International Journal of Economic Plants

https://ojs.pphouse.org/index.php/IJEP

IJEP February 2024, 11(1): 038-047

Article IJEP5039b

Full Research

Doi: HTTPS://DOI.ORG/10.23910/2/2024.5039b

# Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits of Bread Wheat (*Triticum aestivum* L.) Genotypes

**Demeke Zewdu[1*], Fikru Mekonnen[2], Negash Geleta[1] and Kibret Abebe[3]**

[1]Ethiopian Institute of Agricultural Research, Kulumsa Agricultural Research Center, P.O. Box 489 Asella, Ethiopia
[2]Dept. of Plant science, Wollo University College of Agriculture, Dessie, Ethiopia
[3]Dept. of Plant Science, College of Agriculture and Natural Resource Mekdela Amba University, Ethiopia

**Corresponding Author**

Demeke Zewdu
*e-mail*: demekezewdu21@gmail.com

**Article History**

Received on 05th December, 2023
Received in revised form on 10th February, 2024
Accepted in final form on 18th February, 2024

## Abstract

Wheat (*Triticum aestivum* L.) is a self-pollinating annual plant extensively grown as staple food source in the world. Information on the extent of genetic variability, heritability and genetic advance among different traits of bread wheat genotypes is essential to designing breeding strategies. The research was conducted at Kulumsa in (8th July–16th November, 2021) with the objective to assess the extent of genetic variability, heritability and genetic advance among different traits of bread wheat genotypes. A total of 64 bread wheat genotypes were evaluated for 16 traits in 8*8 simple lattice design. ANOVA revealed a highly significant ($p \leq 0.01$) difference among the tested bread wheat genotypes for all studied traits. High PCV and GCV were observed from grain yield, yield head$^{-1}$, head weight, biomass yield and moderate thousand kernel weight, peduncle length, number of effective tillers plant$^{-1}$ and number of kernel spike$^{-1}$. High broad sense heritability coupled with high genetic advance as percent of mean were obtained from grain yield, biomass yield, yield head$^{-1}$, peduncle length and thousand kernel weight whereas, head weight, harvest index and number of kernel spike$^{-1}$ had moderately high heritability and high genetic advance as percent of mean. Therefore, the attention should be given for those traits for wheat breeding program, because the phenotypic expression of these characters governed by additive gene action. Hence, direct selection for these traits will be improved grain yield.

***Keywords:*** Genetic advance, genetic variability, heritability, yield related traits

## 1. Introduction

Wheat (*Triticum aestivum* L.), is a self-pollinating annual plant, it is in the true grass family, *Gramineae*, is extensively grown as staple food source in the world (Mollasadeghi and Shahryari, 2011). And it is one of the most important crop among the prime cereals at the global level (Wani et al., 2018). Bread Wheat evolved through years of cultivation in the southern Caspian plains (Feldmann, 2001). Wheat is the second important food crop after rice worldwide (Nishant et al., 2018) and it provides 20% of the calories and protein and feeding about 40% of the world population (Braun et al., 2010, Shiferaw et al., 2013). Mollasadeghi and Shahryari, 2011)

The world wheat production reaches about 776.5 mt in 2020, also estimated and forecasted to be 778.3 and 770.3 mt by 2021 and 2022 respectively (Anonymous, 2022). Wheat is not only the most important food security crop but also it is currently becoming strategic as a cash crop at the global level (Tadesse et al., 2017, Crespo-Herrera et al., 2018). World wheat trade in 2020/21 was pegged at a record 186.6 million tonnes, 1.2% (2.3 mt) exceeding the previous season (Anonymous, 2021).

Ethiopia is one of the largest wheat producer country in Africa (Yasin, 2015, Regasa, 2019) in Ethiopia, wheat production is based on two modern species: hexaploid wheat (*Triticum aestivum* L, 2n=6x=42, AABBDD) and durum or tetraploid wheat (*T. turgidum* subsp. durum, 2n=4x=28, AABB). Wheat ranks second next to maize in terms of yield production (57,801,305.96 q) and third in terms of area coverage (1,897,405.05 hectares) following tef and maize among cereals for rain fed production in Ethiopia ( Anonymous, 2021).

Wheat production in Ethiopia for 2021/22 is projected to 5.18 mt, up by 1.6% over the 2020/21 production estimated. This is due to more Government of Ethiopia engagement in irrigation, better input supply, and mechanized farming in the lowland and central parts of the country (Anonymous, 2021), Rapid population growth associated with increased urbanization and change in food preference for easy and fast food such as bread, biscuits, pasta and porridge (Tadesse et al., 2018). However, wheat production and productivity is relatively small by global standards. The main reason is that mostly subsistence farming of wheat is produced by small-scale farmers through rain feed production system with less irrigated production (Anteneh and Asrat, 2020) and constrained by several infectious diseases including rust and Septoria leaf blotch diseases which are the major problem of wheat production in Ethiopia (Hailu and Woldeab, 2015; Tadesse et al., 2018)

The major wheat producing areas in Ethiopia are located in Oromiya region (Arsi, Bale, Shewa, Walega, Jima, Guji and Harerghe), in Amhara region (North, south and central Gondar zone, East and west Gojam, North and South Wollo, North Shewa and Awi ) in Southern Nations Nationalities & Peoples Region, Tigray region, Benishangul Gumuz region and Afar region (Anonymous, 2021).

Precise knowledge about germplasm variability, heritability and genetic advance is a pre-requisite for crop improvement programs, as it helps in the development of superior recombinants for all traits of interest (Rauf et al., 2012, Tilahun et al., 2020). The existence of genetic variability is very essential to meet the present and future crop breeding challenges (Hailu, 2011), Such as breeding for increasing yield, wider adaptation, desirable quality, drought tolerance, insect and disease resistance (Ferdous et al., 2011). Therefore the present study was conducted with the objective to assess the extent of genetic variability, heritability and genetic advance for different traits of bread wheat genotypes.

## 2. Materials and Methods

### *2.1. Experimental site and time*

The research was conducted at Kulumsa agricultural research center main station in 2021 (8 July-16 November) main cropping season. The experimental site is located at at 08$^{o}$01’10”Nlongitude and 39$^{o}$09’11”E latitude at an altitude of 2200 meters above sea level. The mean annual rain fall of the site is 820 mm with an average annual temperature of 16.5°C.

