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PHENOTYPIC AND ISOZYME DIVERSITY IN TETRAPLOID WHEATS (*TRITICUM TURGIDUM* L.) FROM BALE AND WELLO REGIONS OF ETHIOPIA

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Addis Ababa University, June, 2001

PHENOTYPIC AND ISOZYME DIVERSITY IN TETRAPLOID WHEATS (*TRITICUM TURGIDUM* L.) FROM BALE AND WELLO REGIONS OF ETHIOPIA

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In memory of my brother Wakuma Eticha.

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ABSTRACT

Phenotypic and isozyme diversity of 32 landrace populations of tetraploid wheats originating from two regions (Bale and Wello) of Ethiopia was analysed in this study. A total of 2559 individual plants (45-110 plants per population) representing each landrace were considered for the phenotypic diversity investigation. Investigations were also made on the species richness (biological diversity) of the populations whereby individuals in each landrace were classified into their own taxonomic classes and analysis of the species diversity was made for each population, altitudinal class and region of collection. Seven heritable qualitative traits (seed color, glume color, awn color, glume hairiness, beak awn, spike density, and awn length) were studied. The frequencies of each phenotypic class were used to compute the Shannon-Weaver index (H') to estimate and analyse the diversity at different levels. For isozyme analysis, three enzyme systems, Esterase (EST), Aspartate amino transpherase (AAT), and Leucine amino peptidase (LAP) were used to study the genetic variation in 14 landrace populations selected based on the clustering of the populations from the phenotypic frequencies. Each population was represented by twenty individuals.

The analysis of species diversity indicated that seven species of wheats from two ploidy levels, tetraploid and hexaploid, are planted in mixtures at varying proportions, Triticum turgidum ssp. durum *was the most dominant species accounting for about 67.32 % of the total population. A maximum of four species was recorded per each population. Analysis of phenotypic frequencies and diversity indices were done for tetraploids lumped together and for durum alone. Considering tetraploid species, seed color and beak awn contributed the highest diversity index (H' = 0.92 for both). Awn color contributed the lowest diversity index (H' = 0.59). When durum treated alone, glume color followed by beak awn and seed color contributed the highest diversity index (H' = 0.90, 0.84, and 0.84, respectively), whereas glume hairiness had the lowest diversity index (H' = 0.48).*

Traits such as awn color, awn length, glume color and seed color showed statistically significant differences ($p < 0.05$) between regions while significant differences ($p < 0.05$) were observed for awn length, beak awn, glume hairiness and seed color across gradients of

altitudinal classes in tetraploid wheats. Significant differences were also observed between altitudes and regions for traits in durum treated alone. Variations were, however, largely due to the differences in the level of the different characters within populations. On regional basis, higher mean diversity index was observed for Wello than Bale. Awn color was monomorphic and fixed for color types in collections originating from Bale whereas a variety of frequencies were observed in Wello. Considering tetraploids, the overall diversity index was computed to be H' = 0.81 ± 0.08. The overall region value of H' for durum wheat is 0.63 ± 0.08 indicating a decline in the amount of diversity in durum wheat as compared with the index for tetraploid wheats.

The isozyme assay resulted into a total of 5 isozyme loci; 2 of the distinct polymorphic regions of enzyme activity (banding pattern) detected for EST, 2 for AAT, and one for LAP. The isozyme data also indicated presence of allelic polymorphism was detected at all loci. The mean number of alleles per locus ranged from 1.4 to 2.2. Considering the genetic variability at the 5 loci, the percentage polymorphic loci varied from 40% to 80%. A pair-wise comparison of populations over five isozyme loci indicates that the unbiased genetic identity ranged from 0.904 to 1.00. Whereas the genetic distance ranged from 0.00 to 0.053, indicating that there is small amount of variation among populations. Populations were grouped/clustered into six clusters. The landraces from Bale and Wello grouped differently similar to that of clustering that was based on phenotypic frequencies.

1. INTRODUCTION

In Ethiopia, wheat (*Triticum* spp.) is one of the most important cereals both in terms of production and acreage (Tesemma and Belay 1991). It stands fifth following 'tef', maize, barley and sorghum in terms of area of production. But in total grain production, it ranks fourth after maize, 'tef' and sorghum (CSA, 1996).

