.2	40.9	42.2	9.3	9.4	97.1	13.0	20.1
Days to maturity	139.1	135-143	0.7	4.6	5.2	1.5	1.6	87.3	4.6	3.3
Plant height	85.4	49.7-115.6	31.9	67.6	99.5	9.6	11.7	68.0	19.9	23.3
Panicle length	8.4	5.2-14.1	0.4	1.2	1.6	13.3	15.1	76.6	2.5	30.2
No of productive tillers	3.5	2-5.8	0.4	0.6	1.0	22.9	29.1	61.8	2.0	58.1
No of spikelets per spike	17.6	14.9-21	1.4	2.1	3.5	8.2	10.6	60.0	3.7	21.1
1000-kernel weight	69.7	40.7-90	69.6	60.6	130.3	11.2	16.4	46.5	22.8	32.7
Harvest index	0.3	0.11-0.67	0.0	0.0	0.0	34.9	42.7	66.6	0.3	86.0
Grain per head	65.2	43.8-79.7	8.4	77.1	85.5	13.5	14.2	90.2	18.5	28.3
Kernels per spike	3.8	2.8-4.6	0.1	0.2	0.3	11.3	14.4	61.9	1.1	28.7
Yield (kg/ha)	4099.2	1830-6745	5974.	14560.7	19604.7	28.9	34.5	70.1	2824.9	68.9

N.t: δ2e= Environmental variance, δ2g= Genotypic variance, δ2p= Phenotypic variance, GCV= Genotypic coefficient of variation, PCV= phenotypic coefficient of variance, H= Broad sense heritability, GA = genetic advance, GA%= Genetic advance as percentage of mean.

In general, phenotypic coefficient of variation value was relatively greater than genotypic coefficient of variation value although the differences were small. Narrower difference between the values of GCV and PCV indicated that the environmental effect was small for the expression of these characters and these traits are governed by additive gene action. The results obtained were in agreement with the results for yield and its contributing characters reported by Chethana and Rudranaik (2017).

Heritability

According to Singh (2001) heritability of a character is very high if 80% or more, moderate if ranging from 40-80%, but low heritability for a character with less than 40%. In the present study heritability estimated ranged from 46.5 to 97.2%, showing the traits are grouped into moderate and high (Table 4). High heritability was recorded for days to heading, days to flowering, days to grain filling, days to maturity and number of kernels per spike. These traits which exhibited high heritability suggested improvement through selection could be fairly easy and successful because there would be a close correspondence between genotype and phenotype due to a relatively smaller contribution of environment to phenotype. Similar findings in wheat have also been reported by Zakirullah et al. (2017). Plant height, spike length, number of productive tillers, grain yield, harvest index and number of kernels per

spike show moderate heritability value (40-80%). In harmony to this investigation, Mesele et al. (2016) also reported moderate heritability estimates for harvest index and spike length.

Estimates of genetic advance

Genetic advance expressed as a percentage of the mean ranged from 3.3% for days to maturity to 68.9% for grain yield (Table 4). Deshmukh et al. (1986) classified genetic advance as low (0-10%), medium (10-20%) and high (≥20%). Based on classification, high genetic advance as percentage of mean (GA%) was observed for grain yield, productive tillers, number of kernels per spikelet, number of kernels per spike, Thousand-kernels weight, spikelet per spike and plant height (Table 4). This result is in agreement with Kifle et al. (2016) who reported that the highest genetic advance as percentage of mean was recorded for grain yield, spikes per plant, productive tillers per plant. Moderate genetic advance as percentage of mean was computed for days to heading and days to flowering. However, very low (3.3%) genetic advance was observed for days to maturity. This implied that the variations in these traits were mostly environmental, leading to low expected genetic gains from selection. The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action, whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1993).

The importance of considering both the genetic advance and heritability of traits rather than considering separately in determining how much progress can be made through selection was suggested (Johnson et al., 1955). In this study, high heritability accompanied by high genetic advance was observed for grain yield followed by number of productive tillers. This indicated that these traits were highly heritable and selection of high performing genotypes is possible to the improvement of the characters. Most likely the heritability of these traits is due to additive gene effects and selection may be effective in early generations for these characters (Ali et al., 2013). Likewise, Salman et al. (2014) reported high and intermediate heritability and genetic advance for plant height, spike length, productive tillers per plant, number of spikelets per spike, thousand seed weight, and harvest index, number of kernels per spikelet and grain yield (Table 4). High heritability associated with low genetic advance was exhibited for days to maturity. This could be because of predominance of non-additive gene action in the expression of this character.

