

Morphological Variations in Bread Wheat (*Triticum aestivum* L.) Genotypes in Gechi District, South West Ethiopia

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Abstract: With the aim of describing variance in morphological features of bread wheat genotypes using frequency and Shannon-Weaver diversity index, the current study was conducted on forty-nine genotypes of bread wheat, including two released varieties (Wane & Lemu). The experiment was laid out in a 7x7 simple lattice designs. White glumes was the most frequent (67.3 %) within the genotypes and red/brown glume color was the less frequent (20.4%), while purple/black glumes was the least frequent phenotypic frequency (12.2%). The present study indicates that most of the studied traits showed polymorphism exception of glume hairiness. Shannon Weaver diversity index ranged from low ($H' = 0.4$) for glume hairiness to high (0.98) for spike density. The highest diversity index was observed for spike density ($H' = 0.98$) followed by seed vitreousness ($H' = 0.94$) and seed size ($H' = 0.84$) which showed the presence of high diversity among genotypes for these traits. These results demonstrated the comparatively significant diversity of the germplasm. Programs for improvement can benefit from this genetic variability. However, drawing firm conclusions from the current results based just on morphology is not possible. Therefore, it is advised that research be done on molecular characteristics as well as other quality attributes such protein content.

Keywords: Bread Wheat, Diversity Genotypes, Polymorphism, Shannon-Weaver Diversity

1. Introduction

Over one-third of the global population consumes bread wheat (*Triticum aestivum* L.), making it the most popular cereal grain [1]. This self-pollinating annual plant was domesticated 10,000 years ago and is now grown all over the world. The development of the bread wheat (*Triticum aestivum*) ($2n = 6x = 42$, AABBDD) has been the focus of extensive research and heated debate for a number of years. Nowadays, it is thought that a hybrid between the diploid species *Aegilops tauchii* var. *strangulata* ($2n = 2x = 14$, DD) and the tetraploid wheat species *T. turgidum* ($2n = 4x = 28$, AABB) produced hexaploid wheat [2]. It is one of the most important staple crops for ensuring food security worldwide, contributing more than 35% of the calories from cereals

consumed directly in underdeveloped countries, 74% in affluent countries, and 41% worldwide [3]. Wheat is used in Ethiopia to make bread, boiled grain (nifro), roasted grain (kolo), local beer (tela), and porridge (genfo) [4]. The crop is farmed in Ethiopia between 6 and 16°N latitude and 35 and 42°E longitude, at an elevation of 1500–3000 m above sea level. Agro-ecological zones between 1900 and 2700 m.a.s.l., however, are the most ideal [5]. Wheat is produced on a variety of soil types, including waterlogged heavy vertisol and fertile, well-drained soils [6]. Arsi, Bale, Shewa, Ilubabor, Western Hararghe, Sidamo, Tigray, Northern Gondar, and Gojam zones are Ethiopia's principal wheat-producing regions [5]. The degree of genotypic diversity in a population for a trait determines the development of an improved cultivar that can yield more under different agroclimatic

conditions [7]. Rahman *et al.* [8] state that determining the genetic variability of the genotypes that are currently available for the desired features is the initial stage in the production of varieties. Since the selection of appropriate parents determines the effectiveness of improving yield and quality traits, the search for optimal genotypes is an ongoing activity. For the successful selection of varieties for yield, it is crucial to understand nature, the extent of variations present in the breeding materials that are now available, and the linkages between the quantitatively inherited features in grain yield [9, 10].

Genetic resources should be thoroughly assessed for characterisation and genetic variety before being exploited. Recording traits that are highly heritable, easily observable with the naked eye, and expressive in all settings is the process of characterization [11]. A uniform record of easily measurable plant characteristics should be provided by characterization, as these are crucial in identifying an accession [12]. It is a description of the germplasm of plants. Actually, bread wheat is a cereal crop that is highly versatile and flexible [13]. Its genetic heterogeneity and variability set its landraces apart. Thus, it is necessary to identify and quantify this genetic diversity as it could be helpful for managing and conserving plant genetic resources as well as for breeding programs [14]. Selecting appropriate materials for crop improvement breeding projects may involve evaluating genetic variability based on morphological traits of economic interest [15]. Furthermore, because morphological features are easier to identify and have a simpler mechanism of inheritance than quantitative traits, they play a more significant role in genetic research than biochemical traits [16].