The great majority of tetraploid (2n = 4x = 28) wheat (*Triticum turgidum* L.) cultivars grown in Ethiopia today are landraces consisting of distinct morphotypes (Tesemma and Belay, 1991). Vavilov suggested Ethiopia as a center of origin of tetraploid wheats (Vavilov, 1951). But due to the absence of wild relatives, Ethiopia has been considered only as a center of diversity for this crop (Harlan, 1971).

Beyene *et al.* (1991) and Gebre-mariam (1991) reported that tetraploid wheat, which is produced exclusively by small-scale farmers, covers about 60% of the total wheat area and the remaining 40% is covered by bread wheat (*Triticum aestivum* L.). However, recent survey indicates that bread wheat and tetraploid wheat each occupy 50% (Efrem Bechere, pers. comm.). Gebre-mariam (1991) also indicated that out of the current total wheat production area, 75.5% is located in Arsi, Bale and Shewa regions. The dominant tetraploid wheat growing areas include Shewa, Gonder, Gojam, Wello and Bale.

Quantitative estimates of genetic diversity and some measures of genetic structure are prerequisites for a sound genetic conservation strategy (Bekele, 1983a). Comparisons of genetic composition and distribution of landrace populations could give the limits of genotypes needed in each population. It could also be used to determine the sites of *in situ* conservation and to minimize the drawbacks of current genebank activities, including the freezing of the evolutionary process, and to gain more insight into genotypic structure and interactions of the various hosts and pathogens in the sites under study (Jain, 1975). It may also indicate the role of genetic composition in the maintenance of stability of a desired trait and of genetic diversity of a population.

Belay *et al.* (1997) pointed that the genetic and phenotypic diversity studies so far carried out on tetraploid wheats of Ethiopia were in a lump without classifying them into their taxonomic species and they noted that this area is considered to be a gap for further study. The present study tried to fill this gap through the isozyme and phenotypic diversity analyses of tetraploid wheats obtained from two regions (Bale and Wello) of Ethiopia. Moreover, the landraces of tetraploid wheats included in the present investigation were of recent collections (since 1997) which were not included in any of the previous studies. Attempts were made to estimate the level of genetic erosion that occurred through time in Ethiopian tetraploid wheats by the comparisons made between the previous findings of indices of genetic and phenotypic diversities on tetraploid wheats with that of the present study regardless of the areas of collection of landraces.

OBJECTIVES

A. General objectives:

1. To know the composition of the taxonomic species in the landrace populations
2. To estimate the magnitude of morphological and genetic variations that exist within and among taxonomic species of tetraploid wheats
3. To study phenotypic variations and isozyme genetic diversity of Ethiopian tetraploid wheats (*Triticum* sp.)

B. Specific objectives:

1. To group the species in each collection (landrace population) into its taxonomic species based
   on their spike morphology and other morphological traits
2. To observe the morphological diversity of Ethiopian tetraploid wheats as a complement to previous studies
3. To compare the magnitudes of morphological diversities observed in this study with that previously reported on Ethiopian tetraploid wheats and thereby estimate the rate of genetic erosion that has occurred through time.
4. To study isozyme diversity of the landrace populations and show the magnitude of genetic diversity existing within population or among the taxonomic classes.

2. LITERATURE REVIEW

2.1. EVOLUTIONARY ORIGIN AND TAXONOMY OF WHEAT (*TRITICUM* SPP.)

Wheats evolved from wild grasses found growing in the Eastern Mediterranean and the Near East areas (Purseglove, 1978). According to him, wheat was probably domesticated around 10,000-15,000 BC in the Near East area known as Fertile Crescent, a mountainous-hilly region in the upper reaches of the Tigris-Euphrates drainage basin.

The cultivation of wheat is prehistoric in the Old World (de Candolle, 1967). It spread rapidly and widely throughout Asia and Europe after its domestication in the Middle East. It had reached far northern China in very early times (Purseglove, 1978). According to Berrie (1977), wheat is classified under the tribe Hordeae or *Triticeae,* the cereal tribe. This tribe also includes other two important cereals, barley and rye. According to him the main genera of this tribe include *Triticum* L.- the wheats, *Hordeum* L. – the barleys and *Secale* L. – the rye.