### *2.2. Experimental materials and design*

The experiment was laid out in an 8 x 8 simple lattice design with two replications. The 64 introduced bread wheat genotypes from International Maize and Wheat Improvement Center (CIMMYT) and International Center for Agricultural Research in Dry Areas (ICARDA) were randomly selected for study (Table 1).

### *2.3. Data collected*

Data was collected from the mean of ten sample plants for

Table 1: Materials used in the study

| Entry | source | Pedigree |
|---|---|---|
| 1 | CIMMYT | rolf07*2/3/prinia/pastor//huites/4/2*sup152/akuri//sup1 |
| 2 | ICARDA | 06w31476//milan/pastor/4/heilo/3/sw89.5277/borl95//skauz |
| 3 | ICARDA | usher-18/wafir-6 |
| 4 | CIMMYT | nd643/2*trch//mutus/3/sup152/4/kachu #1/kiritati//kachu |
| 5 | ICARDA | munia//chen/altar 84/3/chen/aegilops squarrosa (taus)//bcn/4/marchouch-8/5/afif |
| 6 | CIMMYT | francolin#1/7/reh/hare//2*bcn/3/croc_1/ae.squarrosa(213)//pgo/4/huites/5/t.speltapi348599/6/reh/hare//2*bcn/3 |
| 7 | ICARDA | NAVJ07/SHORTENED SR26 TRANSLOCATION/3/ATTILA/BAV92//PASTOR |
| 8 | CIMMYT | bavis/3/attila/bav92//pastor/5/croc_1/ae.squarrosa(205)//borl95/3/prl/sara//tsi/vee#5/4/fret2/6/mutus//wbll1*2/brambling/3 |
| 9 | ICARDA | attila/4/weaver/tsc//weaver/3/weaver/5/brbt1*2//tui/clms/6/teg/mian yang 20//chum18/5*bcn |
| 10 | CIMMYT | chipak/3/swsr22t.b./2*blouk #1//wbll1*2/kuruku |
| 11 | CIMMYT | sokoll/3/pastor//hxl7573/2*bau*2/6/oasis/5*borl95/5/cndo/r143//ente/mexi75/3/ae.sq/4/2*oc |
| 12 | CIMMYT | kachu*2/3/nd643//2*prl/2*pastor/4/kachu/danphe |
| 13 | ICARDA | sw89-5124*2/fasan/3/cazo/kauz//kauz/4/wbll1/5/ac8528/sova/6/milan/s87230//babax |
| 14 | ICARDA | usher-16//kamb2/pandion/3/huites/pandion |
| 15 | CIMMYT | altar 84/ae.squarrosa (221)//3*borl95/3/ures/jun//kauz/4/wbll1/5/mutus*2/6/danphe #1/kenya sunbird//danphe |
| 16 | ICARDA | kronstad/3/fret2/kukuna//fret2/6/altar84/ae.squarrosa(jbangor)//esda/3/heilo/5/cno79//pf70 |

Table 1: Continue...

| Entry | source | Pedigree |
|---|---|---|
| 17 | ICARDA | nabuq-1//kamb2/pandion/5/02w50807/4/pfau/seri.1b//amad/3/waxwing |
| 18 | CIMMYT | wbll1*2/brambling*2//bavis/3/kachu #1/kiritati//kachu |
| 19 | ICARDA | nesser/seri//milan/pastor/3/florkwa-2/asfoor-5 |
| 20 | ICARDA | kronstad/3/fret2/kukuna//fret2/6/altar 84/ae.squarrosa (jbangor)//esda/3/heilo/5/ cno79//pf70354/mus/3/pastor/4/babax |
| 21 | CIMMYT | mutus//nd643/2*wbll1/3/swsr22t.b./2*blouk #1//wbll1*2/kuruku |
| 22 | CIMMYT | tacupetof2001/brambling//pvn/3/iwa8600211//2*pbw343*2/kukuna/4/pbw343*2/kukuna*2//frtl/pifed/5/mutus/akuri-5 |
| 23 | ICARDA | attila-7/sunco//05w90045 |
| 24 | CIMMYT | kachu#1//wbll1*2/kukuna/3/brbt1*2/kiritati/6/rolf07*2/5/reh/hare//2*bcn/3/croc_1/ae.squarrosa(213)//pgo/4/huites/7/borl14 |
| 25 | CIMMYT | kachu/becard//wbll1*2/brambling*2/3/frncln*2/tecue #1 |
| 26 | ICARDA | katila-9/3/ning mai 96035/finsi//heilo |
| 27 | CIMMYT | grack/tecue #1//frncln*2/5/site/mo//pastor/3/tilhi/4/waxwing/kiritati |
| 28 | ICARDA | cham-10/3/tnmu//milan/tui/4/sandall-5 |
| 29 | ICARDA | 02w50807/rsmf8 704//mace |
| 30 | CIMMYT | kutz*2//kfa/2*kachu |
| 31 | CIMMYT | wbll1*2/kuruku//heilo/3/kanchan*2/juchi/4/parus/francolin #1 |
| 32 | ICARDA | nejmah-14/4/bl2064//sw89-5124*2/fasan/3/tilhi/5/05w90045 |
| 33 | CIMMYT | premio/4/croc_1/ae.squarrosa (205)//kauz/3/pifed/5/borl14 |
| 34 | CIMMYT | trap#1/bow/3/vee/pjn//2*tui/4/bav92/rayon/5/kachu#1/6/toba97/pastor/3/t.dicocconpi94624/ae.squarrosa(409)//bcn/4/bl |
| 35 | ICARDA | girwill-13/2*pastor-2//sids-1/3/gladius |
| 36 | CIMMYT | fret2*2/shama//kachu/3/mutus*2/muu |
| 37 | ICARDA | bow #1/fengkang 15//nesma*2/261-9/3/ducula/4/sids-1/5/gladius |
| 38 | CIMMYT | mayil//mutus*2/haril #1/3/mayil |
| 39 | CIMMYT | kiritati/4/2*seri.1b*2/3/kauz*2/bow//kauz/5/cmh81.530/6/manku |
| 40 | ICARDA | prl/2*pastor//seri/4/milan/kauz//prinia/3/babax/5/hubara-3*2/shuha-4/6/kamb2/pandion |
| 41 | CIMMYT | francolin#1/7/huites/5/t.speltapi348599/6/reh/hare//2*bcn/3/croc1/ae.squarrosa/8/trap#1/bow/3/vee/pjn//2*tui/4/bav92/rayon/5 |
| 42 | CIMMYT | sntl/3/kachu//wbll1*2/brambling |
| 43 | ICARDA | worrakatta/2*pastor//aguilal/flag-3 |
| 44 | ICARDA | pastor/3/gen*2//buc/flk/4/pastor/5/kamb2/pandion/ 6/02w50807/rsmf8 704 |
| 45 | CIMMYT | mayil/8/seri.1b*2/3/kauz*2/bow//kauz/4/pbw343*2/tukuru/5/c80.1/3*batavia//2*wbll1/6/cmh75a.66/seri/7/munal #1/9/manku |
| 46 | CIMMYT | chrz//bow/crow/3/wbll1/4/croc_1/ae.squarrosa (213)//pgo/5/borl14 |
| 47 | CIMMYT | becard/frncln//borl14 |
| 48 | CIMMYT | ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE |
| 49 | ICARDA | kabowsh-7/5/shuha-6//ns732/her/4/croc-1/ae.squarrosa (205)//fct/3/pastor |
| 50 | CIMMYT | borl14*2/7/muu/5/wbll1*2/4/yaco/pbw65/3/kauz*2/trap//kauz/6/wbll1*2/shama |
| 51 | CIMMYT | saual/3/achtar*3//kanz/ks85-8-4/4/saual*2/5/attila*2/pbw65//muu #1/3/francolin #1 |
| 52 | ICARDA | hubara-15/zemamra-8//massira/4/frame//milan/kauz/3/pastor |

