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Evaluating Yield Performance and Morpho-agronomic Characters of Landraces and Released Varieties of selected Bread Wheat (*Triticum aestivum L.*) Genotypes at Bale Zone, Agarfa Woreda, Oromia Region, Ethiopia

ABSTRACT

Bread Wheat (*Triticum aestivum L.*) is an annual cereal crops belonging to the family *Poaceae* Sixteen bread wheat varieties (8 of them farmers varieties and 8 of them improved varieties) were tested to compare yield performance, genetic variability, association among the traits on the grain yield. The genotypes were grown in Randomized complete block design at Goro and Agarfa community seed bank in 2017/18. Analysis of variance revealed that there were highly significant differences among the genotypes for most of the traits at individual and across locations. From the combined analysis of variance, significant (p≤0.05) effect due to location, varieties and G×E was observed for most of the traits. The varieties showed wider variability in mean grain yield of 666.67--4000 kg ha-1, 1333.33--8333.33 kg ha-1 and 666.67 – 8333.33 at Goro, Agarfa and across location, respectively. PCV was higher than the genotypic coefficients of variation (GCV) in most of the traits. At Agarfa GCV ranged from 0.34% (aboveground biomass) to 689% (kernel number per spike), whereas PCV ranged from 0.4% (days to tillering) to 790% (kernel number per spike).At Goro GCV ranged from 2.23% (kernel number per spike) to 29.9% (grain yield), whereas PCV ranged from 2.6% (kernel number per spike) to 36.2% (grain yield). Phenotypic coefficient of variability ranged from 11.54% (day to emergence) to 70.28% (grain yield). Genotypic coefficient of variability ranged from 7.4% (days to emergence) to 46.13% (plant height).Highest heritability estimates were recorded (>80%) for the characters; days to heading (89.8%) and spikes length (82.9%),kernel per spike (87.2%),1000 seed weight(83.8%) and harvest index(348.9%) at Agarfa and plant height(95.7%), and spikes length (91.1%),at Goro. Similarly, the result from combined analysis indicated that Phenotypic coefficient of variability ranged from 11.54% (day to emergence) to 70.28% (grain yield). Genotypic coefficient t of variability ranged from 7.4% (days to emergence) to 46.13% (plant height). The expected genetic advance as the percent of means expressed as a percentage of the mean ranged from 0.72% for above ground biomass to 264.8% for 1000 kernel weight at Agarfa and at Goro the expected genetic advance expressed as a percentage of the mean ranged from 0.95% for spike length to 49.14% for grain yield. Grain yield

showed significant (p≤0.01) positive phenotypic correlations with thousand kernels weight, above ground biomass, harvest index and plant height at each location. Similarly, significant (p≤0.01) positive and negative phenotypic and genotypic correlations between the yield components were observed at each location. The highest grain yield was recorded in Bokate variety (80.01kunt/hect and the lowest grain yield was recorded in Ayuba variety (16.67kunt/hect) from farmers varieties, while Hidase variety (61.67 kunt/hect) and Ejerso variety (35.01 kunt/hect) the highest and lowest grain yield from improved varieties at Agarfa location. In Goro the highest grain yield was recorded in Tikur goshmber variety (33.34kunt/hect and the lowest grain yield was recorded in Tate variety (11.67kunt/hect) from farmer's varieties, while Kekeba variety (39.01kunt/hect) and Digalu variety (10.01 kunt/hect) the highest and lowest grain yield from improved varieties. Generally, it has been observed the presence of variability among the genotypes, heritability and relationships in the tested traits of the genotypes studied. Hence, Selection and hybridization on farmers and released varieties based on the trait with high GCV, heritability, genetic advance, positive correlation coefficient and high grain yield can be recommended for farther yield improvement of bread wheat at respective location.

Key words: Heritability, Genetic Advance, correlation, Grain yield, farmers' varieties, improved varieties.

1. INTRODUCTION

Bread Wheat (*Triticum aestivum* L.) is an annual cereal crops belonging to the family *Poaceae*. Tribe Triticeae that adapted to cool moist climate with moderate temperature. Wheat are the universal cereals of old world agriculture and the world foremost crops plant (Feldman *et al.*, 1995), followed by rice and corn. It is the most widely cultivated food crop and is the stable food in more than 40 countries and for over 35% of the global population. Wheat and barley constituted the principal grain stock upon which old world agriculture was founded. These were among the earliest domesticated crop plants, 10,000 years ago (Valdes *et al*., 1997).

The tribe Triciceae is economically the most important group of the family Gramineae.It has given rise to cultivated wheat, barley, ayes oats and number of important range grasses. Hybridization among genera within the tribe has allowed the exchange of genetic material and given rise to polyploidy in the form of amphiploidy. The wheat (genus *Triticum*) comprise a series of diploid, tetraploid and hexaploid forms, the polyploidy having arisen by amphiploidy between Triticum species and diploid species o the genus Aegilops (Miller,1987).

Modern wheat cultivars belong primarily to two specie (1) hexaploid bread wheat, Triticum aestivum (2n=42 chromosomes), and (2) tetraploid, hard or durum type wheat, T. turgidum (2n =28) used for macaroni and low rising bread wheat, are almost fully self pollinated; hence genetic diversity is represented in the wild by numerous clones and in cultivation by some 25,000 different cultivars. Cultivated primitive wheat forms have hulled grains, whereas advanced cultivars wheat is free threshing (Patrick ,1972)

Today, wheat ranks first in the world's grain production and account for more than 20% of the total food calories and protein in human nutrition .Wheat are now extensively grown across the temperate, Mediterranean and subtropical parts of both hemispheres of world, from 67^0N in Norway, Finland and Russia to 45 ^{0}S in Argentina. However, in subtropics and tropics, the cultivation of wheat is restricted to higher elevations (Vander ,2011)

In Ethiopia, tetraploid (2n = 4x = 28) wheat have been under cultivation since ancient times

and the country is considered as the center of genetic diversity for these wheat (Vavilov 1997; Worede , 1997). Agriculture in Ethiopia is pre- dominantly traditional and thus mainly landraces are grown. This is mainly attributed to problems of adaptability and stability of improved varieties to the adverse farming conditions that prevail on small peasant farms and also due to the unavailability of seeds of improved varieties to farmers in sufficient quantity (Tessema and Bechere 1998). Brown (1978) described landraces as geographically or ecologically distinctive populations, which are conspicuously diverse in their genetic composition both among populations (i.e., among landraces) and within them. Harlan (1975) indicated that landraces possess genetic variation for useful quantitative and qualitative characters.

In Ethiopia, grain crops that include cereals, pulses, oilseeds, vegetable, root crops, fruit fibers, stimulants and sugarcane are grown on 16.5 million hectares of land in different agro ecological zones o the countries. Among all crops are the important field crops occupying about 86% of the area planted. Out of 12.6 million hectares of cultivated land by smallholder farmers, major crop production accounts for 11 million hectares or 87.9 % of the total average. Teff (24.3%) ,wheat(13.3%),maize (16.8%) and sorghum (14.6%) refer to the largest shares of the total production area and represent the major crops that are cultivated by the greatest number of smallholders. Wheat production in Ethiopia increases from 10210.22 Qt in 1994/94 to 42315.59 Qt in 2014/15.The yield of wheat increases from 15.57 Qt/ha in 2004/05 to 25.43Qt/ha in 2014/15 (CSA, 2014/15).However, the most important import good in Ethiopia is wheat, which accounts for more than 60% of import volume to fill the consumption gap of the country population (FAOSTAT, 2015).Wheat cultivars are superior to most other cereals in their nutritive value. Besides 60-80% starch, 10-15% protein, Fate 1.54g,dietary fibers 12.2g vitamin 0.8g ,minerals 8.17g water 31.1g selenium 70.7mg and energy 1368KJ (USAD data base, 2015).

In sub-Saharan Africa Ethiopia ranks 3rd next to South Africa interns of total wheat production area and production. According to CSA (2007), wheat in Ethiopia is an important cereal crop and it ranks third in total production next to teff and maize. It is largely grown in the highlands of the country and constitutes roughly 20-30% of the annual cereal production and plays an appreciable role of supplying the production with carbohydrates, protein and minerals (Schthess *et al*., 2000)

In spite of growing wheat in most part of Ethiopia the country is not sufficient in production and consequently a large quantity of bread wheat is imported ever year. The national average of wheat in country, which is 14qt/ha, is 24%, is still below the average of South Africa yield and 48%, below that of the world's (FAO, 2004).This low production and productivity is mainly due to diseases, frost drought, poor soil fertility, lack of adaptability of released variety, lack of packages for landraces and lack of knowledge on the extent of genetic variation (Kahrizi *et al*., 2010)

Several genetic diversity studies have been conducted on different crop species based on quantative and qualitative traits in order to select genetically distant parents for hybridization (Arega *et al.,* 2007).Genetic

variability is an essential prerequisite for crop improvement program for obtaining high yielding varieties. On the other hand, yield is a complex character and is associated with some yield contributing characters. The understanding of association of characters is of prime importance in developing an efficient breeding program. The correlation studies provide information about association between any two characters. The path coefficient analysis provides the partitioning of correlation coefficients into direct and indirect effects giving the relative importance of each of the causal factors (Allard, 1996).

Despite the importance of such investigation and much works done to improve the production and productivity of this crop, but there is no sufficient work has been done regarding landraces for understanding and describing the nature and extent of GCV, PCV, heritability in broad sense, genetic advance, association among yield and yield related traits and product performance of bread wheat varieties developed for south east high land Ethiopia Therefore, this work has been designed with the following objectives:

1.2. General Objective

The general objective of the present study is

- ❖ To evaluate yield performance and morpho-agronomic characters of Bread wheat (*Triticum aestivum L.*) Farmer's varieties in contrast to improved Varieties for on farm conservation for yield and yield related traits.