Numerous investigators have documented the existence of genetic variation concerning qualitative characteristics in wheat. Levy and Feldman [17] have revealed that spike qualitative and quantitative features play a crucial role in determining genetic diversity and distinguishing closely related types, making them a popular choice for evaluating and characterizing wheat properties. Moreover, wheat types are identified by the size, color, and form of their seeds [18]. As a related trait yield and vigor, Dubey *et al.* [19] state that seed size is a key component of both basic plant research because it has a substantial impact on seed formation and development in plant reproduction and cereal breeding. Two of the primary goals of wheat breeding projects are grain size and form [20]. Furthermore, [19] noted that as seed color influences the quality and appeal of processed grain, it is therefore a crucial breeding criteria for cereal varieties. Therefore, evaluating genetic variety and defining genetic resources is crucial for improving the output of bread wheat.

2. Material and Methods

2.1. Description of the Study Site

The field experiment was carried out at Gito, Gechi district, Buno Bedele, Southwest Ethiopia, during the 2019–2020

growing season. The experimental site is situated at a height of 2132 meters above sea level and is located geographically at 08° 12' 0" N latitude and 36° 18' 0"E, at an altitude of 2132 m. a. s. l. The average annual temperature and rainfall at the experimental site are 21°C and 1850 mm, respectively. The experimental site's soil had deep, well-drained Nitosoil, 2.56 CEC, and a pH of 4.3. To reduce the acidity issue, 4.22 t ha⁻¹ of lime stone was applied to the area. Major crops grown in the research region and in Buno Bedele were tef, wheat, sorghum, barley, and maize.

2.2. Experimental Materials

Wane and Lemu, two released bread wheat varieties, were among the 47 advanced genotypes of bread wheat that made up the experimental materials. In order to establish a variety, Kulumsa Agricultural Research Center (KARC) initially introduced the advanced bread wheat genotypes used in this study from CIMMYT during the nursery stages. The supplies used in this experiment at the National Variety Trial (NVT) of Variety Development Stages were provided by KARC. The lines with advanced genotypes are homozygous. The Kulumsa Agricultural Research Center (KARC) announced the two genotypes that were used as checks in 2016: Lemu (ETBW 6861) and Wane (ETBW6130).

2.3. Experimental Design and Field Management

The experiment was laid out in a simple lattice design (7 x 7) with two replications. An experiment's entire area measured 488 m³ (23.8 m x 20.5 m), with a 3 m³ plot size (2.5 m x 1.2 m). Blocks, replications, and plots were spaced 0.5, 1.0, and 0.5 meters apart, respectively. In July 2019/20, the seeds were manually drilled into six rows, spaced 20 cm apart and 2.5 meters long. 150 kg ha⁻¹ of seed was used, or 45 g plot⁻¹. Nitrogen, Phosphorus, Sulfur, and Boron (NPSB) blend fertilizer was applied at a rate of 100 kg ha⁻¹ right before seeding, and 100 kg ha⁻¹ of split UREA was sprayed throughout planting and the crop's knee stage before to heading.

2.4. Data Collected

Table 1 lists the morphological features that were investigated and recorded using the bread wheat descriptor list (IBPGR, 1985; CPVO, 2008).

Table 1. Data collected for qualitative traits.

Glume hairness	0	Absent
	1	Present
	3	Lax
Spike density	5	Intermediate
	7	Dense
	3	Short
Beak length	5	Medium
	7	Long
	1	White
Awn color	2	Red/brown
	3	Purple/black
	1	Straight
Beak shape	3	Slightly curved

	5	Moderately curved
	7	Strongly curved
Glume color	1	White
	2	Red/brown
	3	Purple/black
Spike color	1	White
	2	Colored
Spike shape	1	Tapering
	3	Parallel sided
	3	Ovoid
Seed shape	5	Semi-elongate
	7	Elongated
Seed color	1	White
	2	Red/brown
	3	Purple/black
Seed size	3	Small
	5	Medium
	7	Large
Seed plumpness	3	Plump
	5	Partly plump
	7	Shriveled
	3	Vitreous
Seed vitreousness	5	Partly vitreous
	7	Non-vitreous

2.5. Data Analysis

2.5.1. Phenotypic Frequency

Each qualitative trait's phenotypic frequency distribution was computed to assess variation across all genotypes.