Table 1: Continue...

| Entry | source | Pedigree |
|---|---|---|
| 53 | ICARDA | hubara-1/3/munia/chto//milan/4/goumria-8/5/afif |
| 54 | CIMMYT | slvs/attila//wbll1*2/3/gondo/cbrd/4/borl14 |
| 55 | ICARDA | altar84/ae.squarrosa(jbangor)//esda/3/heilo/5/cno79//pf70354/mus/3/pastor/4/babax/6/02w50807_1/rsmf8 704 |
| 56 | ICARDA | gonglase-4/4/croc_1/ae.squarrosa (205)//kauz/3/2*kauz*2/yaco//kauz/5/teg/mianyang 20//chum18/5*bcn |
| 57 | ICARDA | soonot-10/hubara-15//jawahir-14 |
| 58 | CIMMYT | saar//inqalab 91*2/kukuna/3/villa juarez f2009*2/4/fret2*2/shama//kiritati/2*trch/3/baj #1 |
| 59 | ICARDA | nada-1/5/milan/munia/3/pastor//munia/altar84/4/milan/ducula/6/huites/pandion |
| 60 | ICARDA | kronstad/3/fret2/kukuna//fret2/6/altar84/ae.squarrosa(jbangor)//esda/3/heilo/5/cno79//pf70354/mus/3/pastor/4/babax |
| 61 | ICARDA | miskeet-18/3/cbrd/wbll1//pandion/5/ald/coc//ures/3/ducula /4/metso |
| 62 | ICARDA | qafzah-33/florkwa-2//excalibur/3/doukkala-33 |
| 63 | ICARDA | weebill-1/2*qafzah-21//kamb2/pandion/3/teg/mian yang 20//chum18/5*bcn |
| 64 | CIMMYT | muu/kbird//2*kachu/kiritati |

the characters like plant height, effective tillers plant$^{-1}$, tillers plant$^{-1}$ and spikelets spike$^{-1}$, spike length, kernels spike$^{-1}$, head weight, yield head$^{-1}$, peduncle length and spike length. However, plot base data were collected for the characters such as days to heading and maturity, grain yield, harvest index, hectoliter weight, thousand kernels weight and above-ground biomass yield.

### *2.4. Data analysis*

### *2.4.1. Analysis of variance (ANOVA)*

The analysis of variance (ANOVA) was performed using the R software version 4.1.2 for simple Lattice Design (R core team, 2021). The ANOVA was conducted using the following mathematical model:

$P_{ijk}=\mu+g_i+r_j++b_{k(j)}+e_{ijk}$ , Where: Pijk=phenotypic value of i$^{th}$ genotype under j$^{th}$ replication and k$^{th}$ incomplete block within replication j; μ = grand mean; gi = the effect of i$^{th}$ genotype; rj = the effect of replication j; bk(j)=the effect of incomplete block k within replication j and eijk=the residual or effect of random error

### *2.4.2. Estimation of phenotypic and genotypic variance*

Genotypic and phenotypic variance components and coefficient of phenotypic and genotypic variability were estimated according to the statistical procedure of SAS software (SAS, 2014) using mixed model (i.e. treatment as random and replication and block as fixed to generated genotypic variance and residual (error variance)) and calculated other components with excel by using the formula as follows (Burton and Devane, 1953):

Genotypic variance ($\sigma^2g$)=(MSg-MSe)/r,

Phenotypic variance ($\sigma^2p$)=$\sigma^2g+\sigma^2e$

Where:-, $\sigma^2e$=Environmental variance, r=Number of replication, MSe=Error, MSg=Mean square of genotype. Phenotypic and genotypic coefficients of variations were expressed as a percentage of the corresponding phenotypic and genotypic standard deviations as described by Johnson et al. (1955)

Phenotypic coefficient of variation (PCV)=$(\sqrt{\sigma^2p}/\bar{X})\times100$ ,

Genotypic Coefficient of Variation (GCV)=$(\sqrt{\sigma^2g}/\bar{X})\times100$, Where:-$\bar{X}$= grand mean.