Specific objectives

- ➢ To estimate morpho-agronomic characters of Bread wheat (*Triticum aestivum L.*) Farmer's varieties in contrast to improved Varieties
- ➢ To compare product performance of bread wheat farmer's varieties in contrast to improved varieties.
- ➢ To assess the extent of association among agronomic characters of Bread wheat farmer's varieties in contrast to improved varieties

2. MATERIALS AND METHODS

2.1. Description of the Study Site

The study was conducted in Oromia regional state, Bale Zone Agarfa and Goro Woredas. Agarfa Community Gene Bank, which is located 457km South East of Addis Ababa .The average annual mean temperature, is 18 ^{0}C & 22 ^{0}C, night and day respectively. The geographic location of Agarfa community seed bank is 8^0 32'32'' N longitudes and $39^0$14'03''E latitude with an elevation of 2460 meters above sea level. The center represents high lands of Bale with average annual rainfall of 850-2000mm. The dominant soil type is black and slightly acidic.

Goro wareda Chafe Mana Community Gene Bank, which was located 487km South East of Addis Ababa .The average annual mean temperature, is 18 ^{0}C & 24 ^{0}C, night and day respectively. The geographic location of Chefe Mana is 77^0 56'25''N longitudes and 65^0 37' 75'' E latitude with an elevation of 2034 masl. The center represents high lands of Bale with average annual rainfall of 700-1560mm. The dominant soil type is brown and slightly acidic.

2.2. Experimental Material

16 bread wheat varieties were used .Out of these 8 of them were farmer's varieties and 8 of them were released varieties. The source of different wheat varieties were SARC and EBI Gene bank and was planted in 2017 main summer season for study. The descriptions of wheat varieties were used in the study are list in table 1 below.

Table1.Description of Released and farmers varieties of Bread Wheat in Ethiopia was used in the Study

No.	Accessions names	Farmers varieties /Released	Source
1	Tate	Farmers varieties	EBI
2	Garando	>>	EBI
3	Tikur goshmber	>>	EBI
4	Nech goshmber	>>	EBI
5	Konte	>>	EBI
6	Bawunde	>>	EBI
7	Bokate	>>	EBI
8	Setakur	>>	EBI
9	Danda'a	Improved varieties	OSE
10	Eerso	>>	OSE
11	Huluka	>>	OSE
12	Sherume	>>	OSE
13	Hidase	>>	OSE
14	Digalu	>>	OSE
15	Kekeba	>>	OSE
16	Ogolcho	>>	OSE
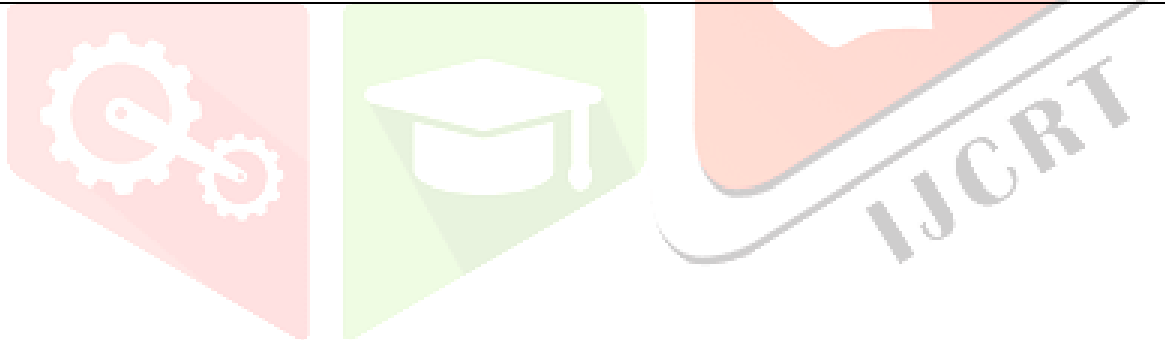
2.3 Experimental Design and Trial Management

The experiment was conducted using Randomized Complete Block Design (RCBD) with two replications. Each plots were consist of six rows of spacing 20cmx 2.5m long. The plot area was $3m^2$(2.5mx1.2m). A1.5m distance is maintained between replications. Four middle rows were harvested, dried, threshed and cleaned for data collection for 12 quantitative characters. Natural fertilizer (compost) was applied at the rate of 20Qt/ha before one week of planting. Seedling was done at rate of 150kg/ha was applied. Seed and natural fertilizer was drill uniformly by hand. Weeding and other agronomic practice was carried out as per recommendations of respective location. Neither herbicides nor insecticides were applied.   .

2.4 Data to be collected

Data on quantities and qualitative was collected either on the plot bases or from four central rows randomly selected plants of wheat genotypes on the following characters.

1. **Plant height (PH)-** the height was measured in cm from the ground level to the top of the plant.
2. **Day to tillering (DT**) - . The days from the date of sowing to the date at which the 50% tillering appears per plots.
3. **Spike length (SL):-** the average length of the longest spike expressed in cm at physiological   maturity from four central rows randomly selected.
4. **Kernel number per spike (KNS**):- the number of kernels were counted for each spike of the four central rows randomly selected
5. **Day to emergence (DE):-** day to emergence was record when 50% of the plant in each   plot emerged out. .
6. **Day to head emergence (DHE):-** The days from the date of sowing to the date at which the first head appears per plots.
7. **Day to physiological maturity (DM**):- was recorded as the day from emergence to maturity when 50% of the plant population per plot have turned yellowish or showed sign of senescence.
8. **Grain yield per plot (GYP) (kg):-** The ratio of grain yield in kilogram per plot.
9.**1000 kernel weight (TKW)**: the weight of 1000 kernel was selected randomly from five plants per Plots.
10. **Above ground Biomass Weight per plant (AGB in kg/m2):-** Whole above ground plant parts on the plant were harvested, sun dried and weighted from four selected rows from each plot. This value again converted to kg hectare.
11. **Harvest index (HI):-** this will be calculated by the following formula:

$$\text{Harvest Index (HI)} = \frac{\text{seed yield per plot(kg)}}{\text{Biomass per plot (kg)}} \times 100\%$$

2.5 Data Analysis Method

The descriptive stastics of each trait was conducted and followed by an analysis of variance (ANOVA).These stastical analysis was performed using appropriate procedures of the SAS soft ware version 9.1 (SAS 9.1 Institute Inc. Cary .NC,USA).

2.6 Statistical procedures

2.6.1 Analysis of variance

Data was collected   and are subjected to analysis of variance using the linear model equation $y_{ij}=$ Ti $+B_i+$ ij , where y_{ij} = the overall mean , T_i = the effect of the ith treatment B_j = the effect of the jth block, and   ij= the random effect associated with the experimental unit assigned to the ith treatment and occurring in the jth plot to determine the differences existing among the 6 wheat genotypes. The variance was analyzed using the standard   procedure applicable to Randomized Complete Block Design (RCBD) as suggested by (Gomez, 1984) using appropriate procedures of the SAS soft ware version 9.1 (SAS 9.1 Institute Inc. Cary .NC,USA).The least significance difference (LSD) was also worked out for mean separation at 1% and 5% probability levels.

Table.2 Analysis of variance

S.V	D.F	Mss	EMS
Replication	r-1	Mr	$\delta^{2e}+\delta 2r$
Genotypes	g-1	Mg	$\delta^2+r\delta^2 g$
Error	(r-1)(g-1)	Me	$\delta^2 e$

Where S.V=source of variation   D.F=degree of freedom , mss=mean sum square, EMS=expected mean square Mr =mean sum square of replication , Mg =mean sum square of genotype , Me = mean sum square of error, $\delta^2 e$ =error variance, $\delta^2 g$ =genotypic variance, r= number of replication

2.6.2 Phenotypic and genotypic variability

The variability present in the population was estimated by simple measures namely range, mean, standard error, phenotypic and genotypic variance coefficient of variations. The phenotypic and genotype according to the methods suggested by Burton and Derane (1953)   as follows:

$\delta^{22p} = \delta^{2}\,^2 g + \delta^{2e}$ where ∂ p = phenotypic variance

$$\partial^2 g = \frac{Mg - me}{r}$$ g= Genotypic variance

me= environmental (error) variance (error mean square)

Ms= Mean sum square of genotype

M<= Mean sum square of error

R= number of replication

Phenotypic coefficient of variation (PCV) $= \frac{\sqrt{2\delta 2}}{x}$ X 100

Genotypic Coefficient of Variation (GCV) $= \frac{\sqrt{\delta 2}}{x}$ 100

Where x =population mean.

2.6.3. Estimates of heritability in broad sense

Heritability was computed for each character based on formula developed by Allard (1960) as.

$$h^2 = \frac{\sqrt{\delta 2}}{\delta 2 \, p} \text{ X } 100 \quad \delta^2$$

Where 2 p= Phenotypic Variance

$\cdot \delta^2$ g= Genotypic Variance

$\delta^{2 \, p} = \partial 2 \, g + \delta^{2 \, e}, \delta^{2 \, e}$ =Environmental (error) variance.

2.6.4. Estimation of expected genetic advance

The genetic advance (GA) for selection intensity (K) at 5% was calculated by formula suggested by Allard (1960) as:

    GA= (K) (δp) (h^2)

Where, GA= Expected genetic advance, δp= the phenotypic standard deviation, h^2 $^=$ the heritability, k=selection differential (K= 2.06 at 5% ^{X} selection intensity).

The genetic advance as percent of mean is calculated as $\frac{GA}{X} X^{100}$ Where , X= population Mean

2.6.5 Correlation analysis

To estimate the correlation it is necessary to calculate the covariance. The covariance was computed from the analysis of covariance table below

Table 3. Analysis of covariance

S.V	D.F	MSP	EMSp
Replication	(r-1)	Mspr	δ exy+g δ rxy
Genotype	(g-1	Mspg	δ exy+r δ gxy
Error	(r-1)(g-1	Mspe	δ exy

where, S.V =source of variation

    D.F =degree of freedom

    Mspg= mean sum products due to genotypes for character   x and y

    Mspe = mean sum product of environment (error) for character   x and y

    Emsp = expected mean sum product

      r= number of replications

COV   exy = Mspg-Mspe

COV   pxy = COV   gxy +COV (exy)

Where, COV (gxy)=genotype covariance between characters   x and y

    COV pxy= phenotypic covariance between characters   x and y,

    COV exy = environmental covariance between x and y

The correlation was estimated using the formal suggested by miller estal (1958).

   where rp= phenotypic correlation coefficient

$$rp = \sqrt{(\delta2px * \delta2py)}$$

   pcov xy = phenotypic covariance b/n character x and y

     px = phenotypic variance for character   x.

$$rg = \frac{P\cos xy}{\sqrt{(\delta2gx * \delta2by}} \quad \text{py = phenotypic variance for character y.}$$

     where ,   rg = Genotypic correlation coefficient

        Gcov x.y = Genotypic covariance between character   x and y

         gx = Genotypic variance for character x

         gy = Genotypic variance for character   y.

