SOIL & CROP SCIENCES | RESEARCH ARTICLE

Phenotypic performance, genetic advance and regression analysis in bread wheat (*Triticum aestivum* L.) genotypes in Northwestern Ethiopia

Misganaw Ferede¹*, Fisseha Worede² and Getachew Alemayehu³

**Abstract:** The study was initiated to explore genetic advance and rate of genetic progress over years of bread wheat genotypes in Ethiopia. Twelve bread wheat genotypes released in between 1995 and 2012 were used as experimental treatments. The experimental treatments were laid out on randomized complete block design with three replications across locations over 2 years. The study was conducted at Adet, Debretabor, Finoteselam, Injibara and Simada in 2014 and 2015 cropping seasons. The combined analysis of variance of genotypes, environments and their interactions showed significant difference (P < 0.05) among bread wheat genotypes for all studied traits. The higher grain yield was recorded on the genotypes Gambo and Ogolcho which showed 47.3% and 39.5% grain yield advantage, respectively, as compared to the older variety Kubsa. In the genetic linear regression analysis over years, only thousand seed weight showed positive significant increment, whereas grain yield, biological yield, days to physiological maturity, plant height and test weight showed positive non-significant increment. The traits spike length and number of seeds per spike showed negative non-significant decrement over years. Therefore, breeders should consider the yield-related traits to bring the

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**PUBLIC INTEREST STATEMENT**

In Ethiopia, wheat research has been started since 1970s. Ethiopia has been released about 89 bread wheat varieties during 1970-2018. However, due to climate changes as well as evolving of new rust races, a lot of released wheat varieties were obsolete from production. Although the wheat variety release has been continued year after year, only few varieties are used as genetic material for wheat production and productivity. Studies on genetic variability, heritability, advance and regression over years are valuable information to design the plant breeding approaches and techniques. In Northwestern Ethiopia, the climate is fluctuated from location to location and season to season as well. Therefore, this type of study is pertinent to exploit the degree of genetic advance and rate of genetic improvement over years to developed demanded and climate-resilient wheat varieties to farmers’ agro-ecologies as well as to consider scientific gaps in the future wheat breeding investigations.
desired genetic enhancement as well as to develop demanded genotypes in the future bread wheat breeding investigations.

Subjects: Agriculture & Environmental Sciences; Crop Science; Agriculture and Food

Keywords: bread wheat; breeding investigation; genetic progress; genetic variation; grain yield

1. Introduction
Wheat is a staple food all over the World. In the World among 125 wheat-producing countries, Ethiopian wheat area coverage and productivity are ranked 25th (1.7 million hectares) and 63th (28,126 kg/ha), respectively. Its productivity is by far lower compared to wheat-producing countries such as Ireland (101,746 kg/ha), New Zealand (98,633 kg/ha) and Netherlands (90,936 kg/ha) (FAOSTAT, 2017). In Ethiopia, bread wheat variety development research program has been started since 1970s, and 89 bread wheat genotypes have been released in between 1970–2017 through landrace collection, introduction and intra-specific hybridization (Ministry of Agriculture and Natural Resource [MoANR], 2019). The productivity of bread wheat is affected by factors such as genotypes, environments, management practices and their interactions (Misganaw, 2017; Fentaw et al., 2015; Arega et al., 2013; Haile et al., 2013; Tesfaye et al., 2013) as well as pests in particular wheat rusts. However, it is difficult to estimate simultaneously the interaction effects of these factors over years.