2.5.2. Shannon Weaver Diversity Index

H' was estimated based on the phenotypic frequency data. It was computed to assess the phenotypic diversity for each character; entire accession. H' was calculated as described by Hutcheson [21].

$$H' = -\sum_{i=1}^n p_i(\log p_i)$$

Where p_i is the proportion of accessions in the i^{th} class of an n -class character and n is the number of phenotypic classes for a character. Each value of H' was divided by its maximum value, $\log n$, and normalized in order to keep the values between zero and one.

3. Results and Discussion

3.1. Phenotypic Frequency

The frequency distribution of thirteen studied quality traits of bread wheat was discussed below. Most of the genotypes showed absence (91.8%) and presence (8.2%) of glume hairiness. This indicates that the studied genotypes were less diversified for this trait. In agreement with the present findings, [22] reported only 10% of accession had hairy glumes while he studied 293 entries of Ethiopian wheat. The lowest diversity value for glume hairiness in Ethiopian tetraploid and hexaploid wheat was reported by Mulugeta [23]. White glumes was the most frequent (67.3 %) within the genotypes and red/brown glume color was the less frequent (20.4%), while purple/black glumes was the least frequent phenotypic frequency (12.2%). In line with this

result, Negash and Heinrich [24] reported a large frequency (74.5%) of white glume in bread wheat.

White seed color accounted for about 57.1% of genotypes, red/brown for 38.8%, and purple/black for 4.1%. In a similar vein, [25] observed that unusual purple seed color and white seed color for most genotypes. [26] observed a high percentage of white seed color in bread wheat genotypes, which is consistent with this data. Ethiopian farmers greatly favor white seeded wheat due to market prices. [19] stated that the increasing milling efficiency and consumer choice for various products made white grain more in demand. Hexaploid wheat rarely has purple grains, and the current small number of Ethiopian accessions that do may be the result of tetraploid genes being incorporated into ordinary wheat [23]. After being discovered for the first time in Abyssinia (modern-day Ethiopia) in the 1870s, purple tetraploid wheat (*T. durum*) was brought to Europe and extensively disseminated by botanists. Eventually, bread wheat was blended with the purple grain color. [27] suggested that end-use product preferences and habits may also contribute to the prevalence of white-grained wheat in several nations, such as Pakistan, Libya, and India. Wheat landraces in Ethiopia are frequently mixed species [28]. Therefore, additional cytological investigation is still required to confirm the ploidy level of the current purple genotypes.

Most of the genotypes had intermediate (42.85%), dense (28.57%), and lax (28.57%) spike density. Similarly, [29] reported the majority of accession studied had intermediate spike density in durum wheat. Genotypes having large seed sizes were 46.9%, followed by medium (44.9%) and small (8.16%). The majority of medium-to big-sized seeds showed a high selection pressure by Ethiopian farmers and contemporary breeders in favor of large seed size. Both seed weight and size are crucial yield factors, particularly when there are only a certain number of seeds available per unit area. Greater output, better stand establishment, and enhanced seedling vigor and hardiness are frequently linked to larger seed sizes [30]. Large seed genotypes, along with other desirable agronomic features such as resistance to disease and lodging, are valued in variety improvement programs. [31] revealed that the size and the shape of wheat grain had a substantial effect on grain weight and flour yield. Grain size is a factor in seedling vigor, according to [20], whereas grain shape refers to the proportion of the grain main growth axis. In hexaploid wheat, [23] observed big to medium seed sizes.

The majority of the genotypes possessed vitreous seed type (51.02%), partly vitreous (24.49%), and non-vitreous (24.49%). As mentioned by Rasheed et al. [32] vitreousness is well connected with increased flour output. As a result, compared to non-vitreous (soft) grain varieties, vitreous seeds are of higher quality. The current findings shown that basic selection from these genotypes can yield the optimum seed quality for hexaploid wheat. This supports the hypothesis put out by Hutcheson [22] that a high frequency of large, vitreous seed suggests that these genotypes may be used in a high-quality breeding program. Mulugeta [23] observed that in hexaploid wheat, the majority of accessions were

somewhat vitreous to vitreous kinds. White awn color was dominant (69.4%) which followed by red/brown (28.6%) and purple/black (2.04%). The seed shapes of most genotypes were Ovoid (67.3%) followed by semi elongated (24.5%) and elongated (8.2%). About 67.35% of genotypes had plump seeds followed by partly plump (24.49%) and shriveled (8.2%). In line with the present result, [23] reported the majority of studied hexaploid wheat had Ovoid seed and semi-elongated (90%) shape and plumped seed (85%). Beak shape showed polymorphic distribution within genotypes. Strongly curved beak shape was more frequent (69.4%) followed slightly curved (14.3%) and moderately curved