The Coefficient of correlation at phenotypic level are tested for their significance by comparing the values of correlation with tabulated r; value at g-2 degree of freedom however, the tested for their significance using the formula described by Robertson (1959) indicated below

$$Z = \frac{rgxy}{SEgxy}$$

Where g= number of accessions

SEgxy= standard error of the genotypic correlation rgxy= Genotypic correlation   rgxy=Genotypic correlation coefficient of x and y calculated t value is compared with the tabulated "Z" value at g-2 degree of freedom at 5% level of significance.

$$SEgxy= \sqrt{\frac{(1-r2gx)2}{2hx.hy}}$$

Where. g= number of genotypes

Hx= heritability of character x

Hy= heritability of character y

3. RESULTS AND DISCUSSION

3.1. Quantitative Characters

3.1.1 Minimum, maximum, and mean values of 12 characters of Field pea.

The minimum, maximum and mean values for 11 characters are showed in Table 4,5 and 6 for Agarfa, Goro, and combined analysis respectively. Wide ranges variations were recorded for most of the Character studied both locations.

The minimum values for days to emergence (6 days) variety sherume and maximum value was recorded by Ejerso variety. Days to tillering (57) and 78 , days of heading 63 and 90 ,days of maturity (107), and 128, plant height 65.6 and 129,spike length7.2 and 12 ,kernel per spike 39.2 and 64.8,grain yield 0.4 and 2.2, 1000 seed weight 30 and 44,above ground biomass 1.4 and 3.5 ,harvest index 26 and 91.6 minimum and maximum values respectively at Agarfa.

In Goro location minimum values for days to emergence (7 days),days to tillering (59 days),days to heading (66) ,days of maturity (112), plant height (73),spike length(6.2),kernel per spike(43.2),1000 kernel weight(24),above ground biomass(1.0),grain yield per plot (0.2kg) and harvest index (20) while variety Bawunde had the maximum values for days to heading(90),days to tillering (78), plant height (129),spike length(12),kernel per spike(64.8) and above ground biomass(85),while variety Bokate had the highest grain yield(2.5kg) at Agarfa .At Goro variety Tikur goshmber had maximum grain yield(1.2kg),above ground biomass(3.0kg)and kernel per spike(80),variety Bawunde had maximum 1000kernel weight(42g),days to tillering (75)and days to heading(80)and variety setakur had maximum spike length (11.6),plant height (150cm),days to maturity (142) and days to emergence(9 days). The result from both location indicated that the landraces varieties were more competent than released varieties. From combined analysis minimum values for days to emergence (6 days),days to tillering (57 days),days to heading (63),days of maturity (107), plant height (65),spike length(6.2),kernel per spike(39.2),1000 kernel weight(24),above ground biomass(1.0),grain yield per plot (0.2) and harvest index (20) similar result were reported by Mistewa (2013) Harvest index (HI) has been used to describe the proportion of harvestable biomass. Current modern wheat varieties have HI of 0.45−0.50 (spring type) and 0.50−0.55 (winter type), approaching its theoretical maximum value (c. 0.64 in winter wheat) (Foulkes et al., 2011; Alamu Dabi.,2016). In this study, harvest index ranged from 0.2 to 0.91 with an average value of 0.45. The score of the variable was lower than its theoretical maximum value (0.64) at both locations.

Grain yield is the final result that can be studied through its yield components. Grain yield varied from 0.4 kg to 2.5 kg (mean of 0.937 kg) The minimum genotype Tate and the maximum genotype Bokate In Goro grain yield varied from 0.2 kg to 1.2 kg (mean of 0.71 kg) The minimum genotype Digalu and the maximum genotype Tikur goshmber The grain yield performance was better at Agarfa than Goro indicating its potential for wheat production.. .Gezahegn et al. (2015) reported a wide variation of grain yield per hectare which ranged from 2115 kg ha-1 (Menze) to 5955 kg ha-1 (Alidoro) in bread wheat.

Table 4. Minimum and Maximum scoring genotypes and Mean values for the 11 character of the 16 bread wheat genotypes evaluated at Agarfa

Characters	Minimum		Maximum		Mean	Variance	SD($\pm$)
	Value	Genotypes	Value	Genotypes			
Days to emergence	6	Sherume	11	Ejerso	7.6	1.04	1.02
Days heading	63	Kekeba	90	Bawunde	73	59.3	7.7
Days tillering	57	Kekeba	78	Bawunde	66.1	44.9	6.7
Days of Maturity	107	Sherume	128	Bokate	117.6	33.6	5.8
Plant Height(cm)	65.6	Tate	129	Bawunde	93.6	193.2	13.9
Spike length(cm)	7.2	Ejerso	12	Bawunde	8.39	10.04	1.02
Kernel per spike(g)	39.2	Ayuba	64.8	Bawunde	51.7	82.8	9.1
Grain Yield per plot(g)	0.4	Ayuba	2.5	Bokate	1.35	0.22	0.47
Thousand Seed Weight(g)	30	Tate	44	Setakkur	36.6	10.9	3.3
Above ground Biomass(g)	1.4	Tikur seregegna	3.5	Bawunde	2.2	0.19	0.44
Harvest index(g)	26	Nech sergegna	85	Sherume	53.6	256	16

SD($\pm$) = Standard deviation

Table 5. Minimum and Maximum scoring genotypes and Mean values for the 11 character of the 16 bread wheat genotypes evaluated at Goro

Characters	Minimum		Maximum		Mean	Variance	SD(±)
	Value	Genotypes	Value	Genotypes			
Days to emergence	7	Kekeba	9	Setakur	7.9	1.04	0.91
Days heading	66	Kekeba	80	Bawunde	72.5	59.3	4.02
Days tillering	59	Kekeba	75	Bawunde	67.8	44.9	4.08
Days of Maturity	112	Huluka	142	Setakur	127.4	33.6	9.75
Plant Height(cm)	73	Tate	150	Setakur	100.7	193.2	22.60
Spike length(cm)	6.2	Digalu	11.6	Setakur	8.39	10.04	1.46
Kernel per spike(g)	43.2	Tate	80	Tikurgoshmber	59.2	82.8	7.98
Grain Yield per plot(g)	0.2	Digalu	1.2	Tikurgoshmber	0.71	0.22	0.25
Thousand Seed Weight(g)	24	Tate	42	Bawunde	36.6	10.9	4.81
Above ground Biomass(g)	1.0	Digalu	3.0	Tikurgoshmber	1.92	0.19	0.56
Harvest index(g)	20	Digalu	50	Kekeba	36.6	256	7.40

SD(±) = Standard deviation

Table 6. Minimum and Maximum scoring genotypes and Mean values for the 11 character of the 16 bread wheat genotypes evaluated at Agarfa and Goro

Characters	Maximum		Minimum		Mean	Variance	SD(±)
	Value	Genotypes	Value	Genotypes			
Days to emergence	11	Ejerso	6	Sherume	7.906	0.91	0.954
Days heading	90	Bawunde	63	Kekeba	66.93	37.33	6.11
Days tillering	78	Bawunde	57	Kekeba	72.7	31.36	5.60
Days of Maturity	142	Setakur	107	Ogolcho	121.4	100.80	10.04
Plant Height(cm)	150	Setakur	65	Tate	97.65	365.57	19.12
Spike length(cm)	12	Bawunde	6.2	Ejerso	9.08	2.04	1.43
Kernel per spike(g)	80	Danda'a	39.2	Ayuba	54.92	90.06	9.49
Grain Yield per plot(g)	2.5	Bokate	0.2	Digalu	1.04	0.190	0.436
Thousand Seed Weight(g)	44	Setakur	24	Tate	37.2	16.89	4.11
Above ground Biomass(g)	3.5	Ejerso	1.0	Digalu	2.034	0.264	0.514
Harvest index(g)	91.6	Ogolcho	20.0	Digalu	45.12	237.77	15.42

SD(±) = Standard deviation

3.2. Analysis of Variance of studied traits

.Wide ranges of variation were recorded for most of the traits studied at Agarfa , Goro and combined analysis of was carried out for 11 characters recorded from ANOVA result. There was a highly significant difference among the genotypes (P<0.01) for traits including days to maturity and plant height in Goro, days to heading, days to tillering and 1000 kernel weight in Agarfa. While days to heading, days to tillering and 1000 kernel weight, grain yield, 1000 kernel weight, spike length and harvest index and above ground biomass in Goro and days to maturity, spike length, kernel per spike, harvest index and above ground biomass in Agarfa have significant genotypic variances. Combined analysis studied at individual locations confirming the genetic variability for yield and its components. Alemu Debi(2016), Obsa (2014) and also reported considerable genetic variability for grain yield and its component characters in studied bread wheat genotypes in Ethiopia. Other authors also reported considerable genetic variability for grain yield and its component characters in durum wheat (Khan.et al. (2013). Gezahegn et al. (2015) reported highly Significant and significant differences among genotypes (P<0.01) for days to heading, days to maturity, day to tillering,1000 kernel weight, plant height, spike length, grain yield per plot and harvest index. However, El Abidine Fellah (2017) reported non significant differences among bread wheat genotypes for plant height and spike length. The high ly significance result from genotypic variances indicating there were variability in studied genotypes. Hence, selection could be effective for different quantitative characters or for inclusion in crossing program for creating variability. Such variability with in studied genotypes was also reported by Alemu Debi (2016).