Knowledge on nature and magnitude of variation in genotypes is of great importance to develop genotypes for high yield and other desirable traits (Chekole et al., 2016). The magnitude of genetic variability, heritability and genetic advances in selection of desirable traits are pertinent and compulsory issues for the plant breeder to consider the traits during crossing in breeding program (Bello et al., 2012). Periodic measurement of genetic advance allows the efficiency of new technologies incorporated into a breeding program for crop production and productivity (Benhilda et al., 2017). As Mekuria (2018) reported, estimation of genetic progress in variety development helps breeders to make a decision on the increment of productivity as well as to consider the breeding strategies in the future. As Upasna et al. (2019), Mekuria et al. (2018), Tesfaye et al. (2016), Kifle et al. (2016), and Arega et al. (2010) Studies on the extent and magnitude of genetic variability, heritability, genetic gain and advance as well as genetic progress over years of introduced exotic genotypes, land races, early generation crowed hybridized genotypes and released varieties are vital to genetic improvements on the available resources through direct selection and promotion and scale up of released varieties in a short period of time and also to design breeding techniques. Hereby the study was initiated with the objectives of to analyze the extent and magnitude of genetic variability, heritability, genetic advance and genetic improvement progress over years of grain yield and agronomic traits in bread wheat released genotypes over years.

2. Materials and Methods

2.1. Description of the study areas
The study was conducted in bread wheat producing moisture deficit to acidic prone highland areas in Northwestern Ethiopia. The experiment was done at Adet Agricultural Experimental sites, namely Adet, Debretabor, Finoteselam, Injibara and Simadain 2014 and 2015 cropping seasons. The agro-ecological data of the experimental sites are listed in Table 1.

2.2. Experimental materials and procedures
The experimental bread wheat genotypes were selected purposively which are used as genetic materials for production. The treatment consisted of twelve bread wheat genotypes which are released in between 1995–2012. Description of the experimental genotypes data is given in Table 2. The experimental land was ploughed three times and labeled manually at the time of
### Table 1. Geographical locations and climate data of the experimental sites

| Testing sites | Code | Altitude (masl) | Geographical | Climate data for two cropping seasons |
|---------------|------|----------------|--------------|--------------------------------------|
|               |      |                | Latitude     | Longitude   | RF (mm) | Average temp (° C) | RF (mm) | Average temp (° C) |
| Adet          | E1   | 2240           | 11°16’ N     | 37°29’E     | 658.6   | 17.53             | 948.9   | 19.4               |
| Simada        | E2   | 2460           | 11°03’ N     | 37°30’E     | 736.1   | 13.27             | 770.6   | 15.07              |
| Debretabor    | E3   | 2591           | 11°51’ N     | 38°01’E     | 1102.7  | 15.48             | 958.1   | 15.94              |
| FinoteSelam   | E4   | 1917           | 1042 N       | 3716E       | NA      | 18.76             | NA      | NA                 |
| Injibara      | E5   | 2560           | 1057 N       | 3656E       | 1562    | NA                | NA      | NA                 |

Source: AARC (2014) and ANRSMA (2014 and 2015)

RF (mm) = total amount of rainfall in the cropping season; Average temp (° C) = average temperature in the cropping season and NA = Not Available.
Table 2. Description of bread wheat genotypes used as experimental entries

| Genotypes                | Code | Breeder center | Year of release | Grain yield (t/ha) at time of release at time | Recommended Agro-ecology Zone |
|--------------------------|------|----------------|-----------------|---------------------------------------------|-------------------------------|
|                          |      |                |                 | On station | On farm | Alt(masl) | RF(mm) |
| Hidase (ETBW 5795)       | V1   | KARC           | 2012            | 4.4-7      | 3.5-6   | 2200-2600 | >500   |
| Huluka (Flag 5)          | V3   | KARC           | 2012            | 4.4-7      | 3.8-6   | 2200-2600 | 500-800 |
| Ogolcho (ETBW 5520)      | V2   | KARC           | 2012            | 2.8-4      | 2.2-3.5 | 1600-2100 | 400-500 |
| Shorima (ETBW 5483)      | V11  | KARC           | 2011            | 2.9-7      | 2.3-4.4 | 2100-2700 | 700-1100|
| Gambo (QUIAU#2)          | V4   | KARC           | 2011            | 3.5-5.7    | 4.5     | 750       | NA     |
| Tsehay (HAR 3837)        | V9   | DBARC          | 2011            | 3.8        | 2.8-3.5 | 2600-3100 | >900   |
| Dando’a (DANPHE#1)       | V5   | KARC           | 2010            | 3.5-5.5    | 2.5-5   | 2000-2600 | >600   |
| Balol (HAR 3816)         | V8   | DBARC          | 2009            | 2.8-3.5    | 2.3-3.3 | 2580-3100 | >904   |
| Menze (HAR 3008)         | V10  | DBARC          | 2007            | 1.9-3.3    | 1.5-2.7 | 2800-3100 | >904   |
| Gassay (HAR 3730)        | V6   | ADARC          | 2007            | 4.4-5      | 3.5-4.7 | 1890-2800 | >700   |
| Tay (ET-12 D4/HAR-604(1)) | V7   | ADARC         | 2005            | 2.5-6.1    | 3.4-5.8 | 1900-2800 | >700   |
| Kubsa (HAR 1685)         | V12  | KARC           | 1995            | 5.8-6.3    | 4.4-5   | 1850-2800 | 500-800 |

