



# Evaluation of genetic variability in bread wheat (*Triticum aestivum* L.) genotypes at Holeta, Central Ethiopia

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## ABSTRACT

The experiment was conducted in an alpha-lattice design at Holeta Agricultural Research Center in the 2021 main cropping season with two replications at experimental area of research farm. Analysis of variance revealed that there were statistically significant differences among the genotypes for most of their traits. The varieties showed wider variability in grain yield (1027.2-5620.8 kg ha<sup>-1</sup>). The study was undertaken to inheritance of grain yield and its components in bread wheat genotypes. Analysis of variance revealed that genotypes were significantly differed for all characters and suggested considerable variability for all yield and its attributing characters in the present material. High GCV and PCV values (>20) were obtained from grain yield, thousand kernel weight, days to heading, plant height whereas moderate GCV and PCV values (10-20%) were obtained from days to maturity. High heritability estimates (>80%) were obtained for grain yield (99.8%), thousand kernel weight (98.8), plant height (97), days to maturity (97), days to heading (96.9). The higher heritability was observed for days to heading, 1000 kernel weight, grain yield, and days to maturity and plant height. High heritability coupled with high genetic advance recorded for traits grain yield, and 1000 kernel weight and these characters are governed by additive gene effects; a directional selection for these characters would be more effective for the planned genetic improvement.

**Keywords:** Genetic advance; Genotypic coefficient of variation; Phenotypic coefficient of variation; Heritability

## INTRODUCTION

Bread wheat (*Triticum aestivum* L.), is an annual self-pollinating plant with in Gramineae (Poaceae) family of true grasses, it is the foremost cereal crop appreciably grown in the world. Wheat was thought to have been domesticated around 10,000 years ago. The world's wheat production is based almost entirely on two modern species, namely durum wheat (*Triticum turgidum* ssp. durum, tetraploid, 2n=4x=28, AABB) and bread wheat (hexaploid, 2n=6x=42, AABBDD).

Global wheat grain production must be increased in 2% annually to meet the requirement of consistently increasing world population (around 9 billion) by 2050 [1]. The leading wheat producing countries in the world are China, India, Russia Federation, the United States, and France; and the global average wheat productiveness is 3.54 t ha<sup>-1</sup> with a total production of about 778.6 million tons [2]. Wheat ranks first in terms of area coverage and second in terms of total production after maize and offers extra nourishment than any other food crops in the world [3].

South Africa and Ethiopia are the largest wheat producers in sub-Saharan Africa [4]. Ethiopia's annual production is about 5.8 million tons with mean productivity of 3 tons per hectare (tha<sup>-1</sup>) (CSA, 2021), which is relatively lower than the attainable yield of the crop, the attainable yield of the crop reaches up to 5 tha<sup>-1</sup> [5].

It is necessary to reshuffle the gene using hybridization in the suitable parents to boost the current yield level and overcome yield stagnation. Then, the genetic stocks harboring the desired genes must be identified in light of various yield contributing characters. This can be achieved by studying the genetic variability and association of different traits in a breeding population. Therefore, this study was carried out to study genetic variability in bread wheat (*Triticum aestivum* L.)

## MATERIALS AND METHODS

An experiment was conducted in alpha lattice design with two replications at experimental area of research farm, during 2021-2022. The experimental material consisted of 100 bread wheat genotypes. The sowing was done by dibbling seeds in rows with spacing of 20 cm apart and 4-6 cm within row on June 30 (Timely sown environment 2021-22). Observations were recorded on randomly selected 5 plants for grain yield and different yield contributing traits viz., plant height (cm), days to heading, 1000 grain weight (g), grain yield (kg/plot), days to maturity in each plot. The phenotypic and genotypic coefficients of variation which measured the magnitude of phenotypic and genotypic variation present in a particular character were computed by the formulae given by Burton and de Vane [6]. The coefficient of variation was proposed by Dabholkar [7]. The estimation of expected genetic advance from selection G (s), was obtained by the formula suggested by Robinson, Comstock, and Harvey and genetic advance as percent of mean was classified as low, moderate and high by Johnson et al. [8]. Heritability in per cent in broad sense was estimated by Falconer [9]. Heritability values were categorized as low, moderate and high by Robinson et al.