The location × genotype interaction was highly significant for days to heading, days to maturity, days to tillering, spikes length and grain yield while 1000 kernel weight, plant height and kernels per spike had significant genotypic variance indicating different performance of bread wheat genotype across the two locations or genotypes responded differently to the different environmental conditions suggesting the importance of the assessment of genotypes under different environments in order to identify better performing genotypes for a particular environment. The finding in agreement with Tesfaye *et al*. (2014) who reported significant differences among genotypes for most of the traits including day to heading, days to maturity, plant height, thousand seed weight and hector liter weight across environments

Table 7. Analysis of variance (Mean squares) for the 11 characters of 16 bread wheat genotypes grown evaluated at Goro

Characters	Goro Location					Agarfa Location				
	Error (df= 30)	Genotypes (df= 15)	Replication (df= 1)	CV(%)	LSD	Error (df= 30)	Genotypes (df= 15)	Replication (df= 1)	CV(%)	LSD
Days to emergence	0.52	0.86	5.6**	9.1	0.54	0.85	1.2	1.3	11.8	0.69
Days heading	7.6	28.6**	1.87	3.8	2.05	11.29	112*	0.52	4.6	2.5
Days tillering	6.9	30.4**	2.04	3.9	1.9	7.3	86.4*	0.29	4.1	2.04
Days of Maturity	26.4	190.6*	2.3**	4.0	3.8	14.9	47.6**	122.7**	3.35	2.9
Plant Height(cm)	25.4	1173.8*	141.6**	5.0	3.8	79.7	328*	66*	9.4	6.7
Spike length(cm)	0.59	4.08**	0.024	9.2	0.57	0.35	1.82**	0.024**	6.1	0.45
Kernel per spike(g)	58.7	70.8**	56.8**	12.9	5.7	20.1	148**	35**	8.8	3.38
Grain Yield per plot(g)	0.021	0.11**	0.15**	20.4	0.11	0.19	0.24**	0.27**	38.1	0.35
Thousand Seed Weight(g)	14.7	5.9**	0.91	10.5	2.8	3.3	18.7*	1.3**	4.8	1.37
Above ground Biomass(g)	0.13	0.57**	0.29**	18.8	0.27	0.16	0.23**	0.11	18.8	0.3
Harvest index(g)	29.6	82.7**	123.6**	14.8	4.1	215	274.6	101.6	32	12.9

Goro in 2018.

df = degree of freedom, CV = Coefficient of Variance, G = Genotype   and **,* = Indicate   significance at the 0.05 and 0.01

probability levels, respectively.

Table 8. Combined Analysis of variance (Mean squares) for the 11 characters of 16 bread wheat genotypes grown evaluated at Goro and Agarfa

Characters	Error (df= 30)	Genotypes (df= 15)	Replication (df= 1)	Location (df=1)	G*L (df=13)	CV(%)	LSD
Days to emergence	0.84	1.38	1.0	0.062	0.59	11.61	0.62
Days heading	9.08	87.44*	0.76	1.26**	56.92*	4.14	2.27
Days tillering	6.95	69.63*	1.56	52.56	49.81*	3.93	1.97
Days of Maturity	20.26	107.09*	150.06	2352.25*	121.92*	3.70	3.35
Plant Height(cm)	54.31	1151.21*	73.110	656.96	246.9**	7.54	5.25
Spike length(cm)	0.46	4.58*	0.60	30.52*	1.109*	7.53	0.51
Kernel per spike(g)	40.05	195.95*	71.40	1145.82*	15.91**	11.52	4.54
Grain Yield per plot(g)	0.112	0.145	0.022	3.33*	0.211*	35.80	0.23
Thousand Seed Weight(g)	9.09	43.17*	3.06	18.06**	7.70**	8.12	2.09
Above ground Biomass(g)	0.153	0.34	0.0006	0.85	0.433	19.27	0.29
Harvest index(g)	157.12	4605.31	175.92	0.068*	196.64	27.77	8.5

Goro and Agarfa in 2018.

df = degree of freedom, CV = Coefficient of Variance, GXL = Interaction of Genotype with Location and **,* = Indicate significance at the 0.05 and 0.01 probability levels, respectively

3.2.1. Mean and Range of grain yield and yield components

Range and mean values for the 11 characters and. the mean performance of the 16 genotypes for 11 traits is presented in Tables 4 and 5. The minimum value of coefficients of variances in Agarfa (Table 7) is ranged from 3.35% (day to maturity) to 35.8% (grain yield),in Goro ranged from 3.8%(Days to maturity) to 20.4%(grain yield) and in table 8 combined analysis Coefficients of variation is ranged from3.7% (days to maturity) to 35.8% (grain yield).Coefficients of variation (CV %) were used to compare the precision of the experimentation i.e. means with lower CV% for most of the characters revealed existence of reliability of the data (Gomez and Gomez, 1984).

3.2.2. Phenotypic and genotypic coefficients of variations

The amount of genotypic and phenotypic variability that exist in a species is of utmost importance in breeding to select better varieties and initiating a breeding program. At Agarfa the lowest genotypic variance is ranged from 0.025(grain yield) to 63.9(kernel per spike while phenotypic variances is ranged from 0.215(grain yield) to 203.8 (plant height).In Goro the lowest genotypic variance is ranged from 0.045(grain yield) to 574.2(plant height) while phenotypic variances is ranged from 0.066(grain yield) to 599.6 (plant height)

As indicated in combined analysis data phenotypic variance ranged from 0.133 (grain yield) to 381.28 (plant height).The values for genotypic variances ranged between 0.073 (days to emergence) and 326.79 (plant height). The minimum phenotypic variance was recorded for the grain yield. The minimum genotypic variance was also recorded for the character day to emergence (0.073), grain yield (0.082), above ground biomass yield (0.117). This indicates that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters. The rest characters showed smaller genotypic variability. The finding is in agreement with Alemu Dabi (2016) and Gezehagn et al.,(2015)

Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given genotypes. Estimated genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), broad sense heritability as well as genetic advance for selection of the traits studied are presented in Tables 8, 9 and 10.

Table 9. Estimation of phenotypic (σ2p), genotypic (σ2g) and environmental (σ2e)components of variances, phenotypic (PCV) and genotypic coefficients of variability (GCV), broad sense heritability (H), expected genotypic advance (GA) and genetic advance as percent of the mean (GA%) for 12 characters evaluated at Agarfa

Characters	MsTr	$\delta^2 e$	$\delta^2 g$	$\delta^2 p$	GCV	PCV	h^2	GA	GA%
Days to emergence	7.9	0.85	0.18	1.03	5.4	12.8	42.2	0.87	11.0
Days heading	72.8	11.29	50.4	61.6	9.7	10.8	89.8	12.4	17.02
Days tillering	66	7.3	39.6	46.9	9.5	0.4	23.8	2.84	4.3
Days of Maturity	115.3	14.9	16.4	31.3	3.5	4.9	71.4	11.4	9.9
Plant Height(cm)	94.4	79.7	124	203.8	11.8	15.1	78.1	14.6	15.5
Spike length(cm)	50.7	0.35	0.74	1.09	1.7	2.05	82.9	1.74	3.44
Kernel per spike(g)	1.16	20.1	63.9	84.0	689	790	87.2	24.9	215.5
Grain Yield per plot(g)	37.8	0.19	0.025	0.215	0.4	1.2	3.33	0.32	0.84
Thousand Seed Weight(g)	2.15	3.3	7.7	11.0	129	154	83.8	5.7	264.9
Above ground Biomass(g)	53.6	0.16	0.035	0.195	0.34	0.8	42.5	0.38	0.72
Harvest index(g)	7.9	215	29.8	244.8	69.1	198	348.9	11.5	145.6

PCV = Phenotypic coefficient variance, GCV = Genotypic coefficient variance, GA = Genetic Advance, and GA% = Genetic Advance as percent of Mean, σ2p = Phenotypic variance, σ2g = Genotypic variance, σ2e = Environmental variance, and σ2gl = Genotype and Location interaction variance

At Agarfa GCV ranged from 0.34% (aboveground biomass) to 689% (kernel number per spike), whereas PCV ranged from 0.4% (days to tillering) to 790% (kernel number per spike).Among all characters, moderate PCV values (>10%) were observed for days to emergence (12.8%), days to heading(10.8%) and plant height (15.1%) while harvest index(198%),1000kernel weight(154%) and kernel per spike(790%) had high genotypic and phenotypic coefficient 0f variance. Whereas, plant height (15.1%) had moderate GCV value suggesting sufficient variability and thus scope for genetic improvement through selection for these traits. Navin et al. (2014) reported higher magnitude of GCV and PCV for grain yield per plant, harvest index, spike length and test weight which support this finding. The rest of the characters grouped under low phenotypic and genotypic coefficients of variation, indicating less scope of selection as they were under the influence of environment.

At Goro GCV ranged from 2.23% (kernel number per spike) to 29.9% (grain yield), whereas PCV ranged from 2.6% (kernel number per spike) to 36.2% (grain yield).Moderate GCV values was observed for harvest index (14.1 %) whereas grain yield, spike length and plant height had high GCV values. Moderate PCV values were recorded for character like thousand-kernel weight (10.47%) and days to emergence while above ground biomass (30.8%), spikes length (30.9%), harvest index (20.5%), plant height (24.3%) and grain yield(36.2%) had high PCV values. This indicated that selection will be effective based on these characters and their phenotypic expression would be good indication of the genotypic potential. Similar results of moderate PCV and GCV has been reported for 1000 kernel weight and grain yield in wheat (Gezahegn et al., 2015).Mitsiwa, (2013) also reported low PCV and GCV for grain filling period (1.82%, 1.59%) and days to maturity (3.63%, 3.50%), respectively.

 In general, estimates of phenotypic coefficient of variation in this study were higher than their corresponding genotypic coefficient of variation indicating the influence of environment on the expression of these characters although the differences were small at both locations. Narrower difference between the values of GCV and PCV indicated that the environmental effect was small for the expression of these characters. According to Deshmukh et al.(1986) PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be moderate.