Correlation coefficient analysis

Genotypic and phenotypic correlation coefficients of grain yield with other characters: The correlation coefficient analysis revealed that grain yield had positive and highly significant (p≤0.01) association with plant height, number of productive tillers, number of spikelets per spike and number of kernels per spike at genotypic level (Table 5). Also, it had positive and significant (p≤0.05) correlation with thousand kernels-weight. This result is in agreement with the finding of Kifle et al. (2016). This shows that those traits are the key contributors for grain yield and need more emphasis on these component characters for increasing the grain yield in the genotypes. Conversely, grain yield negatively correlated with days to heading at genotypic level. Number of productive tillers showed positive and highly significant (p≤0.01) association with spikelet per spike and plant height at genotypic level. Days to heading had positive and highly significant association with days to maturity and moderate association with plant height, spike length, number of spikelets per spike, number of kernels per spike at genotypic level, showing genotypes that were reached early at heading had better chance to mature early without affecting most growth traits except those that had shown negative correlation with days to heading such as productive tillers per plants, thousand kernels weight, and grain yield. Similar results were also reported by Degewione et al. (2013), Kumar et al. (2013) and Chimdessa et al. (2014), but contradicting the finding that was reported by Kumar et al. (2010). Days to maturity exhibited negative and weak genotypic correlation with spike length and thousand seed weight but the remaining traits were positively associated with days to maturity.

Table 5. Genotypic correlation coefficients (rg) between grain yield and yield related traits for wheat genotypes

Characters	DTH	DTF	DTM	PHT	SL	NPT	SkPs	TSW	KPS	KPSk	Gy/ha
DTH	1										
DTF	0.07	1									
DTM	0.394**	0.055	1								
PHT	0.112	-0.045	0.046	1							
SL	0.113	-0.083	-0.017	0.208**	1						
NPT	-0.019	-0.042	0.064	0.217**	0.063	1					
SkPs	0.002	0.033	0.112	0.037	0.116	0.263**	1				
TSW	-0.136	0.022	-0.0004	-0.058	-0.025	0.099	0.046	1			
KPS	0.052	-0.044	0.072	0.072	0.106	0.04	0.103	0.075	1		
KPSk	0.075	0.031	0.097	0.193**	-0.032	0.005	0.019	-0.119	-0.042	1	
Gy/ha	-0.031	0.014	0.143	0.316**	0.087	0.378**	0.382**	0.166*	0.273**	0.061	1

N.t: DTH= Days to heading, DTF= Days to flowering, DTM= Days to maturity, PHT= plant height, SL= Spike length, NPT=Number of productive tillers, SkPs= Number of spikelets per spike, TSW= Thousand seed weight, KPS= Number of kernels per spike, KPSk= Number of kernels per spikelet, Gyha^{-1}=Grain yield per hectare, **= highly siginificant difference, *= siginificant difference.

The analysis revealed that grain yield phenotypically had positive and highly significant (p≤0.01) association with number of productive tillers, number of spikelets per spike, number of kernels per spike and kernels per spikelet. Besides, thousand kernel weight, plant height and days to maturity showed positive and significant (p≤0.05) association with grain yield at phenotypic level (Table 6). Similar findings were also reported by Waleed (2014), Chimdessa et al. (2014) and Kifle et al. (2016). This suggested that improvement of these traits would contribute for increment of grain yield. In contrast, days to heading and days to flowering negatively correlated with grain yield at phenotypic level. Days to maturity had positive and highly significant (p≤0.01) association with days to heading and positive and significant (p≤0.05) association with days to flowering. The result justifies that early heading genotypes had a possibility to mature early. The results obtained confirm the results reported by Degewione et al. (2013) and Kumar et al. (2013), but are opposite to those established by Kumar et al. (2010).