All wheats belong to the genus *Triticum,* a member of the grass (*Graminae* or Poaceae) family and the tribe Hordeae (Martin *et al*, 1967). The species and groups (or subspecies) of cultivated wheat in the world are listed in Table 1. This genus *Triticum* is characterized by two-to five-flowered spikelets placed flat at each rachis point of the spike. One or more flowered spikelets are sessile and alternate on opposite sides of a rachis (the main axis of the inflorescence forming a true spike).

Martin *et al.* (1967) reported that a tetraploid, emmer, evolved from a wild type, *Triticum dicoccoides,* that carries the A and B genomes. Mutations of emmer resulted in other tetraploids - durum and Polish wheat. Emmer eventually crossed naturally with *T. tauschii* (*Aegilops squarrosa*), a diploid with the D genomes to produce spelt wheat. Spelt later mutated to produce common wheat (*T. aestivum*), which in turn, mutated to produce club and shot wheats (Martin *et al.,* 1967).

In the wild and semi-domesticated species, the grain (caryopsis) is closely and tightly covered by the glumes. There is no evidence of the origin of naked tetraploid wheats, but it is assumed that the predominant naked tetraploid wheat, *T. turgidum* ssp. *durum,* originated from *T. turgidum* ssp. *dicoccum* by an accumulation of mutations that reduced the toughness of the glumes until free threshing was attained (Morris and Sears, 1967). Other naked grain tetraploids, such as *T. turgidum* ssp. *polonicum*, are of relatively recent origin, deviating from durum in only a single character. Hence, it is apparent that the naked tetraploid wheats originated from *T. turgidum* ssp. *dicoccum* and diversified over the course of domestication (Feldman, 1976).

Cytological and cytogenetic studies showed that wheats fall into three natural groups, each are characterized by having 14 chromosomes (seven pairs) or a multiple of 14 chromosomes in each somatic cell; diploid wheat having 14, tetraploid wheat 28, and hexaploid wheat 42. Two species are recognized at the diploid level; *T. monococcum,* with both wild and cultivated types, and *T. urartu,* a wild species different from *T. monococcum* on genetic, morphological,

and biochemical bases but having in common a basic genome, the A genome (Martin *et al.*, 1967). Kimber and Sears (1987), however, stated that nine diploid species were recognised, some of which were thought to carry genomes somewhat modified from other closely related diploids. And there are 17 polyploid species, subspecies and polyploid forms.

At tetraploid level, two species have been recognized: *T. timopheevii* and *T. turgidum* (de Candolle, 1967). These two species have in common the A genome, which surely comes from the *T. monococcum* complex, but the second genome is different in the two species; it has given the letter G in *T. timopheevii* and the letter B in *T. turgidum*. Kimber and Sears (1987) reported that the origin of B and G genomes were that most likely they derive from ancestors or species belonging to a section of the genus *Aegilops (Sitopsis)* or from a modified genome A. On the other hand, at hexaploid level two basic species were recognized. The first was *T. zhukoveskyi,* in which genome A is represented twice and genome G once. Apparently, it derives from a cross, followed by the doubling of chromosomes, between *T. timopheevii* and a diploid *T. monococcum*. The second species was represented by *T. aestivum,* derived from a cross between a *T. turgidum* (genome AB) and an *Ae. speltoides* (genome D).

Based on the strong morphological similarities between diploid wheat, *T. monococcum* and tetraploid wheat, *T. turgidum,* and from the chromosome pairing observed in hybrids between them, Kimber and Sears (1987) suggested that the A genome of the polyploid wheats must have come from *T. monococcum*. They also established the source of the D genome of hexaploid wheat as it came from *T. tauschii* (*Aegilops squarrosa)*. Moreover, on the basis of their having the genomic constitutions of AA, AABB and AABBDD, all the wild and cultivated wheats known are classifiable into three species, *T. monococcum, T. turgidum,* and

T. aestivum except the tetraploid *T. timopheevii* and the hexaploid *T. zhuskovyi*. The former has a genome G instead of B, thus being AAGG, and the latter is AAAAGG.