### *2.4.3. Estimates of heritability in broad sense*

Heritability is a useful technique that estimates the performance of parents in hybrids. The highest heritability in any character shows its highest transmitting ability to the next generation (Ajmal et al., 2009). Broad sense heritability was categorized as low (0–40%), medium (40–59%), moderately high (60–79%) and very high (>80%) as suggested by Singh (2001). Heritability ($H^2$) was computed by excel for each character based on a formula developed by Allard 1960 as $H^2=(\sigma^2g/\sigma^2p)\times100$

Where:- $\sigma^2p$=phenotypic Variance, $\sigma^2g$=genotypic variance and $H^2$=Broad sense heritability

### *2.4.4. Estimation of expected genetic advance*

There is a direct relationship between heritability and response to selection, which is referred to as genetic progress. The expected response to selection is called genetic advance (GA). High genetic advance coupled with high heritability estimates offers the most effective condition for selection (Tesfaye et al., 2014). Genetic advance as percent mean (GAM) was categorized as low (0–10%), moderate (10–20%) and high (>20%) as suggested by Johnson et al. (1955).The genetic advance (GA) for selection intensity (K) at 5% was calculated with excel by the formula suggested by Allard (1960) as: GA=(K) ($\sigma p$) ($H^2$) Where:- GA=Expected genetic advance at 5% selection intensity, σp=Phenotypic standard deviation, $H^2$=Heritability, K=Selection differential (K=2.063 at 5% selection intensity). Genetic advance as percent of the mean (GAM) was calculated by excel used the formula as (Johnson et al., 1955). GAM=(GA/$\bar{X}$)×100, Where:- GAM= Genetic advance as percent of mean, GA = Genetic advance at 5% selection intensity, $\bar{X}$=Population mean

## 3. Results and Discussion

### 3.1. Analysis of variance (ANOVA)

The results of the analysis of variance (ANOVA) of 16 quantitative characters for the 64 wheat genotypes were presented in Table 2. There were highly significant differences at ($p$<0.01) among the tested genotypes for all studied traits including days to heading, days to maturity, plant height, number of tillers plant$^{-1}$, number of effective tillers plant$^{-1}$, number of spikelets spike$^{-1}$, number of kernel spike$^{-1}$, peduncle length, spike length, head weight, yield head$^{-1}$, biomass yield, grain yield, hectoliter weight, thousand kernel weight and Harvest Index. This significant genetic variation among genotypes suggested that the genotypes were genetically diverse and it could be a good opportunity for breeders to select genotypes for the trait of interest for variety development.

A similar results reported that the analysis of variance revealed that the genotypes possess significant genetic variability among all traits including days to 50% heading, days to 90% physiological maturity, plant height, 1000 kernel weight and grain yield at ($p$<0.01) (Wani et al., 2018) and the same finding also reported for days to heading, days to maturity, plant height, spike length, spikelet spike$^{-1}$, kernel spike$^{-1}$, 1000 kernel weight and grain yield (Semahegn et al., 2021), and confirmed by several scholars there were significant genetic variability among bread wheat genotypes for all traits including days to heading, days to maturity, plant height, grain yield, 1000 kernel weight, hectoliter weight, biomass yield, harvest index, tillers plant$^{-1}$, spikes length, spikelet's spike$^{-1}$ and kernels spike$^{-1}$ (Alemu et al., 2017; Wani et al., 2018; Semahegn et al., 2021; Getachew et al., 2021), Effective tillers plant$^{-1}$ and Peduncle length (Muhammad et al., 2021, Kumar et al., 2013) and yield head$^{-1}$ (Upadhyay et al., 2019).

### 3.2. Mean performance of studied bread wheat genotypes

Genotypes showed a wide range of variability in most traits (Table 3). A range of Variation was recorded days to maturity ranged from 105.75 to 128 days with the mean of 119.91 days

Table 2: Mean squares of 16 characters of 64 bread wheat genotypes evaluated at Kulumsa Agricultural Research center in 2021/22

| Traits | Replication (DF=1) | Block (Replication) (DF=14) | Genotypes (DF=63) | Error (DF=49) | CV (%) | $R^2$ |
|---|---|---|---|---|---|---|
| DTH | 2.26 | 1.36 | 34.14$^{**}$ | 0.43 | 1.01 | 0.99 |
| DTM | 12.50 | 2.41 | 29.09$^{**}$ | 1.06 | 0.86 | 0.97 |
| PHT | 3.06 | 5.64 | 86.35$^{**}$ | 6.58 | 2.63 | 0.94 |
| NTPP | 1.49 | 0.81 | 0.51$^{**}$ | 0.24 | 12.09 | 0.79 |
| NETPP | 0.01 | 0.86 | 0.42$^{**}$ | 0.12 | 10.64 | 0.87 |
| NSPS | 1.76 | 0.29 | 2.62$^{**}$ | 0.33 | 3.11 | 0.91 |
| NKPS | 10.93 | 26.57 | 88.26$^{**}$ | 11.08 | 6.95 | 0.92 |
| PDL | 3.38 | 1.43 | 17.49$^{**}$ | 0.98 | 5.91 | 0.96 |
| SL | 4.13 | 0.14 | 0.93$^{**}$ | 0.15 | 4.61 | 0.90 |
| HW | 0.44 | 0.04 | 0.55$^{**}$ | 0.07 | 11.59 | 0.91 |
| YH | 0.01 | 0.09 | 0.35$^{**}$ | 0.03 | 11.67 | 0.93 |
| BY | 180751 | 1683000 | 17718960$^{**}$ | 680580 | 6.49 | 0.97 |
| GY | 1592291.5 | 365916.2 | 2817865$^{**}$ | 202758.7 | 12.22 | 0.95 |
| HLW | 33.11 | 4.26 | 62.26$^{**}$ | 2.26 | 1.98 | 0.97 |
| TKW | 35.70 | 8.09 | 67.29$^{**}$ | 5.08 | 6.95 | 0.95 |
| HI | 108.62 | 24.53 | 62.69$^{**}$ | 11.02 | 11.64 | 0.89 |

* and **: Indicates significant at ($p$=0.05) and highly significant at ($p$=0.01) probability levels respectively; DTH: Days to heading; DTM: Days to maturity; PHT: Plant height; NTPP: No. of tillers plant$^{-1}$; NETPP: No. of effective tillers plant$^{-1}$; NSPS: No. of spikelet spike$^{-1}$; NKPS: No. of kernels spike$^{-1}$; PDL: Peduncle length; SL: Spike length; HW: Head weight; YH: Yield head$^{-1}$; BY: Biomass yield; GY: Grain yield; HLW: Hectoliter weight; TKW: Thousand kernel weight; HI: Harvest index; CV: Coefficient of variations; DF: Degree of freedom