*Source: MoA, Crop Variety Register (1995–2012).
*ADARC = Adet Agricultural Research Center; Alt = Altitude; DBARC = Debrebirhan Agricultural Research Center; KARC = Kuldusa Agricultural Research Center; RF = Rainfall; SC = Standard Check and NA = Not available.
planting. The treatments were laid out as randomized complete block design with three replications per treatment at each site. Planting was done in the first and the second week of July with seeding rate of 150 kg/ha on the plot area of 1.2 × 2.5 m with a net plot area of 0.8 × 2.5 m. Urea and DAP fertilizers as a source of nitrogen and phosphorus were applied at the rate of 74 kg N/ha and 46 kg P₂O₅/ha for Adet, whereas 120 kg N/ha and 46 kg P₂O₅/ha for Simada, Debretabor, Finoteselam and Injibara. The total amount of DAP and one-third of urea were applied at planting and the remaining two-thirds of urea was applied at tillering after the first weeding. Weeding was done manually two times at tillering stage and booting stage (50–60 days before heading) depending on the weed infestation of the trial sites.

2.3. Data collection and statistical analysis
The phonological data such as days to 95% physiological maturity as well as agronomic traits such as grain yield, biological yield, plant height, spike length, number of seeds per spike, thousand seed weight and test weight were collected in the study.

The data were analyzed using GenStat (18th edn), SAS version 9.0 and Microsoft Excel 2007 software for the analysis of variances as well as genetic variability, heritability, genetic advance and linear regression analysis over years.

The variance components of genotypes over environments were calculated following the equations suggested by Bello et al. (2012) and Isack (2015)

\[
\text{Genetic variance} \left( \delta^2_g \right) = \frac{\text{MSg} \cdot \text{MSge}}{r e}
\]

\[
\text{Variety-by-environment interaction variance} \left( \delta^2_{ge} \right) = \frac{\text{MSge} \cdot \text{MSe}}{r e}
\]

\[
\text{Phenotypic variance} \left( \delta^2_p \right) \text{ due to genetic effects} = \delta^2_g + \delta^2_{ge} + \delta^2_e e
\]

where \( \delta^2_g \) = genetic variance, \( MSg = \) mean square of genotypes, \( MSge = \) mean square of genotype by environment interaction, \( \delta^2_{ge} = \) genotype by environment interaction variance, \( MSe = \) mean square of error, \( \delta^2_e = \) error variance, \( \delta^2_p = \) Phenotypic variance, \( e = \) number of environments and \( r = \) number of replications.

The coefficient of variation of genotypes and phenotypes was calculated as the following equations suggested by Burton and DeDane (1953).

Genetic coefficient of variation (GCV\%) = \( \left[ \sqrt{\frac{\delta^2_g}{\bar{x}}} \right] \times 100 \)

where \( \sqrt{\delta^2_g} = \) the square root of genetic variance and \( \bar{x} = \) grand mean

Phenotypic coefficient of variation (PCV\%) = \( \left[ \sqrt{\frac{\delta^2_p}{\bar{x}}} \right] \times 100 \)

where \( \sqrt{\delta^2_p} = \) the square root of phenotypic variance and \( \bar{x} = \) grand mean, PCV and GCV values were classified as low (0–10\%), moderate (10–20\%) and high (>20\%) values as indicated by Sivasubranian and Menon (1973).