Table 1. Different classes of wheat as grouped into their respective species.

Species	Group	Common name
Triticum monococcum L	Diploid (2n= 14 chromosome) AA genomes	Einkorn
T. turgidum L.	Tetraploid (2n=28 chromosomes) AABB genomes	
	T. turgidum L. ssp. *Turgidum*	??
	T. turgidum L. ssp. *Dicoccon (dicoccum)*	Emmer
	T. turgidum L. ssp. *Durum*	Durum wheat
	T. turgidum L. ssp. *Polonicum*	Polish wheat
	T. turgidum L. ssp. *Carthlicum*	Persian wheat
T.timopheevii Zhuk.	*T.timopheevii* Zhuk *timopheevii*	??
	T.timopheevii Zhuk *zaukovski*	??
T. aestivum	Hexaploid wheat (2n=42 chromosomes) AABBDD genomes	
	T. aestivum ssp. *Spelta*	Spelt
	T. aestivum ssp *vavilovii*	None
	T. aestivum ssp *aestivum(vulgare)*	Common wheat
	T. aestivum ssp *compactum*	Club wheat
	T. aestivum ssp *sphaerococcum*	Shot wheat

Source: Martin *et al.* (1967)

2.2. WHEAT RELATIVES AND MORPHOLOGY

From earliest plant breeding efforts, man must have looked at the characters of the wild relatives of wheat and wondered if there was a way of transferring them into the cultivated forms. Such attempts would have been frustrated by crossability barriers, polyploidy, genomic non-homology and hybrid sterility (Kimber, 1993). Wheat (genus *Triticum*) is related botanically to certain other grass genera that can be crossed with wheats. Several species of *Aegilops* crossed with wheat include goatgrass (*Aegilops cylinderica*), a weedy

plant. Wheat has been crossed with several species of the genus *Agropyron* (wheatgrass) (Martin *et al.*, 1967).

Reviews made by Bechere and Kebede (1997) indicate that the two wild types, *T. araraticum* and *T. dicoccoides,* were both domesticated, *T. araraticum* giving *T. timopheevii* and *T. dicoccoides* first giving domesticated types resembling the present *T. turgidum* ssp. *dicoccum* types. The first species remained in cultivation in limited areas in Armenia and Transcaucasia whereas, *T. turgidum* ssp. *dicoccum* spread from the Near East and to Ethiopia. Later, the more advanced types (characterized by naked kernels and much wider adaptation) belonging to *T. turgidum* and *T. turgidum* ssp. *durum* spread to all Europe, the Middle East, and North Africa.

The spikes of durum wheat are compact and laterally compressed. The glumes are persistent and sharply keeled and the lemmas are awned in the commonly grown varieties. The long stiff awns and thick compact spikes and long glumes often cause layman to confuse with barley. The amber or red kernels are usually long and pointed, the hardest of all known wheat (Martin *et al.*, 1967).

2.3. DISTRIBUTION AND PRODUCTION OF WHEAT (*TRITICUM* SPP.) IN ETHIOPIA

Wheats in Ethiopia are represented by tetraploid (2n=4x=28) and hexaploid (2n=6x=42) species (Tesemma and Belay, 1991). The former is indigenous to the country while the latter are of recent introduction (Bechere *et al.* 1996). Nearly all the tetraploid wheat varieties grown in Ethiopia at present are landraces consisting of a large number of different genetic

lines; even different species are often found to be grown as mixture in wheat fields (Bechere and Kebede, 1997; Bekele, 1984b). It is not uncommon to find three or occasionally four species and often as many as 8-15 botanical varieties in the same field (Tesemma and Belay, 1991).