Table 3: Estimations of mean, range, variance components, broad sense heritability and genetic advance as percent of means

| Traits | Range | Mean±SE | $\sigma^2$g | $\sigma^2$p | $\sigma^2$e | GCV (%) | PCV (%) | ECV (%) | $H^2$ (%) | GA | GAM (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| DTH | 55.31–74.94 | 65.79±0.51 | 16.96 | 17.39 | 0.43 | 6.26 | 6.34 | 1.00 | 97.51 | 8.39 | 12.75 |
| DTM | 105.75–128 | 119.91±0.80 | 13.19 | 14.25 | 1.05 | 3.03 | 3.15 | 0.86 | 92.60 | 7.21 | 6.01 |
| PHT | 76.54–112.03 | 97.42±2.00 | 40.36 | 46.99 | 6.63 | 6.52 | 7.04 | 2.64 | 85.89 | 12.15 | 12.47 |
| NTPP | 2.5–5.6 | 4.04±0.38 | 0.18 | 0.44 | 0.26 | 10.46 | 16.35 | 12.57 | 40.91 | 0.56 | 13.80 |
| NETPP | 2.11–4.74 | 3.26±0.27 | 0.22 | 0.35 | 0.13 | 14.55 | 18.19 | 10.91 | 64.03 | 0.78 | 24.02 |
| NSPS | 15.93–21.65 | 18.48±0.45 | 1.18 | 1.51 | 0.34 | 5.87 | 6.65 | 3.14 | 77.80 | 1.97 | 10.68 |
| NKPS | 28.55–65.96 | 47.92±2.60 | 38.77 | 49.73 | 10.96 | 12.99 | 14.72 | 6.91 | 77.96 | 11.34 | 23.67 |
| PDL | 8.75–25.1 | 16.74±0.77 | 8.13 | 9.12 | 0.99 | 17.04 | 18.04 | 5.94 | 89.17 | 5.56 | 33.19 |
| SL | 6.72–10.02 | 8.43±0.30 | 0.36 | 0.51 | 0.15 | 7.08 | 8.45 | 4.62 | 70.13 | 1.03 | 12.23 |
| HW | 0.98–3.73 | 2.34±0.21 | 0.23 | 0.31 | 0.07 | 20.73 | 23.71 | 11.52 | 76.41 | 0.87 | 37.38 |
| YH | 0.36–2.44 | 1.55±0.14 | 0.15 | 0.19 | 0.03 | 25.32 | 27.86 | 11.63 | 82.57 | 0.74 | 47.46 |
| BY | 5524–20491 | 12703±6.44 | 7731122 | 8413916 | 682794 | 21.89 | 22.83 | 6.50 | 91.88 | 5498.48 | 43.28 |
| HLW | 52.59–83.27 | 76.16±1.17 | 31.53 | 33.79 | 2.26 | 7.37 | 7.63 | 1.98 | 93.30 | 11.19 | 14.69 |
| TKW | 13.04–44.29 | 32.42±1.76 | 33.16 | 38.25 | 5.09 | 17.76 | 19.08 | 6.96 | 86.69 | 11.06 | 34.12 |
| GY | 11.37–38.04 | 28.52±2.59 | 1339980 | 1542538 | 202558 | 31.41 | 33.70 | 12.21 | 86.87 | 2225.77 | 60.40 |
| HI | 844–5849 | 3685±3.52 | 26.46 | 37.43 | 10.97 | 18.00 | 21.41 | 11.59 | 70.70 | 8.92 | 31.23 |

Note. $\sigma^2$g: genotypic variance; $\sigma^2$p: phenotypic variance; $\sigma^2$e: environmental variance; GCV: genotypic coefficient of variation; PCV: phenotypic coefficient of variation; ECV: environmental coefficient of variation; $H^2$: broad sense heritability; GA: genetic advance; GAM: genetic advance as percent of mean; DTH: days to heading; DTM: days to Maturity; PHT: plant height; NTPP: number of tillers per plant; NETPP: number of effective tillers per plant; NSPS: number of spikelet per spike; NKPS: number of kernels per spike; PDL: peduncle length; SL: spike length; HW: head weight; YH: yield per head; BY: biomass yield; GY: grain yield; HLW: hectoliter weight; TKW: thousand kernel weight; HI: harvest index; SE: standard error

No. of spikelet spike$^{-1}$ ranged from 15.94 to 21.65 with mean of 18.48, No. of kernel spike$^{-1}$ ranged from 28.55 to 65.96 with mean of 47.92 **,** Head weight ranged from 0.98 g to 3.73 g with mean of 2.34 g, yield head$^{-1}$ ranged from 0.36 g to 2.44 g with mean of 1.55 g, Thousand kernels weight ranged from 13.04 g to 44.29 g with mean of 32.42 g). Harvest index ranged from 11.37% to 38.04% with mean of 28.52%, Grain yield ranged from 844 kg ha$^{-1}$ to 5849 kg ha$^{-1}$ with mean of 3685 kg ha$^{-1}$ and Biomass yield ranged from 5524 kg ha$^{-1}$ to 20491 kg ha$^{-1}$ with mean of 12703 kg ha$^{-1}$.

The present result agreed with (Fikre et al., 2015, Naik et al., 2015, Alemu et al., 2017, Muhammad et al., 2021) who reported that grain yield and yield related characters of bread wheat genotypes mean performance showed wide range of values and these wide ranges of Variation among genotypes can have high contribution for further improvement of important traits in wheat breeding program.

### *3.3. Estimation of genotypic and phenotypic coefficient of variations*

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged from 3.03% to 31.41% and 3.15%–33.70% respectively. The Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values can be categorized as low (<10%), moderate (10–20%), and high (>20%) (Sivasubramanian and Menon, 1973). Accordingly, High GCV and PCV (>20%) were observed for grain yield maximum value (31.41% and 33.70%) followed by yield per head (25.32% and 27.86%), head weight (20.73% and 23.71%), biomass yield (21.89% and 22.83%) and moderate (18.00%) and high (21.41%) harvest index, respectively.

The present finding lined with Kumar et al. (2019) who reported High PCV and GCV for grain yield and yield per head (kernel weight per head) and also high PCV and GCV reported for grain yield, biomass yield and harvest index (Dutamo et al., 2015). Tilahun et al. (2020). Similarly found high PCV for grain yield and harvest index and moderate GCV for harvest index and in contrast to the present finding moderate GCV for grain yield and moderate PCV and GCV for biomass yield. Oppositely with the present result observed moderate PCV and GCV for Yield per head (Rajput et al., 2019) and (Mohant et al., 2016).