The combined ANOVA results are presented in Table 5. Phenotypic coefficient of variability ranged from 11.54% (day to emergence) to 70.28% (grain yield). Genotypic coefficient of variability ranged from 7.4% (days to emergence) to 46.13% (plant height). Generally, the PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all the traits. Alemu Dabi (2016), was reported similar result for all studied character. Moderate GCV (10%--30%) were observed for character like grain yield (29.71%) and harvest index (25.95%) while the rest had high GCV (>40%) values for rest except day to emergence (7.4%) which score low GCV. Moderate PCV value was observed for days to emergence (11.54%) whereas the rest of traits had high PCV values. Gezahegn et al. (2015), were reported similar result for all studied character. High PCV (>40%) for all traits,1000 kernel weight (64.07%), days to heading (56.6%), harvest index (70.4%),days to maturity(55.33%), spikes lengths (55.89%),above ground biomass(69.79%), gain yield (70.28%) Moderate PCV (11.54) values was observed for days to emergence respectively, indicating high scope of selection as they were under the influence of environment.
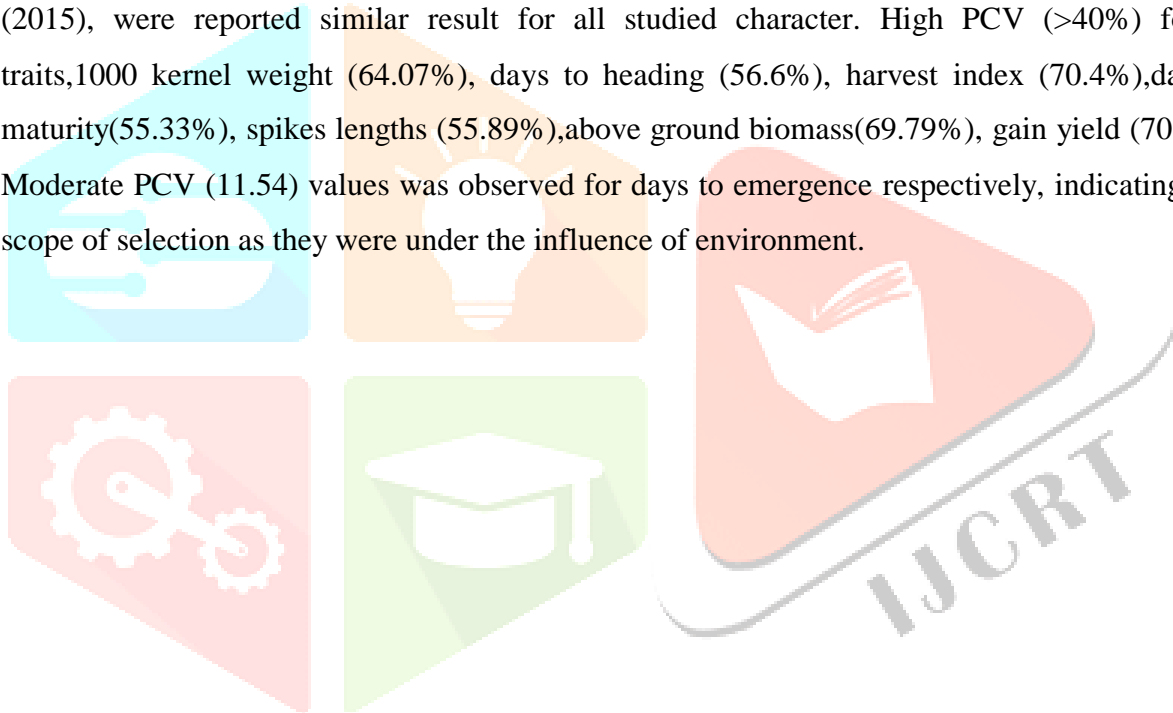
Table 10. Estimation of phenotypic (σ2p), genotypic (σ2g) and environmental (σ2e)components of variances, phenotypic (PCV) and genotypic coefficients of variability (GCV), broad sense heritability (H), expected genotypic advance (GA) and genetic advance as percent of the mean (GA%) for 12 characters evaluated at Goro

Characters	MsTr	δ^2e	δ^2g	δ^2p	GCV	PCV	h^2	GA	GA%
Days to emergence	7.9	0.52	0.17	0.67	5.2	10.4	25.4	0.47	6.02
Days heading	72.6	7.6	10.5	18.1	4.4	5.8	58.0	4.8	6.61
Days tillering	67.8	6.9	17.8	24.7	6.2	7.3	72.0	6.05	8.9
Days of Maturity	127.4	26.4	82.1	108.5	7.1	8.2	75.6	15.18	11.9
Plant Height(cm)	100.7	25.4	574.2	599.6	23.8	24.3	95.7	44.6	44.2
Spike length(cm)	8.37	0.59	6.05	6.64	29.4	30.8	91.1	0.08	0.95
Kernel per spike(g)	59.2	58.7	1.75	2.34	2.23	2.6	74.8	12.02	20.3
Grain Yield per plot(g)	0.71	0.021	0.045	0.066	29.9	36.2	68.2	0.35	49.5
Thousand Seed Weight(g)	36.6	14.7	10.6	25.3	8.9	13.7	41.9	4.14	11.3
Above ground Biomass(g)	1.92	0.13	0.22	0.35	24.4	30.8	62.9	0.72	37.8
Harvest index(g)	36.6	29.6	26.6	56.2	14.1	20.5	47.3	7.21	19.7

PCV = Phenotypic coefficient variance, GCV = Genotypic coefficient variance, GA = Genetic Advance, and GA% = Genetic Advance as percent of Mean, σ2p = Phenotypic variance, σ2g = Genotypic variance, σ2e = Environmental variance, and σ2gl = Genotype and Location interaction variance

3.2.2.2 Estimates of heritability

Broad sense heritability (H^2) which was estimated for the 11 character, ranged from (7.99%) days to emergence to (85.7%) plant height from (Table 3). Pramoda and Gangaprasad, (2007) categorized heritability estimates as low (<40%), medium (40-59%), moderately high (60-79%), and very high (≥80). Accordingly, high heritability estimates were recorded (>80%) for the characters; days to maturity (80.7%) and plant height (85.07%) whereas medium to moderately high heritability were recorded for characters, days to tillering (78.66),days to heading(76.57), grain yield (42.46%), spike length (78.4%), grain yield (62.61%), 1000 kernel weight (47.6%), harvest index (68.19%), spikes length (75.17%), kernels per spike (56.54%), and above ground biomass yield (43.3%). The use of breeding will likely be successful in improving these traits or wheat genotype selections based on phenotype are effective. Low heritability estimates were recorded for harvest index (5.04%) and days to emergence (7.99%) (Table 3).

At Agarfa very high heritability estimates were recorded (>80%) for the characters; days to heading (89.8%) and spikes length (82.9%),kernel per spike (87.2%),1000 seed weight(83.8%) and harvest index(348.9%) while high heritability were recorded for character days to maturity(71.4%) and plant height (78.1%) indicating that the variation observed were mainly under genetic control and were less influenced by the environment and the possibility of progress from selection. Moderate heritability were recorded for days to emergence (42.2%) and above ground biomass yield (58.81%). Grain yield (3.33%) and days to tillering had low heritability values indicating that the variation observed were mainly due to influence of the environment.

At Goro very high heritability estimates were recorded (>80%) for the characters; plant height(95.7%), and spikes length (91.1%), while high heritability were recorded for character days to maturity(75.6%) days to tillering (72%) and kernel per spike (74.8%%),1000, Grain yield(68.2%),above ground biomass (62.9%) indicating that the variation observed were mainly under genetic control and were less influenced by the environment and the possibility of progress from selection. Moderate heritability were recorded for 1000 seed weight(41.9%) ,harvest index(43.3%) and days to heading (58%)while low heritability was recorded by days to emergence(25.4%) had low heritability values indicating that the variation observed were mainly due to influence of the environment

For combined analysis the estimated heritability for the studied traits is presented in Table 5. The heritability values ranged from 7.99% for days to emergence to 85.7 % for height. Highest heritability (>80%) was computed for days to maturity(80.7%) and plant height(85.7%) while days to heading (76.57%),day to tillering (78.66%) and spike length (78.4%) had high heritability indicating selection could be fairly easy and improvement is possible using these traits in breeding. Medium values heritability were recorded for traits above ground biomass (43.3%),1000 seed weight (47.6%),grain yield (42.6%) and kernel per spike (56.54%).Days to emergence (7.99%) and harvest index (35.04%) had low heritability. Adhiena (2015) reported high heritability for days to heading which support this finding. Navin et al. (2014) and Ali

et al. (2008) also reported high heritability estimates for grain yield per plant, number of seeds per spike, plant height and 1000 seed weight which support the present findings. Low heritability was recorded for the characters grain yield (29.28%), harvest index (28.21%) and spikes per plant (20.66%). This result is contradicted with the finding of Gergana and Bozhidar (2015) who reported high heritability for tillers per plant and spikes per plant. Selection may be considerably difficult or virtually impractical for less heritable due to the masking effect of the environment.

3.2.2.3. Estimates of expected genetic advance

Genetic advance as per cent mean was categorized as low (0-10%), moderate (10-20%) and high 20% and above (Johnson et al., 1955). Accordingly, the expected genetic advance as the percent of means expressed as a percentage of the mean ranged from 0.72% for above ground biomass to 264.8% for 1000 kernel weight at Agarfa (Table 9). High GAM was observed in 1000 kernel weight (264.8%), kernel number per spike (215.5%) and harvest index (145.6%). In accordance with finding of Arati et al. (2015) and Navin et al. (2014) who reported similar result with this study. GAM was moderate for days to emergence (11%) and plant height (15.5%) while days to maturity (9.9%), above ground biomass yield (0.72%), days to tillering (4.3%), spikes length (3.44%), grain yield (0.84%). At Goro the expected genetic advance expressed as a percentage of the mean ranged from 0.95% for spike length to 49.14% for grain yield (Table 10), indicating that selecting the top 5% of the base population could result in an advance of 0.17% to 19.14% percent over the respective population mean. GAM was high for grain yield (49.3%)followed by plant height(44.2%),above ground biomass (37.8%), kernel number weight (20.3%) while moderate days to maturity (11.9%),1000 kernel weight (11.3%) and harvest index (19.7%).Low GAM for day to emergence(6.02%),days to heading (6.6),days to tillering (8.9%) and spike length (0.95%) in conformity with the findings by Gezahegn et al. (2015) and Awale.et al. (2013) for the traits, grain yield (14.85%), days to 50% heading (14.70%) and number of grains per plant(14.65%) except for harvest index (15.68%).