According to Porceddu *et al.* (1973), Ethiopian wheats belong to the following species: *Triticum diccocum, T. turgidum* ssp. *durum, T. turgidum, T. turgidum* ssp. *polonicum, T. aestivum, T. compactum* and *T. abyssinicum.* Sylivia (1995) listed the wheats of Ethiopia as *T. polonicum* L., *T. dicoccum* Schrank, *T. aethiopicum* Jakubz., *T. turgidum* L., *T. durum* Desf. and *T. aestivum* L. The presence of continuous variation in Ethiopian wheats is a factor in hindering the result of an unambiguous taxonomic treatment (Bekele, 1984b; Tesemma *et al.* 1991). Another obvious difficulty is that Ethiopian wheats exhibit differences from other wheats because of isolation and differences in agricultural practices (Bekele, 1984b). He also noted that since wheat has a wealth of genetic variability in the absence of clear-cut discontinuities, there is a great controversy over the taxonomy and nomenclature of wheat species and their relatives in the genus *Aegilops*.

Ethiopia, often referred to as a major Vavilovian gene center, is considered as one of the world's most important centers of crop diversity. But since a diploid (2n = 2x = 14) einkorn wheat (*T. monococcum*) is not grown in Ethiopia and hexaploid (2n = 6x = 42) is a late introduction, wheat evolution in Ethiopia is restricted to the tetraploid (2n=4x=28) wheat (Tesmma and Belay, 1991). Therefore, this made Ethiopia to be considered as a center of diversity rather than being the origin for tetraploid wheats.

Durum wheat shares 10% of the total world wheat area and it is grown on almost 22 million hectares (Bechere and Kebede, 1997). In Ethiopia, durum wheat is one of the most important crops grown exclusively on vertisols by small-scale farmers under rain fed conditions at altitudes ranging from 1800-2800 m above sea level (masl) (Tesemma and Belay, 1991). It is an indigenous species and one of the predominant wheat species grown in Ethiopia.

All the known tetraploid wheats in Ethiopia belong to the AABB genomic group (Tesemma and Belay, 1991; Belay, 1997). Cytogenetic analysis by an assessment of chromosome number of randomly selected accessions collected from Ethiopia showed greater proportion of tetraploids indicating that the durum wheats are the most predominant landraces cultivated (Messele, 1989). From cytogenetic studies Belay *et al.* (1994) found that the Ethiopian tetraploid wheats as a whole had pairs of two satellited, eight median and four sub-median chromosomes. They finally state that despite the presence of cytotypes, however, the chromosome arm ratio remained highly stable after centuries of wheat cultivation in Ethiopia.

2.4. IMPORTANCE OF GENETIC DIVERSITY

Diversity is expressed as genetic differences between species, subspecies, varieties, populations or individuals (Jarvis *et al.*, 2000). Assessment of characteristics of plant germplasm collections is one of the tasks of plant genetic resource centers. The germplasm is characterized for future use and may contribute to improvement and stabilization of crop yields (Fuentes *et al.*, 1999). Germplasm provides a repository of useful genes for the plant scientist and also provides a source of new genes to solve the future crop production problems (Cole-Rodgers *et al.*, 1997).

Hawkes (1986) summarized genetic diversity within a species that results from broad environmental differences acting on it over different parts of its distribution range. Where the environmental differences are slight over a great distance the changes in genetic diversity will also be slight. Where environmental changes are abrupt, as with changes in altitude or soil type, correspondingly abrupt changes in genotypes may be expected. The second type of diversity lies within a small area where a mosaic of population results in what is spoken of as inter-population diversity. The third type is to be seen within populations, necessitating proper population sampling techniques.

The indigenous landraces of crop plants provide the basic material for any crop improvement program. Landrace is a crop variety bred and cultivated by farmers and adapted to local environmental conditions (Jarvis *et al.*, 2000). It is a genetically diverse population composed of different genotypes each possessing particular characteristics (Harlan, 1975). Landraces are essential in the development of cultivars with stable yield, adaptation to biotic and abiotic stresses as well as other characters of interest to breeders (Demissie, 1986; Bechere *et al.* 1996). For instance, Purseglove (1978) reported the presence of disease resistance against *Puccinia graminis,* in landraces like emmer, *T. dicoccum* and durum wheat, *T. turgidum* ssp. *durum*.