Broad sense heritability (\( H^2 \)) of genotypes across environments was calculated as suggested by Falconer and Mackay (1996) and Bello et al. (2012)

\[
H^2 = \frac{\delta^2_g}{\delta^2_p} = \frac{\delta^2_g}{\delta^2_g + \frac{\delta^2_{ge}}{r e} + \delta^2_e e}
\]

where heritability was classified as suggested by Robinson et al. (1949) into low (0–30\%), moderate (30.1–60\%) and high (>60\%).
Genetic advance (GA) between genotypes over environments was calculated according to Bello et al. (2012)

\[ GA = \sqrt{\frac{\delta^2 P}{H^2}} \]

Genetic advance as a percent of means (GAM) in genotypes was done using the following formula according to Bello et al. (2012)

\[ GAM = \frac{GA}{X} \times 100 \]

where the GA as percent of mean categorized as suggested by Johnson et al. (1955)

0–10% = Low, 10–20% = Moderate and >20% = High.

Linear regression analysis on dependent variable Y and independent variable X is represented by the equation: \( Y = \beta X + \alpha \)

where \( Y \) = the value of the dependent variable, \( X \) = the value of independent variable, \( \alpha \) = the intercept of the line, \( \beta \) = the regression coefficient (slope of the line), or the changes in y per unit change in X (Yan & Su, 2009). The relative annual genetic advance per year was determined as a ratio of genetic advance to the corresponding mean value of oldest variety.

3. Results and Discussion

3.1. Performance in bread wheat genotypes over environments

The combined analysis of variance of genotypes, environments and their interactions showed a significant difference (P < 0.05) among bread wheat genotypes for all studied traits as depicted in Table 3. The genotypes Gambo and Ogolcho showed higher grain yield response with cumulative effect of higher in biological yield, harvest index, thousand seed weight and test weight, whereas medium in maturity, plant height, spike length and number of seed per spike across environments. As a result, Gambo and Ogolcho had 47.3% and 39.5% grain yield advantage, respectively, as compared to the older variety Kubsa. In Upasna et al. (2019), Mekuria et al. (2018), Tesfaye et al. (2016), Kifle et al. (2016), and Arega et al. (2010) reports, all the studied traits showed significant differences among bread wheat tested genotypes. The magnitude of variation in agronomic traits and grain yield advantages were varied due to the agronomic performance of the older variety, genetic nature and diversity of tested genotypes and the diversity and number of tested environments as well.

3.2. Genetic variability, heritability and advance in bread wheat genotypes

The coefficients of variations in between genotypic and phenotypic variance were narrow differences in all studied traits in bread wheat tested genotypes as depicted in Table 4. As Gezahegn et al. (2015) reports the narrow differences between genotypic and phenotypic coefficient of variation in bread wheat genotypes which indicates the effect of environment in expression of bread wheat traits is less than the genetic effect. In the study, all studied traits showed higher broad sense heritability in the tested bread wheat genotypes as indicated in Table 4. As Chekole et al. (2016), Gezahegn et al. (2015), Isack (2015), Moslem et al. (2014), and Bello et al. (2012) report, the higher in broad sense heritability means that the traits performance variations are mainly under genetic control and less influenced by environments.