Moderate range of genotypic and phenotypic coefficient of variation (10–20%) were observed for thousand Kernel Weight (17.76% and 19.08%), peduncle length (17.04% and

18.04%), and number of effective tillers plant$^{-1}$ (14.55% and 18.19%), number of kernel spike$^{-1}$ (12.99% and 14.72%) and number of tillers plant$^{-1}$ (10.46% and 16.35%) respectively. Similarly Fikre et al. (2015) reported moderate PCV and GCV for thousand Kernel Weight, number of kernel spike$^{-1}$ and number of productive tiller and Rajput et al. (2019) reported low PCV and GCV number of tillers plant$^{-1}$. Contrasted to the present result Dutamo et al. (2015a) observed high PCV and GCV for thousand Kernel Weight, number of kernel per spike and number of fertile tillers and Atinafu et al. (2020) reported high PCV and GCV for peduncle length.

The low values of phenotypic and genotypic coefficient of variation (<10%) were observed for spike length (8.73% and 7.42%), Hectoliter Weight (7.46% and 7.19%), plant height (7.00% and 6.48%), days to heading (6.32% and 6.24%), number of spikelets spike$^{-1}$ (6.57% and 5.78%) and minimum value of PCV and GCV was observed in days to maturity (3.24% and 3.12%) respectively. The present result in agreement with Tilahun et al. (2020), Kabir et al. (2017) and Obsa et al. (2017) Who reported low PCV and GCV for plant height, days to heading and days to maturity, Tilahun et al. (2020) and Obsa et al. (2017) observed low PCV and GCV for spike length, Tilahun et al. (2020) recorded low PCV and GCV for Hectoliter Weight, Similarly, Obsa et al. (2017) reported low PCV and GCV for number of spikelets spike$^{-1}$.

### *3.4. Estimation of heritability and genetic advance*

Broad sense Heritability ranged from 40.91% for number of total tillers plant$^{-1}$ to 97.51% for days to heading. Broad sense heritability was categorized as low (0–40%), medium (40–59%), moderately high (60–79%) and very high (>80%) as suggested by Singh (2001). Based on these categories traits such as days to heading (97.51%), Hectoliter Weight (93.30%), days to maturity (92.60%), biomass yield (91.88%), peduncle length (89.17%), grain yield (86.87%), Thousand Kernel Weight (86.69%, plant height (85.89%) and yield per head (82.57%) had very high broad sense heritability. Similar result were documented that high estimates of heritability for days to heading, days to maturity and plant height (Rajput et al., 2019, Upadhyay et al., 2019), and 1000 kernel weight (Fikre et al., 2015, Kabir et al., 2017), biomass yield (Muhammad et al., 2017; Atinafu et al., 2020, Sami et al., 2021) and also high heritability was noticed for peduncle length ( Upadhyay et al., 2019). similarly high heritability for biomass yield and grain yield (Sami et al., 2021) and high heritability for yield head$^{-1}$ (Mohant et al., 2016) and for peduncle length (Muhammad et al., 2017, Muhammad et al., 2021).

Number of kernel spike$^{-1}$ (77.96), number of spikelets spike$^{-1}$ (77.80%), head weight (76.41%), spike length (70.13%), harvest index (70.70%) and number of effective tillers plant$^{-1}$ (64.03%) were observed moderately high broad sense heritability, whereas number of total tillers plant$^{-1}$ (40.91%) was observed medium broad sense heritability. Earlier work reported that moderately high heritability was noticed for number of kernel spike$^{-1}$ (Muhammad et al., 2021, Tilahun et al., 2020), spike length (Yadav et al., 2014) and moderately high broad sense heritability for number of spikelets spike$^{-1}$ and spike length (Mohant et al., 2016). And for spike length and harvest index (Puneet et al., 2020). Medium heritability for tiller plant$^{-1}$ (Muhammad et al., 2021).

Genetic advance as percent of mean ranged from 6.01% to 60.40% for days to maturity and grain yield respectively. The genetic advance as percent mean (GAM) was categorized as low (0–10%), moderate (10–20%) and high (>20%) as suggested by Johnson et al. (1955). Accordingly, Traits which had high genetic advance as percent of mean were grain yield maximum value (60.40%), yield head$^{-1}$ (47.46%), biomass yield (43.28%), head weight (37.38%), thousand Kernel Weight (34.12%), peduncle length (33.19%), harvest index (31.23%), number of effective tiller plant$^{-1}$ (24.02%) and number of kernel spike$^{-1}$ (23.67%).

Similar finding reported by Upadhyay et al. (2019) High GAM for grain yield, yield head$^{-1}$, thousand Kernel Weight and peduncle length and Kabir et al. (2017) reported high GAM for grain yield plot$^{-1}$ and ha$^{-1}$ and harvest index. Similarly Mohant et al. (2016) reported high GAM for yield head$^{-1}$ and Kumar et al. (2020) reported hight GAM for grain yield and biomass yield and contrast to the present study moderate GAM for harvest index.

Moderate genetic advance as present of mean was observed from Hectoliter Weight (14.69%), number of tillers plant$^{-1}$ (13.80%), days to heading (12.75%), plant height (12.47%), spike length (12.23%) and number of spikelets spike$^{-1}$ (10.68%) however, days to maturity had low (6.01) genetic advance as present of mean. Earlier work reported by Obsa et al. (2017) that Plant height, spike length and spikelets spike$^{-1}$ had moderate GAM and Fikre et al. (2015) reported moderate GAM for spike length, plant height,tillers plant$^{-1}$ and effective tillers plant$^{-1}$ and low GAM for days to maturity. Similarly, moderate GAM for pant height and low GAM for days to maturity (Kabir et al., 2017) and moderet GAM for spike length (Kumar et al., 2020) and Mohant et al. (2016) reported moderate GAM for spike length and number of spikelets spike$^{-1}$.

Very high heritability coupled with high genetic advance as present of mean observed from traits such as grain yield, biomass yield, yield head$^{-1}$, peduncle length and thousand Kernel Weight whereas, head height, harvest index and number of kernel spike$^{-1}$ had moderately high heritability and high genetic advance as percent of mean. Therefore, these traits are useful for improvement of studied bread wheat lines by direct selection because high heritability coupled with high genetic advance indicates the presence of additive gene actions in the mode of inheritance of those traits. High broad sense heritability associated with high genetic advance over mean was observed for the traits such as Grain yield, biomass yield, yield head$^{-1}$, head weight, peduncle length, number of kernel spike$^{-1}$, thousand kernel weight and harvest index.

which indicated the dominance of additive genes action in controlling the expression of these traits (Upadhyay et al., 2019).