Genetic advance expressed as percentage of mean from the combined analysis (Table 11) were days to heading (14.55%), 1000 kernel weight (10.83%), days to emergence (19.6), days to tillering (12.6) and above ground biomass (11.84) had moderate genetic advance as percent of mean.. Gergana and Bozhidar (2015) reported moderate for spikes length (31.83%) and thousand grains weight (33.76%). High Genetic advance expressed as percentage of mean for characters plant height (35.01%),spike length (99.3%) and harvest index(38.69) This suggested selection could be effective in genotypes for these traits and the possibility of improving bread wheat grain yield through direct selection for grain yield related traits. Low genetic advance as percent of the means were not recorded for combined analysis. The result is not in line with finding of Gergana and Bozhidar (2015) who reported high genetic advance as a percent of the mean for the characters plant height which are low in this study. Characters like days to heading, 1000 seed weight and spike length showed high heritability coupled with moderate genetic advance. Therefore, these

characters should be given top priority during selection breeding in wheat. The results are in accordance with reports of Navin et al. (2014) which indicated that heritability was due to additive gene effects and selection may be effective in early generations for these traits. High heritability associated with low genetic advance was exhibited by days to maturity. This may be because of predominance of non-additive gene action in the expression of this character. The high heritability of these traits was due to favorable influence of environment rather than genotypic and selection for these traits may not be rewarding

Table 11. Phenotypic ($\delta^2 p$), Genotypic ($\delta^2 g$), Environmental variance ($\delta^2 e$) and Genotype X Location interaction variance ($\delta^2 gl$) for 16 field pea genotypes from combined ANOVA over locations (Agarfa and Goro).

Characters	MsTrt	$\delta^2 e$	$\delta^2 g$	$\delta^2 p$	$\delta^2 gl$	GCV	PCV	h^2	GA	GA%
Days to emergence	0.986	0.84	0.073	0.913	0.125	7.4	11.54	7.99	1.55	19.6
Days heading	68.45	9.08	29.68	38.76	47.84	43.3	56.6	76.57	9.74	14.55
Days tillering	58.20	6.95	25.62	32.57	21.43	44.02	55.96	78.66	9.17	12.61
Days of Maturity	189.79	20.26	84.76	105.02	50.83*	44.65	55.33	80.70	16.88	13.9
Plant Height(cm)	708.26	54.31	326.79	381.28	96.29	46.13	53.83	85.7	34.19	35.01
Spike length(cm)	3.811	0.46	1.67	2.13	0.324	43.82	55.89	78.4	2.34	99.35
Kernel per spike(g)	145.46	40.05	52.70	93.20	12.07	36.22	64.07	56.54	11.13	20.26
Grain Yield per plot(g)	0.276	0.112	0.082	0.194	0.0495	29.71	70.28	42,46	0.38	40.55
Thousand Seed Weight(g)	25.63	9.09	8.27	17.36	0.691	32.26	67.73	47.6	4.03	10.83
Above ground Biomass(g)	0.387	0.153	0.117	0.27	0.14	39.53	69.76	43.3	0.24	11.84
Harvest index(g)	326.69	157.12	84.78	241.9	19.76	25.95	70.04	35.04	17.46	38.69

σ2p = Phenotypic variance, σ2g = Genotypic variance, σ2e = Environmental variance, and σ2gl = Environmental and environmental interaction variance

. 3.3. Association of Characters

Estimates of genotypic and phenotypic correlation coefficients between each pair of characters were studied for studied locations (Table 6 and 8). In most cases, the phenotypic correlation coefficients were less in magnitude than the genotypic correlation coefficients that revealed the presence of inherent genetic relationships among various characters and less dependent on environment. In this study, at both locations genotypic correlation coefficients were found to be higher in magnitude than that of phenotypic correlation coefficients in most of the traits, which clearly indicated the presence of inherent association among various characters.

3.3.1 Correlation of yield with yield related traits

At Agarfa (Table 11) among the studied character harvest index had significant and positive correlation with days to emergence, days to tillering, days to heading and kernel per spike at phenotypic level whereas spike length, and 1000 kernel weight at genotypic level. While significant and negative correlation with days to maturity, spike length, plant height and above ground biomass at both phenotypic and genotypic level, indicating improvement of these characters can increase the grain yield of wheat. Similar association in winter wheat was also reported by Alemu Dabi (2016).

Days to heading showed significant positive correlation with days to maturity (r= 0.88), above ground biomass (r=0.757**), days to heading (r=0.469*), kernels per spike (r=0.629**) spike length (r=0.975*),1000kernel weight(r=0.437**) and negative significant correlation with plant height (r=-0.649**). The result is in agreement with Awal et al. (2013) for the association of days to heading with days to maturity and grains filling period. Days to maturity showed positive significant correlation with 1000 kernels weight (r=0.839*)), spike length (r=0.327**), days to heading(r=0.866*), grain yield(r=0.775*) and negative significant correlation with plant height (r=-0.272) and harvest index (r=-0.850***).1000 kernel weight showed significant positive correlation with harvest index (0.669**), kernel per spike (r=0.984*), grain yield (r=0.866*), and days to maturity(r=0839*) .Number of kernel per spike and positive correlation with 1000 kernel weight, harvest index, grain yield and spike length. Plant height exhibited highly significant positive association with days to tillering, days to maturity kernels per spike and above ground biomass. Degewione and S. Alamerew, 2013 reported significant positive phenotypic association

of plant height with spike length, biological yield and grains yield. Spike length and kernel per spike showed highly positive correlation with each other which is in accordance with the finding of Alemu Dabi (2016).

At the genotypic level, grain yield showed highly positive significant correlation with number of kernel weight (r=0.456*), days to maturity(r=0.476**), above ground biomass (r=0.253*), harvest index (r=0. 0.988*),1000 kernel weight(r=0.866*) and spike length (r=0.828*) and significant association with the plant height (Table 11). Tewodros Tesfaye et al. (2013) reported significant positive genotypic correlations of above ground biomass, kernels per spike and plant height with grain yield.

Above ground biomass showed significant positive correlation with days to heading (r= 0.352**), days to tillering (r=0.475*), days to emergence (r = 0.349**), grain yield (r=0.255*) and negative significant correlation with harvest index (r = -0.274). Plant height showed highly significant positive coloration with above ground biomass(r=0.339**), and kernel per spike(r=0.723*). The result is in line with the finding of Tewodros Tesfaye et al. (2013)) for above ground biomass and spike length. On the other hand, this finding contradicted with Daniel et al., (2011) and Gezahegn et al.,(2015)) who reported weak above ground biomass association with plant height, indicating that more biomass can be achieved in short plants, which is essential for lodging resistance. Spikelet per spike showed positive highly significant association with kernel per spike and spike length at genotypic level.

Table. 12. Genotypic and phenotypic correlation coefficients among 11 characters of 16 field pea genotype studied at Agarfa, 2018.

	EM	DT	MAT	DHE	KNS	SL	PH	TKW	AGM	HI	PY
EM	1	0.388*	0.524**	0.279*	-0.368	0.869*	-0.178	-0.157*	0. 349**	0.449**	-0.342
DT	-0.217	1	0.157*	0.469**	0.629**	0.975*	0.649**	0.437**	0.475*	0.757*	0.241
MAT	0.078	0.549**	1	0.866*	0.376**	0.327**	0.272*	0.839*	-0.642	-0.859**	0.775*
DHE	0.875*	0.957*	0.493**	1	-0.794	0.264**	-0.316*	-0.216	0.352**	0.656**	0.575**
KNS	0.695**	-0.359**	0.575*	0.457*	1	0.828*	0.723*	0.984*	-0.869	0.632**	0.259*
SL	-0.159	0.256**	0.742**	0.347**	-0.378	1	-0.456	0.275**	-0.256	-0.934*	0.439**
PH	-0.239**	0.496**	0.452**	0.479*	0.349**	0.469*	1	-0.716	-0.125	-0.324**	-0.065
TKW	-0.075	-0.459	-0.469	0.336*	0.672*	0.597*	-0.368	1	-0.676	-0.327	0.558*
AGB	0.958*	0.627**	-0.356	0.484	0.696*	0.327**	0.339**	0.727*	1	-0.722*	-0.638*
HI	-0.919*	-0.227	-0.225*	-0.175	-0.482	-0.264**	-0.376**	0.669**	-0.274**	1	-0.731**
PY	-0.463**	-0.422	0.476**	-0.316	0.456*	0.828*	-0.794	0.866*	0.255*	0.988*	1

**,* = Indicate significance at the P< 0.05 and 0.01, probability levels, respectively

Table 13. Genotypic and phenotypic correlation coefficients among 11 characters of 16 field pea genotype studied at Goro 2018.

	EM	DT	MAT	DHE	KNS	SL	PH	TKW	AGM	HI	PY
EM	1	-0.779*	0.198	0.038	-0.346	0.432	-.0226	0.341**	0.146	-0.636	-0.505
DT	0.774*	1	0.647*	-0.416	0.502	0.732*	0.663*	-0.283	-0.236	-0.455	-0.475
MAT	0.246	0.647*	1	0.532**	0.721*	0.197	0.316**	0.591	-0.241	-0.359	0.366**
DHE	0.743*	0.967*	0.675*	1	0.531*	0.421**	0.743*	0.123	-0.218	-0.421	0.439
KNS	0.542**	0.744*	-0.246	-0.749*	1	0.364**	0.643*	0.246	0,318	0.378	0.459*
SL	0.497**	0.502*	0.199**	0.531	0.457**	1	0.453**	0.359	-0.272	-0.093	0 221**
PH	0.453	0.636*	0.316	0.700*	0.453*	0.118	1	0.521	0.476	-0.201	-0.172
TKW	-0.232	0.591*	-0.123*	0.206**	0.359*	0.271**	0.439**	1	0.643*	0.139	0.607*
AGB	0.014	-0.236	-0.241	-0.218	-0.271	0.895*	0.770*	0.181	1	0.174	0.649*
HI	-0.063	-0.454	-0.359	-0.421	-0.095	0.729	0.560	0.369	0.125	1	0.850*
PY	0.220	0.636*	-0.366	-0.439**	0.723*	0.434*	0.162	0.929*	0.227	0.936*	1

**,* = Indicate significance at the $P < 0.05$ and 0.01, probability levels, respectively

At Goro, there was significant correlation between few traits and grain yield at both phenotypic and genotypic level (Table 12). At phenotypic level, grain yield showed highly significant and positive correlation with kernel per spike (r = 0.459*), 1000 kernel weight (r = 0.607*) and harvest index (r = 0.850*). While days to maturity (r=0.366**) and spike length (r=0.221**) had significant and positive correlation with grain yield. At genotypic level, grain yield had highly significant correlation with kernel per spike (r = 0.456*), 1000 kernel weight (r = 0.866*), spike length (r=0.221**).harvest index (r=0.988*) and above ground biomass (r=0253* while days to maturity (r=0.476**) had significant and positive correlation with grain yield. Alemu Dabi (2016) and Fikre et al.,(2015) reported biomass yield (r= 0.8) had positive and high correlation with grain yield. Qasim Mohammed (2018) also reported highly significant positive phenotypic correlation of grain yield with above ground biomass and harvest index which support this finding. In the present study grain yield showed significant positive correlation with hectoliter weight and plant height. This indicated that selection based on these characters could be more efficient to maximize grain yield of wheat. The grain yield showed non-significant association with the rest of the character.