Grain yield showed medium genotypic variation, higher phenotypic variation, higher heritability and medium genetic advance to the mean of the population in bread wheat genotypes. The traits biological yield, spike length, number of seeds per spike and thousand seed weight showed medium variation in both genotypic and phenotypic variation, higher heritability and medium genetic advance to the mean of the population. As Bello et al. (2012) reported, the traits showed higher GCV and PCV.
| Year of release | Genotypes | Code | Traits | GY (qt/ha) | BY (qt/ha) | HI(%) | DPM | PH (cm) | SL (cm) | NSPS | TSW (g) | TW (g/hl) |
|-----------------|-----------|------|--------|------------|------------|--------|------|--------|--------|------|-------|----------|
| 1995            | Kubsa     | V12  |        | 33.22      | 94.7       | 33.45  | 113.9| 77.52  | 7.96   | 44.43| 25.94 | 71.64    |
| 2005            | Tay       | V7   |        | 38.4       | 108.4      | 34.75  | 123.8| 95.02  | 9.098  | 54.94| 29.78 | 74.63    |
| 2007            | Gasay     | V6   |        | 35.36      | 105.9      | 33.74  | 122.9| 86.19  | 8.582  | 48.12| 30.9  | 76.25    |
| 2007            | Menze     | V10  |        | 28.73      | 89.5       | 32.24  | 130.2| 93.24  | 6.561  | 54.78| 26.74 | 73.7     |
| 2009            | Bolo      | V8   |        | 30.02      | 95         | 31.85  | 130.8| 94.48  | 6.64   | 55.01| 27.33 | 74.16    |
| 2010            | Dand’a    | V5   |        | 35.19      | 110.4      | 33.05  | 127.7| 94.61  | 8.103  | 49.35| 33.48 | 72.14    |
| 2011            | Gambo     | V4   |        | 48.92      | 125.7      | 39.41  | 119.2| 89.69  | 8.077  | 48.86| 33.71 | 77.37    |
| 2011            | Tsehay    | V9   |        | 39.3       | 100.9      | 38.98  | 115.4| 86.79  | 8.309  | 50.39| 32.9  | 76.17    |
| 2011            | Shorima    | V11  |        | 42.25      | 110.4      | 38.15  | 118.3| 86.45  | 8.82   | 43.72| 30.85 | 76.7     |
| 2012            | Hidase     | V1   |        | 34.55      | 94.3       | 37.94  | 113.6| 80.3   | 7.724  | 45.11| 32.7  | 71.94    |
| 2012            | Ogolcho    | V2   |        | 46.34      | 117.8      | 39.4   | 119.4| 89.92  | 8.109  | 47.68| 33.63 | 77.05    |
| 2012            | Huluka     | V3   |        | 37.39      | 100.5      | 37.68  | 123.6| 80.33  | 7.942  | 44.68| 28.84 | 74.53    |
| Mean            |           |      |        | 37.47      | 104.5      | 35.89  | 121.57| 88.88  | 7.99   | 48.92| 30.57 | 74.69    |
| CV              |           |      |        | 9.9        | 9.6        | 7.3    | 3.05 | 4.5    | 5.7    | 9    | 7.1   | 2.4      |
| LSD (5%)        |           |      |        | 5.98       | 16.07      | 4.2    | 1.6  | 6.43   | 0.73   | 7.06 | 3.48  | 2.93     |
| Genotypes       |           |      |        | **         | **         | **     | **   | **     | **     | **   | **    | **       |
| Environments    |           |      |        | **         | **         | **     | **   | **     | **     | **   | **    | **       |
| Var*Env         |           |      |        | **         | **         | **     | **   | **     | **     | **   | **    | **       |

GY = Grain yield, BY = Biological yield, HI = Harvest index, DPM = Days to 95% physiological maturity, PH = Plant height, SL = Spike length, NSPS = Number of seeds per spike, TSW = Thousand seed weight, TW = Test weight, Rep = Replications, Env = Environments, Var by Env = Genotypes by environments, CV = Coefficient of variance and LSD = Least significant difference.
Table 4. Mean squares, genetic and phenotypic variability, heritability and genetic advance of bread wheat genotypes across environments