High broad sense heritability and Moderate genetic advance as present of mean recorded from characters such as days to heading, plant height, number of spikelets spike$^{-1}$, spike length and Hectoliter Weight. Whereas, number of effective tiller plant$^{-1}$ had medium broad sense heritability and Moderate genetic advance as present of mean. Number of tillers Plant$^{-1}$ had medium heritability and Moderate genetic advance as present of mean. Whereas, days to maturity was observed very high broad sense heritability coupled with low genetic advance as percent of mean. This trait controlled by non-additive gene action.

## 4. Conculusion

The ANOVA showed highly significant difference ($p$<0.01) for all studied traits. High PCV and GCV were observed for most studied traits. High heritability coupled with high genetic advance as percent of mean were obtained from grain yield, biomass yield, yield head$^{-1}$, peduncle length and thousand kernel weight whereas, head weight, harvest index and number of kernel spike$^{-1}$ had moderately high heritability and high genetic advance as percent of mean. Thus, attention should be given for those traits for breeding program.

## 5. Acknowledgement

The authors would like to thank for the financial support provided by Ethiopian Institute of Agricultural Research, and we are also grateful to Kulumsa Agricultural Research Center for its support in providing experimental materials and site to conduct this study.

## 6. References

Adugnaw, A., Dagninet, A., 2020. Wheat production and marketing in Ethiopia: Review study. Cogent Food & Agriculture, 6, 1778893.

Ajmal, S.U., Zakir, N., Mujahid, M.Y., 2009. Estimation of genetic parameters and character association in wheat. Journal of Agriculture and Biological Science 1(1), 15–18.

Alemu, D., Firew, M., Tadesse, D., 2017. Genetic variability and association among grain yield and yield related traits of bread wheat (*Triticum aestivum* L.) genotypes. Journal of Plant Breeding and Crop Science 11(2), 41–54, 2019 DOI:10.5897/JPBCS2016.0600

Anonymous, 2021. Crop prospects and food situation - quarterly global report No. 1, March 2021. Rome. Available from https://doi.org/10.4060/cb3672en. Accessed on March 21,2024

Anonymous, 2021. The Federal Democratic Republic of Ethiopia Central Statistical Agency Agricultural Sample Survey 2020/21 (2013 E.C.) Volume I Report on Area And Production of Major Crops. Available at http://www.statsethiopia.gov.et/wp-content/uploads/2021/05/2013-meher-report.final_.pdf. Accessed on December 17, 2023

Anonymous, 2021. Ethiopia grain and feed annual report Global Agricultural Information Network USDA Foreign Agriculture Service report rumber ET-0008 Available at https://apps.fas.usda.gov/newgainapi/api/Report/DownloadReportByFileName?fileName=Grain%20and%20Feed%20Annual_Addis%20Ababa_Ethiopia_03-15-2021, Accessed on December 17, 2023.

Anonymous, 2022. Crop Prospects and Food Situation – Quarterly Global Report No. 2, July 2022. Rome.Available from https://doi.org/10.4060/cc0868en. Accessed on March 21,2024

Anteneh, A., Asrat, D., 2020. Wheat production and marketing in Ethiopia: Review study. Cogent Food & Agriculture, 6(1), 1778893.

Atinafu, D.M., Alayachew, S.A., Heterat, K.Z., 2020. Study of genetic variability in some bread wheat accessions (*Triticum aestivum* L.) in gurage zone, Ethiopia. Asian Journal of Biological Sciences DOI: 10.3923/ajbs.2020.309.317.

Burton, G.W., Devane, E.H., 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. Agronomy Journal 45(10), 478–481.

Chimdesa, O., Mohammed, W., Eticha, F., 2017. Analysis of genetic variability among bread wheat (*Triticum aestivum* L.) genotypes for growth, yield and yield components in Bore district, Oromia regional state. Agriculture, Forestry and Fisheries 6(6), 188-199.

Dutamo, D., Alamerew, S., Eticha, F., Assefa, E., 2015. Genetic variability in bread wheat (*Triticum aestivum* L.) germplasm for yield and yield component traits. Journal of Biology, Agriculture and Healthcare 5, 140–147.

Endale, H., Getaneh, W., 2015. Survey of rust and septoria leaf blotch diseases of wheat in central Ethiopia and virulence diversity of stem rust *Puccinia graminis* f. sp. tritici. Advances in Crop Science and Technology 3(2), 166

Feldmann, 2001. Origin of cultivated wheat. In: Bonjean, A.P., Angus, W.J. (Eds.), The World wheat book. A history of wheat breeding. Lavoiser Publishing, France, 1, 3–56.

Ferdous, F., Miao, H., Leaird, D., Srinivasan, K., Wang, J., Chen, L., Varghese, L.T.,Weiner, A.M., 2011. Spectral line-by-line pulse shaping of on-chip microresonator frequency combs. Nature Photonics 5, 770–776.

Fikre, G., Alamerew, S., Tadesse, Z., 2015. Genetic variability studies in bread wheat (*Triticum aestivum* L.) genotypes at Kulumsa agricultural research center, South East Ethiopia. Journal of Biology, Agriculture and Healthcare, 5, 89–98.

Hailu, E., Woldeab, G., 2015. Survey of rust and septoria leaf blotch diseases of wheat in central Ethiopia and virulence diversity of stem rust *Puccinia graminis* f. sp. tritici. Advances in Crop Science and Technology 3(2), 166.

Hailu, 2011. Genetic diversity and grain protein composition of tetraploid wheat (*Triticum durum* Desf.) germplasm from Ethiopia, International Serial Book Number 978-91-576-7646-7,Available from https://res.slu.se/id/publ/35956 Accessed on March 21, 2024.

Kabir, R., Israr, A., Rehman, A.U., Qamar, M., Intikhab, A., 2017. Evaluation of bread wheat genotypes for variability and association among yield and yield related traits. International Journal of Biosciences 11(1), 7–14. ISSN: 2220-6655 (Print), 2222-5234.

Kumar, B., Singh, C.M., Jaiswal, K.K., 2013. Genetic variability, association and diversity studies in bread wheat (*Triticum aestivum* L.). The Bioscan 8, 143–147.