The variability has been increased in tetraploid and hexaploid wheats by their ploidy level and by the survival possibility of mutations, which could permit progress in human utilization of these cereals. Tetraploid wheats are certainly allopolyploid in nature (i.e., they do not have four sets of seven basically similar chromosomes, as auto-tetraploid organisms do, but two

sets each of chromosomes only remotely related to each other by having an ancient common ancestors). This allopolyploid nature allows a disomic type of chromosome pairing at meiosis (Harlan, 1981).

Thousands of years of cultivation and continuous human and natural selection have resulted in tremendous variability in the tetraploid wheats derived from the *T. dicoccoides* wild types (Purseglove, 1978). All the domesticated and wild types having genome AABB have been grouped into only one valid species, *T. turgidum* (L.) Thell., which in turn is subdivided into several subspecies and botanical varieties. The differentiation is based mainly on morphological modifications. All of the subspecies are easily intercrossed and fertile; they all have the same chromosome structure and perfect pairing at meiosis; and often, in progeny of crosses several intermediate types are found breeding true (Kimber, 1993).

2.5. GENETIC EROSION AND MAINTENANCE OF GENETIC DIVERSITY

Genetic erosion refers to loss of genetic diversity between and within populations of the same species over time, or reduction of the genetic base of a species. The valuable and immense genetic diversity that has been built up in the germplasm over many years through natural or artificial selection is being threatened by numerous causes of genetic erosion (Bechere *et al.* 1995, unpublished report) among which the following three are very important: Displacement of local landraces by modern improved varieties, natural disasters like drought, and changes in land use.

According to Frankel (1974), of the several species attributes, geographic range had the greatest effect on variation at the species level. They also noted that the breeding system is even more influential than the geographic region.

The collection and preservation of the existing indigenous landraces is highly essential for their rational utilization in the development of modern improved varieties (Demissie, 1986). The varied topographic features and early history of Ethiopia are among the major factors which resulted in the diversity crop diversity, in particular and the vegetation and flora types in general (Tadesse, 1994; Tsegaye, 1997).

There are two approaches of conserving genetic diversity: *in situ* and *ex situ* conservation methods. *In situ* conservation of crop genetic resources can be defined as the continuous cultivation and management of a diverse set of populations by farmers in the agroecosystems where a crop has evolved. In its maintenance of farming systems, *in situ* conservation applies the principle of conservation to all three levels of biodiversity: ecosystem, species and genetic (intraspecific) diversity (Jarvis *et al.*, 2000). *Ex situ* conservation involves conservation out of their original sites in the gene banks and botanical gardens. *Ex situ* conservation has several important advantages for plant genetic resources conservationists. The genetic diversity maintained by these methods is directly controllable: as long as accessions are kept in suitable conditions and regenerated periodically, the likelihood of losing material is low.

The disadvantage associated with *ex situ* conservation is that it removes genetic material from its natural environment. This halts the on-going evolutionary processes that help to make

landraces unique and adaptable to changing environments (Frankel, 1974). Moreover, *ex situ* conservation can be a highly expensive endeavor, making it unsustainable in some settings.

The advantage of *in situ* is that it conserves genetic materials and promotes the processes that give rise to diversity. *In situ* conservation can address the conservation of a large number of species at a single site while this might be difficult for *ex situ* conservation owing to species different requirements for *ex situ* conservation. There are also distinct problems associated with *in situ* approaches to conservation. Among these are difficulties to identify and access the genetic material being conserved. Moreover, on farm approaches rarely allow the close control of germplasm by scientists that *ex situ* approaches facilitate (Frankel, 1974; Jarvis *et al.*, 2000).

2.6. MARKER SYSTEMS USED FOR DIVERSITY STUDY

Either of morphological, biochemical or molecular markers can be considered to study variations between and among different genotypes and populations. Highly heritable morphological traits were among the earliest genetic markers used as scientific investigation and are still in use in germplasm management. Detection of concealed genetic variation is possible using one of several molecular and biochemical techniques (Klug and Cummings, 1994). These variations are measured in the form of differences in amino acid sequences of proteins and by differences in nucleotide base sequences in DNA (Chamberlain, 1998).