Days to heading showed significant positive correlation with days to maturity, plant height, kernel per spike, and spike length at both genotypic and phenotypic level. However its association with days to tillering, days to emergence,1000 kernel weight, and harvest index were negative, this implied that increasing the days to heading would increase days to maturity, plant height, kernel per spike and spike length. This association is similar at each location (Agarfa and Goro) with the diffidence of correlation coefficient value. Zine El Abidine Fellahi et al. (2017) and Alemu Dabi. (2016) reported highly significant association of days to heading with days to maturity and spikelet per spike.

Days to maturity showed positive significant correlation with 1000 kernel weight, days to heading, plant height and grain yield at phenotypic level. It also showed significant correlation with days to heading and spike length at genotypic level. This probably indicated that longer phonological period could result in large biomass accumulation with the maximum contribution to 1000 kernel weight and grain yield. showed highly significant and positive correlation with Spike length,1000 kernel weight, harvest index, plant height, days to maturity and grain yield at both genotypic and phenotypic level suggesting that longer interval between days to heading and

days to maturity had high contribution for increments of kernel per spike and 1000 kernel weight.

Harvest index had significant negative correlation with days to maturity, spike length and significant positive correlation with plant height kernel per spike and days to at both genotypic and phenotypic level. Daniel et al. (2011) reported Biomass per plant showed positive and highly significant correlation coefficients with grain yield per plant and negative association with harvest index on his experiment in titled with estimation of genetic and phenotypic correlation coefficients among grain yield and its components in bread wheat. Alemu Dabi (2016) and Gerana Desheva. (2018) also reported negative association of above ground biomass and harvest index. This indicates that increments in the above ground biomass reduce the harvest index ratio. Hectoliter weight showed highly significant and positive correlation with 1000 kernel weight and harvest index at both phenotypic and genotypic level.

Plant height showed significant positive correlation with day t0 tillering, days to heading, kernel per spike, spike length and days to maturity at both genotypic and phenotypic level and significant negative correlation with 1000 kernel weight and harvest index at phenotypic level. This was clearly indicate that larger above ground biomass is the result of large in plant height. Similarly Gerana Desheva. (2018) reported a positive significant association of plant height and biomass yield (r=0.34). The same author indicates positive association of 1000 kernel weight with plant height which contradicted with this study. Number of kernel per spike exhibited highly significant and positive correlation with tiller per plant and spikelet per spike and significant negative correlation with 1000 kernel weight which has often been seen in wheat. Similar report was indicated by Qasim Muhammed (2018), 1000 kernel weight was consistently negatively associated with grains per spike.

Thousand seed weight revealed significant positive association with plant height, spike length, day to heading, day to tillering and kernel per spike at genotypic level. Alemu Dabi (2016) reported positive and significant correlation of peduncle length with plant height and kernels per spike, suggesting the genotypes with longer peduncle length may also be longer in plant height with more number of kernels per spike. It also showed significant positive correlation at phenotypic level with day to emergence and days to maturity. Spike per plant had highly significant and positive association at both genotypic level and phenotypic level indicating

increasing number of tillers per plant could be result in high number of spike per plant. Indicating a key function of tillering is to establish final spike number per plant Quan (2015).

The results at from combined analysis indicated that at phenotypic level grain yield was significant correlation with thousand kernel weight (r=0.272**), above ground biomass (r=0.669*), harvest index(r=0.864*),kernel per spike (r=0.939**), plant height (r=0.287*),spike length(r=0.261*) and days to maturity (r=0.537*) negative correlation with days to tillering(r=-406*) (Table 12). Grozi Delchev (2018) reported significant positive phenotypic correlations of above ground biomass, kernels per spike and plant height with grain yield. The same outer reported non-significant correlation of thousand kernel weight and harvest index with grain yield which contradicted with this finding. Qasim Muhammed (2018) also reported positive correlations of grain yield with above ground biomass, harvest index, kernel per spike, which in agreement with this study for those traits. Foulkes et al., (2011) reported high biomass is an especially valuable trait to raise yield potential of bread wheat, because HI is approaching the limit of approximately 0.64, and there has been no significant progress since the early 1990s (0.50−0.55).Recent yield improvement has showed an association with increased biomass. (Sadras and Lawson,2011).   .

Table 14. Genotypic and Phenotypic correlation coefficients among 11 characters of 16 bread wheat genotype studied at Agarfa and Goro 2018

	EM	DT	MAT	DHE	KNS	SL	PH	TKW	AGB	HI	PY
EM	1	0.421*	0.324 **	0.387	0.435*	0.479	-0.999	-0.358	0.163	0.858*	-0.145
DT	-0.019	1	0.615*	0.709*	-0.395	0.939*	-0.226	0.018	0.608**	0.988*	-0.406*
MAT	0.723*	0.549**	1	-0.968	0.281	0.399**	-0.554	-0.112	-0.319	0.387**	0.537*
DHE	0.875*	0.957*	0.493**	1	0.984	0.765 *	0.216	-0.680	0.489**	0.352	-0.263
KNS	0.695*	-0.359	0.257	-0.457	1	0.854*	0.342	0.563	-0.449	0.612**	0.939*
SL	-0.159	0.256	-0.074	0.347	-0.318	1	0.932 *	-0.438	0.739*	-0.214	0.261*
PH	-0.234	0.669*	0.452**	0.479*	-0.349	0.943	1	0.654*	-0.526	0.876*	0.287*
TKW	0.958*	0.0627	-0.556	0.148	-0.066	0.327	0.303	1	0.421	0.512**	0.272**
AGB	-0.919	-0.227	-0.225	-0.175	-0.182	0.264	0.337*	0.740	1	0.567**	0.669*
HI	-0.463	-0.423	-0.476**	-0.311	-0.415	0.828*	-0.719	0.255	-0.239*	1	0.864*
PY	-0.752	-0.459	0.461*	-0.334	-0.067	0.977*	-0.368	0.223**	0.432	0.556 *	1

3.4. Compare average yield performance of bread wheat farmer's varieties in contrast to improved varieties of by using compost

.Table15. Average yield in kunt/hectar of bread wheat farmer's varieties in contrast to improved varieties of by using compost at Agarfa location

No	Treatments	Average yield kunt/hect	Rank	No	Treatments	Average yield kunt/hect	Rank
	Wheat Farmers varieties				Wheat Improved varieties		
1	Tate	21.67	7	1	Danda'a	50.0	4
2	Ayuba	16.67	8	2	Eerso	35.01	8
3	Tikur goshmber	23.34	6	3	Ogolcho	40.0	6
4	Nech goshmber	26.67	5	4	Sherume	55.01	2
5	Tikur sergegna	38.34	3	5	Hidase	61.67	1
6	Bawunde	53.34	2	6	Digalu	36.67	7
7	Bokate	80.01	1	7	Huluka	51.67	3
8	Setakur	36.67	4	8	Kekeba	46.67	5

Table16.Average Grain yield in kunt/hectar of bread wheat farmer's varieties in contrast to improved varieties of by using compost at Goro location

No	Treatments	Average yield kunt/hect	Rank	No	Treatments	Average yield kunt/hect	Rank
	Wheat Farmers varieties				Wheat Improved varieties		
1	Bawunde	26.67	6	1	Sherume	21.67	3
2	Tikur seregegna	27.17	5	2	Ejerso	18.34	6
3	Tate	11.67	8	3	Ogolcho	18.44	5
4	Setakur	21.67	7	4	Danda'a	18.64	4
5	Bokate	28.54	3	5	Digalu	10.01	8
6	Nech goshmber	28.34	4	6	Huluka	23.4	2
7	Ayubo	31.67	2	7	Hidase	10.41	7
8	Tikur goshmber	33.34	1	8	Kekeba	30.01	1

As result indicated in Table 15 the highest grain yield was recorded in Bokate variety (80.01kunt/hect and the lowest grain yield was recorded in Ayuba variety (16.67kunt/hect) from farmers varieties, while Hidase variety (61.67 kg/hect)and Ejerso variety (35.01 kunt/hect) the highest and lowest grain yield from improved varieties at Agarfa location. In Goro (Table 15) indicated that the highest grain yield was recorded in Tikur goshmber variety (33.34kunt/hect and the lowest grain yield was recorded in Tate variety (11.67kunt/hect) from farmers varieties, while Kekeba variety (39.01 kunt/hect) and Digalu variety (10.01 kunt/hect) the highest and lowest grain yield from improved varieties. This result contradicted the idea raised by some authors which show farmers varieties have low grain yield when compare with improved varieties.

4. SUMMARY AND CONCLUSION

Sixteen bread wheat genotypes (8 released and 8 farmers varieties) were grown at Goro and Agarfa to determine genetic variability, association among grain yield and yield components and to compare grain yield performance of bread wheat farmer's varieties in contrast to improved varieties by using compost. Highly significant difference among genotypes (p≤0.01) was observed for 11 traits studied at individual location indicating the presence of variability for further improvement yield and yield components of bread wheat.The combined analysis of variance showed significant differences among the genotypes due to genotypes, locations, GxL for most of the characters.

Grain yield showed wide variation i.e.1001 kg ha Digalu to 3334 kg ha-1 with the mean value 2366.7 kg ha-1 and 1667 kg ha-1 Tate to 8001 kg ha-1 Bokate with the mean value 3123.33 kg ha-1 at Goro and Agarfa, respectively. The highest grain yielding genotypes was Tikur goshmber (3334 kg ha-1), followed by Ayubo (3334 kg ha-1), Kekeba (3001 kg ha-1) at Goro and Bokate (8001kgha-1), Hidase (6167 kg ha-1), Bawunde (5334 kg ha-1) and Sherume (5501 kg ha-1) at Agarfa. The grain yield performance was better at Agarfa indicating its potential for wheat production.