Kumar, P., Solanki, Y.P.S., Singh, V., Kiran, 2020. Genetic variability and association of morphophysiological traits in bread wheat (*Triticum aestivum* L.). Current Journal of Applied Science and Technology 39(35), 95–105. Article no.CJAST. 62266 ISSN: 2457-1024.

Mohant, S., Mukherjee, S., Mukhopadhyaya, S., Dash, A., 2016. Genetic variability, correlation and path analysis of bread wheat (*Triticum aestivum* L.) genotypes under terminal heat stress. International Journal of Bio-resource and Stress Management 7(6), 1232–1238.

Mollasadeghi, V., Shahryari, R., 2011. Important morphological markers for improvement of yield in bread wheat. Advances Environmental Biology 5(3), 538–542.

Muhammad, A., Fida, M., Quaid, H., Iqbal, H., Fawad, A., 2017. Heritability estimates and correlation analysis in bread wheat (*Triticum aestivum* L.) under normal and late plantings. Pure and Applied Biology. http://dx.doi.org/10.19045/bspab.2017.600123. 6, 1151–1160.

Muhammad, I., Mahpara, S., Bibi, R., Shah, R.U., Ullah, R., Abbas, S., Ullah, M.I., Hassan, A.M., Elshehawi, A.M., Brestic, M., 2021. Grain yield and correlated traits of bread wheat lines: Implications for yield improvement. Saudi Journal of Biological Sciences.

Naik, V.R., Biradar, S.S., Yadawad, A., Desai, S., Veeresha, B., 2015. Study of genetic variability parameters in bread wheat (*Triticum aestivum* L.) genotypes. Research Journal of Agricultural Science 6(1), 123–125.

Nishant, B., Arun B., Mishra, V.K., 2018. Genetic variability, heritability and correlation study of physiological, yield traits in relation to heat tolerance in wheat (*Triticum aestivum* L.). Biomedical Journal of Scientific & Technical Research 2(1), 1–5. DOI : 10.26717/BJSTR.2018.02.000636.

Rajput, R.S., 2019. Path analysis and genetic parameters for grain yield in bread wheat (*Triticum aestivum* L.). Annual Research & Review in Biology 31(3), 1–8.

Rauf, S., Tariq S.A., Hassan, S.W., 2012. Estimation of pedigree based diversity in Pakistani wheat (*Triticum aestvium* L.) germplasm. Communications in Biometry and Crop Science 7(1), 14–22.

Regasa, D., 2019. Wheat production, marketing and consumption in Ethiopia. Journal of Marketing and Consumer Research An International Peer-reviewed Journal 55, 10–19. ISSN 2422-8451, 55, DOI: 10.7176.

Sami, U.A., Azeem, A., Sher, A., Ijaz, M., Sattar, A., Saleem, M.A., Bibi, M., Abbas, N., Hussain, M., 2021. Assessment of genetic variability and direct-indirect contribution of post-anthesis traits to the grain yield in bread wheat (*Triticum aestivum* L.) at different sowing dates. International Journal of Agriculture and Biology 26(1), 193–200.

Shiferaw, B., Smale, M., Braun, H.J., Duveiller, E., Reynolds, M., Muricho, G., 2013. Crops that feed the world 10. Past successes and future challenges to the role played by wheat in global food security. Food Security 5, 291–317.

Sivasubramanian, S., Menon, N., 1973. Heterosis and inbreeding depression in rice. Madras Agricultural Journal 60, 1139–1144.

Tadesse, W., Halila H., Jamal, M., 2017. Role of sustainable wheat production to ensure food security in the cwana region. Journal of Experimental Biology And Agricultural Sciences 5, 15–32.

Tadesse, W., Bishaw, Z., Assefa, S., 2018. Wheat production and breeding in Sub-Saharan Africa: Challenges and opportunities in the face of climate change", International Journal of Climate Change Strategies and Management 11(5), 696–715. https://doi.org/10.1108/IJCCSM-02-2018-0015.

Tesfaye, T., Tsige, G., Tadesse, D., 2014. Genetic variability, heritability and genetic diversity of bread wheat (*Triticum aestivum* L.) genotype in western Amhara region, Ethiopia. Wudpecker JournalofAgriculturalResearch,3(1):026034. https://www.google.com/url?sa=t&rct=j&q=&esrc= s&source=web&cd=&cad=rja&uact=8&ved=2ahUKEwjC67S5uYWFAxX2a0EAHYFHA1wQFnoECBIQAQ&url=https%3A%2F%2Fwww.semanticscholar.org%2Fpaper%2FGenetic-variability-%252Cheritabilityand-genetic-of Tesfaye Genet% 2Fa0bea 71df63a22 c1a161343b744ac6d44208d427&usg=AOv Vaw1uEA7yDPb1pGmEkM8BFCb&opi=89978449

Tilahun, B., Habtamu, T., Tesfaye, L., 2020. Genetic variability, heritability and genetic advance among bread wheat genotypes at Southeastern Ethiopia. Agriculture, Forestry and Fisheries 9(2), 128–134. doi: 10.11648/j.aff.20200904.15.

Upadhyay, K., Adhikari, N., Sharma, S., 2019. Genetic variability and cluster analysis of wheat (*Triticum aestivum* L.) genotypes in foot hill of Nepal. Archives of Agriculture and Environmental Science 4, 350–355.

Wani, S.H., Sheikh, F., Najeeb, S., Iqbal, A.M., Kordrostami, M., Parray, G., Jeberson, M.S., 2018. Genetic variability study in bread wheat (*Triticum aestivum* L.) under temperate conditions. Current Agriculture Research Journal 6(3), 268–277.

Yadav, S.K., Singh, A.K., Baghel, S.S., Jarman, M., Singh, A.K., 2014. Assessment of genetic variability and diversity for yield and its contributing traits among CIMMYT based wheat germplasm. Journal of Wheat Research 6(2), 154–159.

Semahegn, Y., Shimelis, H., Laing, M., Mathew, I., 2021. Genetic variability and association of yield and yield components among bread wheat genotypes under drought-stressed condition. Australian Journal of Crop Sciience 15(06), 863–870.

Yasin, G., 2015. Effect of integrated nutrient management on wheat: a review. Journal of Biology, Agriculture and Healthcare 5, 68–77.