Table 6. Phenotypic correlation coefficients (rp) between grain yield and yield related traits for wheat genotypes

Characters	DTH	DTF	DTM	PHT	SL	NPT	SkPs	TSW	KPS	KPSk	Gy/ha
DTH	1										
DTF	0.05	1									
DTM	0.377**	0.18*	1								
PHT	0.095	-0.003	0.053	1							
SL	0.101	-0.058	0.028	0.195**	1						
NPT	-0.026	-0.024	0.019	0.177**	0.001	1					
SkPs	0.001	0.011	0.077	0.051	0.076	0.294**	1				
TSW	-0.102	0.039	0.028	-0.028	-0.004	0.042	0.049	1			
KPS	0.043	-0.032	0.056	0.072	0.088	0.052	0.107	0.046	1		
KPSk	0.066	0.017	0.065	0.13162	0.109	-0.004	0.013	0.109	-0.04	1	
Gy/ha	-0.042	-0.004	0.136*	0.267**	0.093	0.358**	0.392**	0.116*	0.245**	0.034	1

N.t: DTH= Days to heading, DTF= Days to flowering, DTM= Days to maturity, PHT= plant height, SL= Spike length, NPT=Number of productive tillers, SkPs= Number of spikelets per spike, TSW= Thousand seed weight, KPS= Number of kernels per spike, KPSk= Number of kernels per spikelet, Gyha^{-1}=Grain yield per hectare, **= highly siginificant difference, *= siginificant difference.

Path coefficient analysis

Direct and indirect effects of various characters on grain yield at genotypic level: The results of path coefficient analysis at genotypic level (Table 7) revealed that grain yield was directly and strongly affected by date of maturity, plant height, and spike length, days to flowering and kernel per spike with positive magnitude. However, spikelets per spike, thousand kernels weight had negative and strong influence in disfavoring grain yield. Days to maturity had the highest positive direct effect on grain yield. Chimdessa et al. (2014) also found that days to maturity had positive and direct effect on yield. Indirectly, days to maturity had positive effect on grain yield via plant height, thousand kernels weight and number of kernels per spike. Plant height had significant and positively affected grain yield. Similar result was also reported by Khan et al. (2013). Plant height had also positive indirect effect on grain yield through days to maturity, spike length, thousand kernels weight and number of kernels per spike, whereas number of productive tillers per plant, number of spikelets per spike, days to heading and days to flowering had negative influence on grain yield indirectly via plant height.

Table 7. Genotypic path coefficients of direct (main diagonal) and indirect effects of the 9 bread wheat characters

Characters	DTH	DTF	DTM	PHT	SL	SkPs	TSW	KPS	KPSk	rg
DTH	**0.04173**	0.0021	0.0065	0.0061	0.0054	0.0000	0.0078	0.0013	0.0009	-0.031
DTF	-0.0296	**0.00297**	0.0005	-0.0005	-0.0040	-0.0003	-0.0013	-0.0011	0.0004	0.014
DTM	-0.0168	0.0017	**0.0170**	0.0006	-0.0008	-0.0011	0.0000	0.0018	0.0012	0.143*
PHT	-0.0048	-0.0004	0.0008	**0.00546**	0.0010	-0.0004	0.0034	0.0018	0.0024	0.316**
SL	-0.0044	-0.0005	-0.0030	0.0014	**0.00478**	-0.0011	0.0015	0.0026	-0.0004	0.087
SkPs	-0.0009	0.0010	-0.0019	0.0021	0.0006	**-0.0098**	-0.0027	0.0025	0.0002	0.382**
TSW	0.0059	0.0007	-0.0001	-0.0032	-0.0002	-0.0005	**-0.00572**	0.0018	-0.0015	0.166*
KPS	-0.0021	-0.0013	-0.0013	0.0004	0.0051	-0.0010	-0.0043	**0.00244**	-0.0005	0.273**
SPSk	-0.0034	0.0009	0.0016	0.0016	-0.0005	-0.0002	0.0068	-0.0010	**0.00126**	0.061

N.t: DTH= Days to heading, DTF= Days to flowering, DTM= Days to maturity, PHT= plant height, SL= Spike length, SkPs= Number of spikelets per spike, TSW= Thousand seed weight, KPS= Kernels per spike, KPSk= Number of kernels per spikelet, rg= Genotypic correlation.