Higher phenotypic and genotypic variance estimates were observed at each location and across location. Days to maturity and plant height in Goro, days to heading, days to tillering and 1000 kernel weight in Agarfa at each location had highly significant. The location × genotype interaction was highly significant for days to heading, days to maturity, days to tillering, spikes length and grain yield while 1000 kernel weight, plant height and kernels per spike had significant genotypic variance indicating different performance of bread wheat genotype across the two locations or genotypes responded differently to the different environmental conditions suggesting the importance of the assessment of genotypes under different environments in order to identify better performing genotypes for a particular environment.

 PCV was higher than the genotypic coefficients of variation (GCV) in most of the traits.At Agarfa GCV ranged from 0.34% (aboveground biomass) to 689% (kernel number per spike), whereas PCV ranged from 0.4% (days to tillering) to 790% (kernel number per spike).At Goro GCV ranged from 2.23% (kernel number per spike) to 29.9% (grain yield), whereas PCV ranged from 2.6% (kernel number per spike) to 36.2% (grain yield). The combined ANOVA results are presented in Table 5. Phenotypic coefficient of variability ranged from 11.54% (day to emergence) to 70.28% (grain yield). Genotypic coefficient of variability ranged from 7.4% (days to emergence) to 46.13% (plant height). Generally, the PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all the traits.

Highest heritability estimates were recorded (>80%) for the characters; days to heading (89.8%) and spikes length (82.9%),kernel per spike (87.2%),1000 seed weight(83.8%) and harvest index(348.9%) while high heritability were recorded for character days to maturity(71.4%) and plant height (78.1%) at Agarfa and plant height(95.7%), and spikes length (91.1%), while high heritability were recorded for character days to maturity(75.6%) days to tillering (72%) and kernel per spike (74.8%%),1000, Grain yield(68.2%),above ground biomass (62.9%) at Goro indicating that the variation observed were mainly under genetic control and were less influenced by the environment and the possibility of progress from selection Similarly, the result from combined analysis indicated that Phenotypic coefficient of variability ranged from 11.54% (day to emergence) to 70.28% (grain yield). Genotypic coefficient t of variability ranged from 7.4% (days to emergence) to 46.13% (plant height). Generally, the PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all the traits

The expected genetic advance as the percent of means expressed as a percentage of the mean ranged from 0.72% for above ground biomass to 264.8% for 1000 kernel weight at Agarfa. At Goro the expected genetic advance expressed as a percentage of the mean ranged from 0.95% for spike length to 49.14% for grain yield, indicating that selecting the top 5% of the base population could result in an advance of 0.17% to 19.14% percent over the respective population mean. Characters like days to heading, 1000 seed weight and spike length showed high heritability coupled with moderate genetic advance. Therefore, these characters should be given top priority during selection breeding in wheat.

Grain yield showed highly significant (P≤0.01) positive phenotypic correlations with number of kernel weight (r=0.456*), days to maturity(r=0.476**), above ground biomass (r=0.253*), harvest index (r=0.0.9s88*), 1000 kernel weight(r=0.866*) and spike length (r=0.828*) and at genotypic level, grain yield had highly significant correlation with kernel per spike (r = 0.456*), 1000 kernel weight (r = 0.866*), spike length (r=0.221**).harvest index (r=0.988*) and above ground biomass (r=0253* Similarly, significant (p≤0.01) positive and negative phenotypic and genotypic correlations between the yield components were observed at each location.

The highest grain yield was recorded in Bokate variety (80.01kunt/hect and the lowest grain yield was recorded in Ayuba variety (16.67kunt/hect) from farmers varieties, while Hidase variety (61.67 kg/hect)and Ejerso variety (35.01 kunt/hect) the highest and lowest grain yield from improved varieties at Agarfa location. In Goro (Table 15) indicated that the highest grain yield was recorded in Tikur goshmber variety (33.34kunt/hect and the lowest grain yield was recorded in Tate variety (11.67kunt/hect) from farmers varieties, while Kekeba variety (39.01 kg/hect) and Digalu variety (10.01 kunt/hect) the highest and lowest grain yield from improved varieties. Hence, Selection and hybridization on farmers and released varieties based on the trait with high GCV, heritability, genetic advance, positive correlation coefficient and high grain yield can be recommended for farther yield improvement of bread wheat at respective location.

Generally, the present study revealed the existence of significant genetic variability among the tested genotypes for different traits helpful for direct and indirect selection. Attention should be given for traits which has

- ❖ Moderate to high heritability and genetic advance in order to bring an effective response of grain yield improvement.
- ❖ Genotypic and phenotypic correlations among characters of crop plants are useful in planning, evaluating and setting selection criteria for the desired characters for selection in breeding program.
- ❖ Therefore, thousand kernel weights, above ground biomass, harvest index, and plant height showed highly significant positive phenotypic and genotypic correlation with the grain yield.
- ❖ The character harvest index and above ground biomass had highly significant direct effect at both genotypic and phenotypic level to grain yield indicating more attention should be given to those character to improve the grain yield of bread wheat.
- ❖ Hence, Selection and hybridization on farmers and released varieties based on the trait with high GCV, heritability, genetic advance, positive correlation coefficient and high grain yield

Finally, the presence of variability among the genotypes, heritability and relationships in the tested traits of the genotypes confirmed possibility to increase farmers and released varieties wheat productivity in target area. Hence, Selection and hybridization on those genotypes based on the trait with high GCV, heritability, genetic advance, and positive correlation coefficient and   grain yield can be recommended for farther yield improvement of bread wheat at respective location.

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Appendix I

Mean values of 11 characters of 16 bread wheat genotypes grown at Agarfa

No.	EM	DT	DM	DHE	KNS	SL	PH	GY	TKW	AGB	HI
Tate	8	74	124	79	58.8	10.4	65.6	0.6	30	1.6	37.5
Ayuba	7	69	124	76	40.8	10.0	85.4	0.4	33	1.5	26.6
Tikur goshmber	8	72	124	78	45.6	10.4	102	0.7	35	2.0	35.0
Nech goshmber	8	68	119	74	54.8	9.20	84.0	1.0	39	2.4	41.6
Tikur sergegna	7	75	116	77	43.4	10.0	120	1.3	36	2.5	52.0
Bawunde	8	78	128	90	41.6	12.0	129	1.1	42	2.2	50.0
Bokate	8	76	128	88	40.0	10.0	122	2.5	40	1.8	50.0
Setakur	7	67	112	74	40.0	10.2	95.4	0.9	44	2.1	42.8
Danda'a	7	63	119	69	61.2	9.20	88.2	1.6	34	2.3	69.5
Eerso	8	63	116	69	60.0	7.20	84.8	2.2	36	3.5	62.8
Ogolcho	7	59	107	65	55.2	9.80	84.0	2.2	38	2.4	91.6
Sherume	7	61	109	67	55.2	10.8	84.6	1.7	39	2.0	85.0
Hidase	11	59	115	66	55.2	9.80	91.2	1.7	40	2.4	70.8
Digalu	8	58	115	65	56.4	8.00	89.4	1.0	36	2.0	50.0
Huluka	6	59	113	65	62.4	11.0	85.4	1.1	38	2.3	47.8
Kekeba	8	57	113	66	57.6	9.60	85.8	1.7	39	2.3	73.9
Mean	**7.68**	**66.1**	**117.6**	**73**	**51.7**	**8.39**	**93.6**	**1.35**	**37.4**	**2.2**	**55.4**
CV	**11.8**	**4.1**	**3.35**	**4.6**	**8.8**	**6.1**	**9.4**	**38.1**	**4.8**	**18.8**	**3.2**
LSD (5%)	**0.63**	**2.04**	**2.9**	**2.5**	**3.38**	**0.45**	**6.7**	**0.35**	**1.37**	**0.3**	**12.9**

Mean values of 11 characters of 16 bread wheat genotypes grown at Goro

No.	EM	DT	MAT	DHE	KNS	SL	PH	GY	TKW	AGB	HI
Sherume	7	66	129	71	62.4	8.2	86.2	0.5	33	1.3	38.4
Ejerso	9	65	139	70	62.4	6.2	79.0	0.6	31	1.4	42.8
Ogolcho	7	72	139	77	60.8	7.6	87.0	0.4	32	1.2	33.3
Danda'a	7	72	137	77	68.8	7.4	85.4	0.3	37	1.1	27.2
Digalu	9	71	134	76	62.4	7.2	78.0	0.2	36	1.0	20.0
Huluka	9	72	116	77	65.6	7.6	76.8	0.6	38	1.5	40.0
Hidase	9	64	118	70	60.8	8.4	85.6	0.7	42	2.6	26.9
Kekeba	9	62	113	66	64.0	8.2	80.0	1.0	40	2.0	50.0
Bawunde	9	74	134	79	58.0	11	141	0.8	42	2.4	33.3
Tikur seregegna	9	64	128	70	55.2	8.8	118	1.0	39	2.4	41.6
Tate	9	63	113	67	65.6	8.6	73.6	0.3	26	1.1	27.2
Setakur	9	72	141	76	66.0	11	146	0.6	38	1.6	37.5
Bokate	9	70	134	74	51.2	8.0	104	0.7	41	2.0	35.0
Nechgoshmber	9	64	130	68	48.0	7.8	115	0.9	40	2.5	36.0
Ayebo	7	65	116	69	50.4	8.2	116	1.1	39	2.6	42.3
Tikur goshmber	7	63	129	68	61.6	11	117	0.8	28	3.0	26.6
Mean	**7.9**	**67.8**	**127.4**	**72.5**	**59.2**	**8.39**	**100.7**	**0.71**	**36.6**	**1.92**	**36.6**
CV	**9.1**	**3.9**	**4.0**	**3.8**	**12.9**	**9.2**	**5.0**	**20.4**	**10.5**	**18.8**	**14.8**
LSD (5%)	**0.54**	**1.9**	**3.8**	**2.05**	**5.7**	**0.57**	**3.8**	**0.11**	**2.8**	**0.27**	**4.1**