| Traits   | Grand mean | Mean squares | Variance Components | Coefficient of variation (%) | H² | GA | GAM(%) |
|----------|------------|--------------|---------------------|------------------------------|----|----|--------|
|          | Rep (3)    | Genotypes (11) | Envi (7) | Var x Envi (77) | R (190) | δ²g | δ²p | GCV (%) | PCV (%) | H² | GA | GAM(%) |
| GY       | 37.47      | 1874         | 883.7**            | 4300.8**                   | 191.8** | 13.8 | 46.1 | 58.9 | 18.1 | 20.5 | 0.78 | 6.0 | 16    |
| BY       | 10.45      | 720.2        | 2744.7**           | 41205**                    | 711.7** | 99.62 | 135.5 | 183.0 | 11.1 | 12.9 | 0.74 | 10.0 | 10    |
| HI       | 35.89      | 6.66         | 210.0**            | 582.61**                   | 52.77** | 6.81 | 10.5 | 14.0 | 9.0  | 10.4 | 0.75 | 2.8  | 8     |
| DPM      | 121.57     | 16.07        | 850.2**            | 5423.18**                  | 28.74** | 3.59 | 56.8 | 56.7 | 6.1  | 6.2  | 0.97 | 7.3  | 6     |
| PH       | 87.88      | 53.03        | 881.0**            | 2134.69**                  | 64.64** | 15.96 | 56.4 | 58.7 | 8.4  | 8.7  | 0.93 | 7.1  | 8     |
| SL       | 7.99       | 0.38         | 13.94**            | 946**                      | 0.56** | 0.25 | 0.9  | 0.9  | 11.8 | 12.0 | 0.96 | 0.9  | 12    |
| NSPS     | 48.92      | 3.63         | 419.0**            | 1345.26**                  | 56.81** | 19.2 | 24.1 | 27.9 | 10.0 | 10.8 | 0.86 | 4.6  | 9     |
| TSW      | 30.57      | 6.59         | 191.9**            | 203.54**                   | 34.09** | 4.68 | 10.5 | 12.8 | 10.6 | 11.7 | 0.82 | 2.9  | 10    |
| TW       | 74.69      | 4.44         | 100.6**            | 184.77**                   | 30.68* | 12.8 | 4.7  | 6.7  | 2.9  | 3.5  | 0.70 | 1.8  | 2     |

GY = Grain yield, BY = Biological yield, HI = Harvest index, DPM = Days to 95% physiological maturity, PH = Plant height, SL = Spike length, NSPS = Number of seeds per spike, TSW = Thousand seed weight, TW = Test weight, Rep = Replications, Envi = Environments, Var x Envi = Genotypes by environments interaction, R = Residual, δ²g = Genetic variance, δ²p = Phenotypic variance, GCV = Genetic coefficient of variation, PCV = Phenotypic coefficient of variation, H² = Broad sense heritability, GA = Genetic advance, GAM = Genetic advance as percent of mean and ** = Significant at P ≤ 0.01.
Table 5. Linear regression analysis of yield and yield-related traits in bread wheat genotypes over years

| Traits     | Mean of traits | $R^2$ | $\beta$ | $a$     | Sig. F level | $Y = \beta x + a$ |
|------------|----------------|-------|---------|---------|--------------|-------------------|
| GY         | 37.47          | 0.15  | 0.50**  | −970.25 | 0.19         | $y = 0.50x - 970$ |
| BY         | 104.5          | 0.12  | 0.77**  | −1448.8 | 0.26         | $y = 0.77x - 4488$|
| HI         | 35.89          | 0.30  | 0.90**  | 1976    | 0.06         | $Y = 0.90x + 1976$|
| DPM        | 121.57         | 0.01  | 0.09**  | 1997    | 0.71         | $Y = 0.09x + 1997$|
| PH         | 87.88          | 0.05  | 0.05**  | 1992    | 0.46         | $Y = 0.05x + 1992$|
| SL         | 7.99           | 0.006 | −0.049**| 2008    | 0.98         | $Y = -0.049x + 2008$|
| NSPS       | 48.92          | 0.008 | −0.033**| 2010    | 0.92         | $Y = -0.033x + 2010$|
| TSW        | 30.57          | 0.43  | 1.13**  | 1973    | 0.01         | $Y = 1.13x + 1973$|
| TW         | 74.53          | 0.2   | 1.08**  | 1927    | 0.13         | $Y = 1.08x + 1927$|