(10.2%) and straight showed the least frequent of beak shape (6.12%). Most of the genotypes showed long (61.224%) followed by medium (32.65%) and short (6.122%) beak length. About 81.6% of genotypes showed white spike color and only 18.4% of the genotypes were showed a colored spike. Similarly, [26] reported white spike color and long beak for most of the genotypes in Tunisian bread wheat. Parallel sided spike shape was dominant (67.3%) and followed by tapering spike shape (32.7%). 67.35% of genotypes showed plumped seed, 24.49% partly plump whereas only 8.163% showed shriveled seed type.

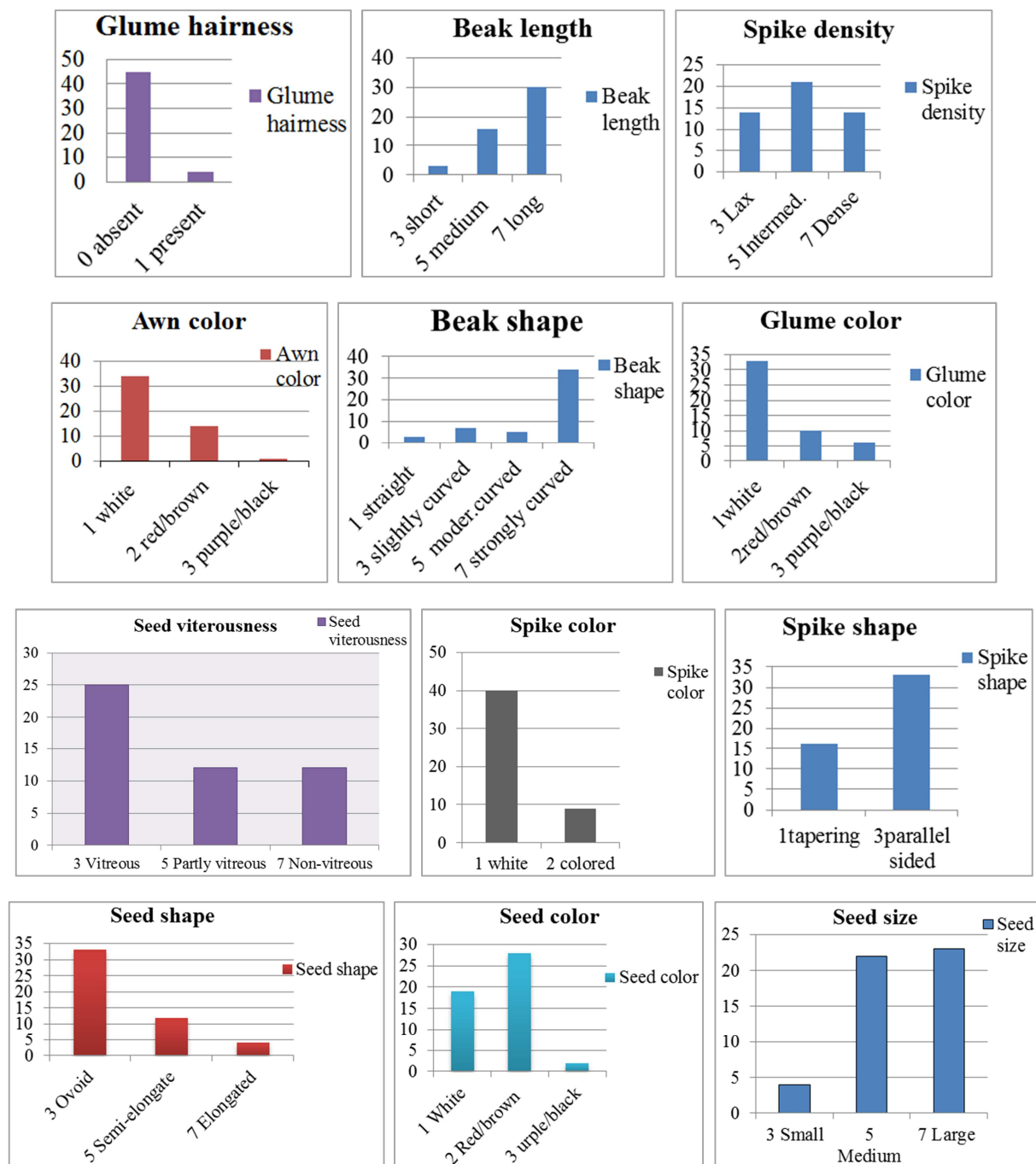


Figure 1. Frequencies distribution of 49 bread wheat genotypes based on different morphological traits.

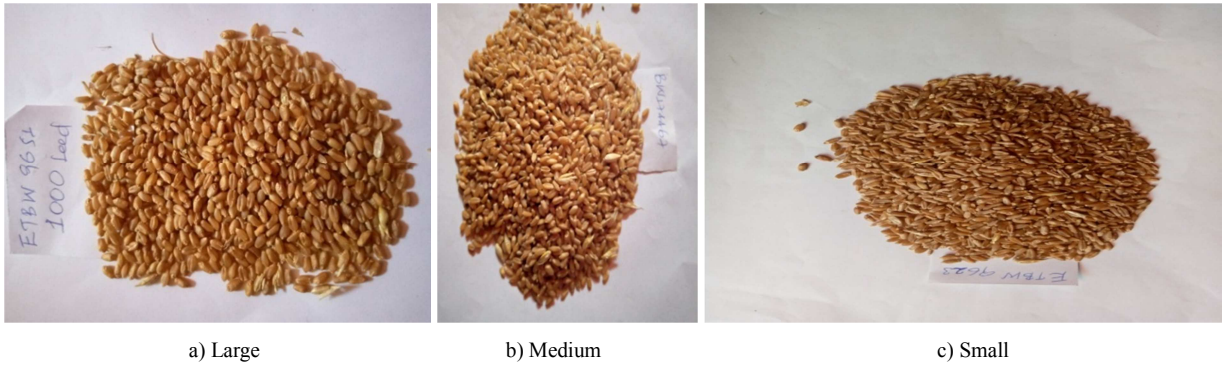


Figure 2. Morphological variation in seed size.

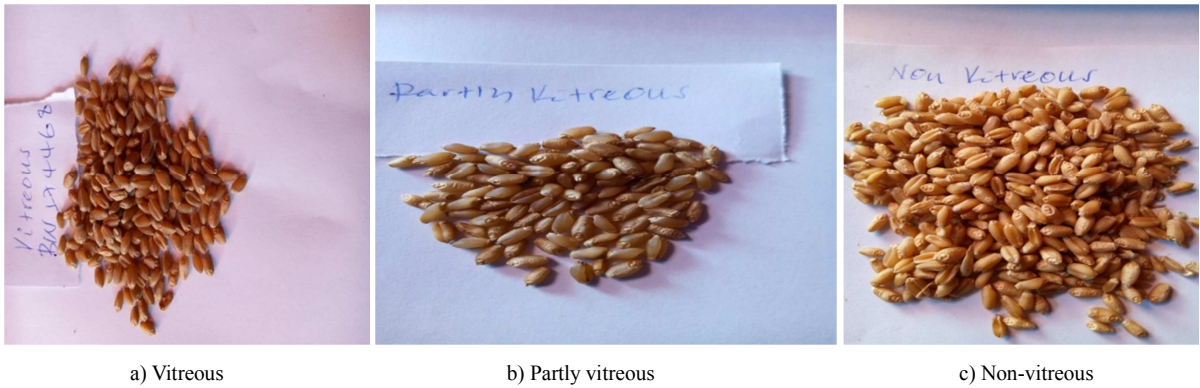


Figure 3. Morphological variation in seed vitreousness.