## RESULTS AND DISCUSSION

Analysis of variance revealed that genotypes were significant for all 5 characters viz., plant height, days to heading, 1000 grain weight, days to maturity and grain yield. Present finding were similar with earlier reports of Zare et al., and Aycicek and Yildirim [10,11]. Mean performance revealed that out of 15 genotypes viz., Elit Ethiopia 172/2020 showed significant highest grain yield (5620.76 g) along with significantly early in days to heading (62.85), dwarf plant height and bolder seed size as reflected by 1000 grain weight. 10HPYT45/2020 was recorded significantly bolder seed size as reflected by 1000 grain weight (45.72 g) with grain yield. Elite Ethiopia 1/2020 was recorded significantly dwarf plant height and late to maturity with grain yield. 10HPYT45/2020 showed significantly late to maturity with grain yield.

Elite Ethiopia 168/2020 showed significantly bolder seed size as reflected by 1000 grain weight and late to maturity with grain yield. Elite Ethiopia 92/2020 showed significantly late to maturity with grain yield. 10HPYT019/2020 showed significantly late to maturity with grain yield. Elite Ethiopia 1/2020 showed significantly dwarf plant height and bolder seed size as reflected by 1000 grain weight, late to maturity with grain yield present finding were confirmed with Bhutto et al.

The estimation of phenotypic and genotypic coefficient of variation was presented in Table 1, Phenotypic Coefficient of Variation (PCV) was high for grain yield (35.978%) and 1000 kernel weight (20.981%). However, it was low for the traits, plant height (5.097%), days to heading (7.390%), days to maturity (3.33%). The high Genotypic Coefficient of Variation (GCV) was observed for the grain yield (35.951%) and thousand kernel weights (20.851%); it was low for rest of the traits that was, days to maturity (3.28%), plant height (5.019%), and days to heading (7.273%).

**Table 1.** Extent of genetic parameters for yield and its attributing characters in wheat genotypes

Traits	Mean	Range	PV	GV	PCV (%)	GCV (%)	H <sup>2</sup> (%)	GA	GAM (%)
Number of days to heading	68.86	60.00-80.00	25.892	25.079	7.39	7.273	96.9	10.153	14.745
Days to maturity	143.19	129.00-151.00	22.782	22.088	3.333	3.28	97	9.533	6.658
Grain yield	3192.96	1027.20-5620.76	1199789	1197839	35.978	35.951	99.8	225290.8	70.527
Thousand kernel weight	31.38	8.52-46.64	43.354	42.816	20.981	20.851	98.8	13.395	42.686
Plant height	92.29	83.00-106.40	22.13	21.458	5.097	5.019	97	9.396	10.181
<b>Note:</b> GV: Genetic Variation; PV: Phenotypic Variation; PCV: Phenotypic Coefficient of Variation; GCV: Genotypic Coefficient of Variation									

Almost equal magnitude of GCV and PCV showed for days to heading, plant height and days to maturity indicating that these characters were less influenced by the environment while grain yield and 1000 kernel weight exhibited high value of PCV over its GCV value, shows that, large amount of variation for these traits was due to environment only. Present finding were in confirmation with Degewione et al., Maurya et al., and Yadav et al. [12-14]. The estimates of broad-sense heritability have been presented in Table 1. The highest heritability was observed for all traits such as days to heading (96.9%) followed by 1000 grain weight (98.8%) and plant height (97%); present finding in line with the finding of Desheva and Cholakov.

The estimates of expected genetic advance (Table 1) was found to be highest for the trait grain Yield (70.527%), followed by that of thousand kernel (42.686%), plant height (10.181%) and number of days to heading (14.745). For rest of the trait it was low; such that for it was 6.658% for days to maturity. High heritability estimates coupled with high genetic advance were shown from 1000 kernel weight, plant height, and days to heading and grain yield, this indicated that, effectiveness of selection for the improvement of these traits. These findings were confirmed with Deoraj et al., and Kabir et al. [15-16].

## CONCLUSION

Bread wheat (*Triticum aestivum* L), is an annual self-pollinating plant with in Gramineae (Poaceae) family of true grasses, it is the foremost cereal crop appreciably grown in the world. Global wheat grain production must be increased in 2% annually to meet the requirement of consistently increasing world population. Ethiopia's annual production is about 5.8 million tons with mean productivity of 3 tons per hectare (tha<sup>-1</sup>), which is relatively lower than the attainable yield of the crop, reaching up to 5 tha<sup>-1</sup>. It is necessary to reshuffle the gene using hybridization in the suitable parents to boost the current yield level and overcome yield stagnation. Then, the genetic stocks harboring the desired genes must be identified in light of various yield contributing characters. This can be achieved by studying the genetic variability and association of different traits in a breeding population. One hundred bread wheat genotypes were grown at Holeta agricultural research center main station to determine genetic variability, heritability, and genetic advance, association among grain yield and yield component traits and identified best performing genotypes. From one hundred bread wheat genotypes, the best performing genotypes were identified and recommended for future breeding work.

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