$R^2$ = Coefficient of determination, $\beta$ = Coefficient of regression/slope of the line, $a$ = Intercept, GY = Grain yield, BY = Biological yield, HI = Harvest index, DPM = Days to 95% physiological maturity, PH = Plant height, SL = Spike length, NSPS = Number of seeds per spike, TSW = Thousand seed weight and TW = Test weight.
as well as higher heritability with higher genetic advance were under the control of additive gene effects. While Chekole et al. (2016) reported, higher heritability with lower genetic advance indicates that the traits expression by additive gene effect is lower than environmental effects. Therefore, in the study, the traits grain yield, biological yield, spike length, number of seeds per spike and thousand seed weight performance variation were mainly under genetic control whereas Days to maturity, plant height and test weight expressions were influenced by environmental effects than genetic effects.

### 3.3. Genetic progress of grain yield and associated traits in bread wheat genotypes

In the study linear regression analysis on bread wheat traits only thousand seed weight showed significant increment per year as depicted in Figure 2. Whereas grain yield, biological yield, days to physiological maturity, plant height and test weight showed no significant increment over 18 years. On the other hand, spike length and number of seeds per spike showed no significant decrement over 18 years in bread wheat genotypes (Table 5). The annual rate of genetic advance of grain yield in bread wheat genotypes was 50 kg/ha/year during 1995–2012, although non-significant per year (Figure 1). In contrary, significant increase in grain yield, biological yield and number of seed per spike, significant decrement in plant height and spike length, non-significant

![Figure 1. Genetic progress of grain yield (qt/ha) (Y = 0.50x - 970) in bread wheat genotypes over 18 years.](image)

![Figure 2. Genetic progress of thousand seed weight (g) (Y = 1.13x + 1973) in bread wheat genotypes over 18 years.](image)
increment in thousand seed weight and similarly non-significant increment in test weight as Nehe et al. (2019), Mekuria et al. (2018), Patricio et al. (2017), Sanchez et al. (2013) and Osmar et al. (2007) reported in wheat genotypes. In the study, the extent and magnitude of genetic progress over years were varied due to the agronomic performance of the older variety, genetic nature and diversity of tested genotypes and the diversity and number of tested environments as well.

4. Conclusions
In the study, the combined analysis of variance of genotypes, environments and their interactions showed significant difference (P < 0.05) among bread wheat genotypes for all studied traits. The higher grain yield was recorded on the genotypes Gambo and Ogolcho which showed 47.3% and 39.5% grain yield advantage, respectively, as compared to the older variety Kubsa. The traits grain yield, biological yield, spike length, number of seeds per spike and thousand seed weight showed medium genetic and phenotypic variation, higher heritability and medium genetic advance to the mean of the population, whereas the traits days to physiological maturity, plant height and test weight showed negligible in both genotypic and phenotypic variation, higher heritability and negligible genetic advance to the mean of the population in bread wheat genotypes. In the genetic regression analysis over years, only thousand seed weight showed significant positive increment, whereas grain yield, biological yield, days to physiological maturity, plant height and test weight showed no significant increment per year. While spike length and number of seeds per spike showed no significant decrement per year of bread wheat genotypes as compared to the older variety. Therefore, breeders should consider the yield-related traits to bring the desired genetic enhancement as well as to develop demanded genotypes in the future bread wheat breeding investigation.

Funding
The authors received no direct funding for this research.

Competing interests
The authors declare no competing interests.

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Citation information
Cite this article as: Phenotypic performance, genetic advance and regression analysis in bread wheat (Triticum aestivum L.) genotypes in Northwestern Ethiopia, Misganaw Ferede, Fisseha Worede & Getachew Alemayehu, Cogent Food & Agriculture (2020), 6: 1746227.

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