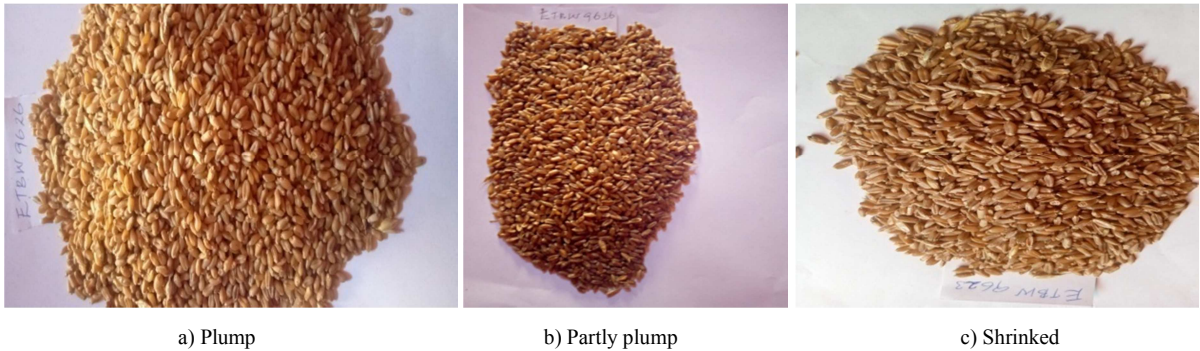


Figure 4. Morphological variation in seed plumpness.



Figure 5. Morphological variations spike color.

3.2. Shannon Weaver Diversity Index (H')

Shannon-Weaver diversity index ranged from low to high (Table 3). The diversity index was classified as high ($H' \geq 0.60$), intermediate ($0.40 \leq H' \leq 0.60$), or low ($0.10 \leq H' \leq 0.40$) [33]. Based on this delineation, high Shannon-Weaver-diversity index was observed for spike density (0.98), seed vitreousness (0.94), spike shape (0.91), seed size (0.84), seed shape (0.81), glume color (0.77), beak length (0.76), seed plumpness (0.74), spike color (0.69), beak shape (0.67) and seed color (0.74) (Table 3). This means that the genotypes had shown most diversity in these traits. Medium Shannon-Weaver diversity index was recorded for awn color (0.59) whereas low Shannon-Weaver diversity index was observed for glume hairiness (0.4) which means that the genotypes were less diverse for these traits. [23] reported that medium to high diversity indices for beak length, awn color, beak shape, glume color, seed shape, seed size whereas low for glume hairiness. Similarly, [26] reported high Shannon-Weaver diversity index for beak shape and seed color. In contrast to this result, the same author reported the lowest diversity indices for spike density. In agreement with this findings the highest Shannon diversity index for seed size, spike density, glume color, seed shape, and seed color was reported by [34, 25]. The higher value of Shannon Weaver diversity index indicated presence of more diversity whereas the lower value showed less diversity among genotypes for specific trait. Therefore, the present finding revealed that there was morphological diversity among genotypes which could be exploited in bread wheat breeding for improving the existing varieties or developing new varieties.

Table 2. Shannon diversity index for thirteen qualitative traits of bread wheat genotypes.

Traits	H'
Glume hairiness	0.4
Spike density	0.98
Beak length	0.76
Awn color	0.59
Beak shape	0.67
Glume color	0.77
Spike color	0.69
Spike shape	0.91
Seed shape	0.81
Seed color	0.74
Seed size	0.84
Seed plumpness	0.74
Seed vitreousness	0.94

4. Conclusion

The present result shows that most of morphological traits showed polymorphism except glume hairiness. The lowest Shannon Weaver diversity index was observed for glume hairiness whereas the highest diversity index observed for spike density. For all accessions, the percentage of frequencies of the phenotypic classes of varied from 4% to 84%. Considerable variation in plant growth habit, Type-II

(indeterminate bush) was the most prevalent among the accessions (55%), followed by Type-I (determinate bush) (45%) growth habits. Characters with wide phenotypic diversity index was observed in seed color ($H'=0.642$) seed coat color ($H'=0.624$), pod color ($H'=0.622$), and seed shape ($H'=0.582$) indicating widely diversified for these characters. In conclusion the current finding revealed the presence of genetic diversity provides opportunity for the breeders to develop new bread wheat varieties or improvement of the existing varieties. However, the present result based on morphological alone can't make definite conclusion. As a result, it is recommended that molecular and other quality traits like protein content studies have to be carried out.

Data Availability

The data supporting the findings of this study are available on request from the corresponding author.

Conflicts of Interest

The authors have no conflict of interest.

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