Direct and indirect effects of various characters on grain yield at phenotypic level: The results of path coefficient analysis at phenotypic level (Table 8) revealed that thousand kernels weight exerted the highest positive direct effect on grain yield followed by maturity. A similar result was reported by Mesele et al. (2016). This justifies that direct selection through these characters could result in reasonable improvement on grain yield. Indirectly, thousand kernels weight can affect grain yield positively via management of days to maturity, days to flowering, days to heading, number of spikelets per spike and thousnad kernels weight, whereas it is negatively influenced by plant height. Similarly, maturity had positive improvement on grain yield via days to heading, days to maturity, plant height, spike length, thousand grain weight, and number of kernels per spike while, indirect and negatively influenced through days to heading and tillers per plant.

Besides, plant height, spike length and number of kernels per spike exerted positive direct influence on grain yield (Table 8). Spike length had moderate positive and non-significant correlation with grain yield, showing non-significant contribution for improvement of yield through selection. The result showed number of kernels per spike significantly correlated with grain yield and also had positive direct effect on yield. Indirectly, kernels per spike can positively influence grain yield via days to maturity, plant height negatively influences days to flowering and days to heading.

Table 8. Phenotypic path coefficients of direct (main diagonal) and indirect effects of the 13 bread wheat characters

Characters	DTH	DTF	DTM	PHT	SL	SpKs	TSW	KPS	KPSk	rg
DTH	**-0.0532**	0.0013	0.0076	0.0049	0.0045	0.0000	-0.0045	0.0013	0.0012	-0.0422
DTF	-0.0270	**0.00254**	0.0080	-0.0002	-0.0026	0.0001	-0.0001	-0.0010	0.0003	-0.004
DTM	-0.0205	0.0010	**0.02108**	0.0027	0.0012	0.0005	0.0001	0.0017	0.0012	0.136*
PHT	-0.0056	-0.0001	0.0013	**0.00513**	0.0087	0.0003	0.0022	0.0022	0.0025	0.267**
SL	-0.0053	-0.0015	0.0059	0.0010	**0.00445**	0.0005	0.0000	0.0027	-0.0006	0.093
SpKs	-0.0006	0.0003	0.0014	0.0026	0.0034	**0.0066**	0.0097	0.0033	0.0002	0.392**
TSW	0.0057	0.0010	0.0006	-0.0015	-0.0002	0.0003	**0.11675**	0.0014	-0.0020	0.116*
KPS	-0.0034	-0.0008	0.0018	0.0003	0.0039	0.0007	0.0054	**0.00305**	-0.0008	0.245**
KPSk	-0.0030	0.0004	0.0018	0.0068	-0.0005	0.0087	0.0042	-0.0012	**0.00187**	0.034

N.t: DTH= Days to heading, DTF= Days to flowering, DTM= Days to maturity, PHT= plant height, SL= Spike length, SkPs= Number of spikelets per spike, TSW= Thousand seed weight, KPS= Kernels per spike, KPSk= Number of kernels per spikelet, rg= Genotypic correlation.

Clustering analysis

The D-square values based on the pooled mean of genotypes resulted in classifying the 180 bread wheat genotypes into ten distinct clusters (Table 9). The genotypes were clustered in such a way that 83 genotypes (46.1%) were grouped into cluster I, 43 genotypes (23.8%) into cluster II, 12 genotypes (6.6%) into cluster III, 13 genotypes (7.2%) into cluster IV, 5 genotypes (2.7%) into cluster V, 13 genotypes (7.2%) into cluster VI, 6 genotypes (3.3%) into cluster VII, 3 genotypes (1.7%) into cluster VIII, 1 genotype (0.6%) into cluster IX and 1 genotype (0.6%) into cluster X. The distribution pattern of genotypes showed that cluster I had maximum number of genotypes (83) followed by cluster II (43), whereas cluster IX and X had the minimum number of genotypes with having the same value of 1 genotype (Table 9).

Table 9. Clustering pattern of 180 genotypes of wheat based on Mahalanobis' D^2-values and the member present in each respective cluster

Cluster	NoG*	Genotype/Accession										
I	83	270	1279	25	6244	85	6212	6207	72	1036	27	1033	1032
		6216	73	71	6208	1037	6218	444	1042	2023	6217	77	160
		1241	2113	2126	1096	1236	2012	2133	2034	6229	2033	6243	6204
		1141	35	1093	6232	1041	1179	87	2104	52	1295	20	2132
		2122	1242	44	2103	2107	6202	6222	70	69	1299	60	1108
		86	6220	22	6225	6236	1087	2013	6213	39	2134	6221	6231
		61	2014	6219	6242	6203	31	2	41	2117	55	1089	
II	43	1172	6246	1092	2121	1035	1097	33	6228	83	1104	40	1162
		45	94	79	120	6	6211	6223	6234	6214	6235	16	2011
		2010	2059	6230	5	6205	34	1029	1034	2136	1294	2131	250
		1102	6210	2125	84	2135	6224	2042					
III	12	1103	6240	47	1099	23	2058	2115	6226	1265	2123	4	2108
IV	13	1185	6237	15	2082	3	1293	1143	12	58	7	82	1143
		9											
V	5	80	6239	2083	1161	74							
VI	13	17	6238	66	6227	63	1015	6241	89	6206	67	6201	6233
		2114											
VII	6	1030	6209	95	1178	6245	1104						
VIII	3	24	6215	1101									
IX	1	51											
X	1	2105											

*Number of Genotypes

Genetic distance analysis

The analysis for inter cluster distance revealed that the maximum distance was recorded between Cluster IV and IX (34633.04) followed by between Cluster IV and VIII (30955.7) and followed by between Cluster II and IV (26880.8) implying that these clusters are genetically more divergent from each other (Table 10). The maximum inter cluster distance, the large magnitude of genetic variability among genotypes and thus the better probability to create wider genetic bases through hybridization. The more diversity of parents, the greater chance of obtaining high heterosis (Zaman et al., 2005). Hence, crossing of genotypes between Cluster IV and IX produce wide range of variability and high heterotic expression in F2 generation for parameters: grain yield, kernels per spikelet, harvest index, effective tillers per plant, spike length. Crossing between cluster IV and IX can be used

to create wider range of variability in the F2 progenies for biological yield and grain yield. Minimum inter cluster distance was observed between Cluster III and Cluster V (2144.7) followed by between Cluster III and VI (2192.3) and between Cluster I and VI (3389.50) indicating that genotypes of these two clusters were relatively less diverse. Thus, crossing of genotypes from these two clusters will produce progenies with less amount of heterotic expression in the F1's and narrow range of variability in subsequent segregating (F2) populations.

Table 10. Average intra (bold) and inter cluster (off diagonal) D2 values among ten clusters in bread wheat genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	.	9786.3	5543.6	18171.3	7688.2	3389.5	3652.5	13986.2	17792.8	7074.4
II		.	15185.8	26880.8	17300.8	13129.4	6213.2	4330.9	8160.7	2953.6
III			.	13674.3	2144.7	2192.3	8973.3	19454.9	23278.3	12585.3
IV				.	12167.9	15348.7	21161.2	30955.5	34633.5	24508.9
V					.	4324.8	11091.7	21581.2	25408.8	14724.68
VI						.	6930.1	17361.5	21174.8	10460.9
VII							.	10493.8	14324.6	3756.87
VIII								.	3834.8	6930.0
IX									.	10721.1
X										.

Conclusion

In the present study a significant variability was noted among bread wheat genotypes for most of the traits and there are opportunities for the genetic gain through selection or hybridization. Heritability in broad sense and genetic advance as percentage of the mean (GAM) were relatively higher for number of kernels per spike and grain filling period, indicating there are additive gene effects and selection may be effective for these traits. Grain yield had positive and highly significant correlation with number of productive tillers, number of kernel per spike and plant height at genotypic and phenotypic levels. The path coefficient analysis result revealed that spike length, plant height and number of kernels per spike had positive direct effect on grain yield on genotypic and phenotypic levels. Divergence analysis (D^2) grouped the total test germplasm into 10 clusters. The highest average inter cluster distance was recorded between Cluster IV and IX followed by between Cluster IV and VIII, and thus the possibility to develop segregating populations upon the crossing of widely related genotypes in those clusters. The information obtained from the study is useful for plant breeders in constructing their breeding materials and implementing breeding strategies with the aim of further improving the yield and associated traits.

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