Allozymes (also known as isozymes) are different alleles of the same enzyme at the same locus. Isozyme polymorphism has been used for characterizing and identifying genotypes and

varieties of crop plants, for studying population genetics and for examining geographical patterns of variation. Isozymes have also been used in genomic analysis of higher plants both to determine phylogenetic and evolutionary relationships among whole genomes and to determine homoeologous relationships among individual chromosomes (Hart, 1996).

Isozyme expressions are known to be independent of environment and hence it is a useful tool to measure genetic variations (Yandgaard and Iloskuldsson, 1985). In general, the analysis of plant isozymes through electrophoresis in starch gels has been a relatively cheap and simple method of choice in genetic studies of different plant species.

3. MATERIALS AND METHODS

3.1. PLANT MATERIALS

Thirty-two landrace populations of tetraploid wheats consisting of 45-110 heads per population were studied. Sixteen of the landraces belong to Bale collection while the rest 16 were from Wello region. These landraces were collected by the National Durum Wheat Improvement Research Program (Debre-Zeit / Ethiopian Agricultural Research Organization) in collaboration with the Institute of Biodiversity Conservation and Research (IBCR), from two regions (Bale and Wello) of Ethiopia. These accessions were collected during the 1997 and 1998 cropping seasons. Planting was done head-to-row following the recommended spacings between and within rows. Data scoring was made based on visual observation of the different traits both in the field and in the laboratory.

3. 2. ANALYSIS OF SPECIES DIVERSITY

The field experiment was conducted at Akaki Research Station, of the Debre-Zeit Agricultural Research Center. The site is located at an elevation of 2200 masl. Identification of taxonomic species was made mainly based on visual observation of spike morphology and kernel characteristics in mixed populations of the landraces. Clustering of taxonomic species was based on the frequencies of seven qualitative traits such as beak awn, awn length, seed color, awn color, glume hairiness, glume color and spike density by the use of MINITAB (1998) software.

Several of the numerous diversity indices so far employed by ecologists (Table 2), including the Margalef index (richness), Berger-Parker (dominance), Simpson index, Shannon evenness

index and Shannon-Weaver diversity indices are widely used by biologists as a means of measuring species diversity (Gomez *et al.*, 2000). These indices were used to measure the level of species diversity in landrace populations of Ethiopian wheats in the current study.

Table 2. Diversity indices, use and their definition

Index	What it measures?	Definition
Margalef (MR)	Richness	$(S-1)/\ln N$
Berger-Parker (BD)	Dominance	$1/(N_{max}/N)$
Shannon Evenness (SE)	Evenness	$H'/\ln S$
Shannon-Weaver diversity index (H')	Combination of richness and evenness	$H'=-\Sigma p_i \ln p_i$
Simpson (SI)	Combination of richness and evenness	$1-(\Sigma p_i^2)$

Where S = number of classes (taxonomic species), N = total number of samples summed over all classes (number of entries within each population), N_{max} = number of samples in the most abundant class, $P_i = n_i/N$, n_i number of classes in class I, P_i proportion of the number of samples in class I relative to the total number of samples

Source: Gomez et al. (2000) as adapted from the literature on species diversity.

According to Gomez *et al.* (2000) species diversity is defined as biological population that consists of not one but two components, the number of species (also known as 'richness') and how equally abundant the species are (also known as 'eveness'). Because diversity indices generally express both of these components in a single indicator, they share the obvious disadvantage of confounding the effects of more than one variable by treating them as one. The simplest measure of richness is a species count (species richness), and depends on sample size. The Margalef index is a measure of richness that adjusts for sampling effect by weighing the number of species counted by the natural logarithm of the sample size. Two widely used diversity indices, the Simpson and Shannon-Weaver, incorporate richness and evenness into a single measure. The Simpson index is a function of the probability that two individuals sampled at random will belong to the same species. The Simpson index weighs the concept of relative abundance more heavily than richness.

The Shannon index is a measure of the average degree of 'uncertainty' in predicting the species to which an individual chosen at random from a collection of S species (e.g., wheat

classes) and N individuals (e.g., wheat samples) will belong. The greater the uncertainty the higher the diversity. The Shannon evenness index is the ratio of the observed to the maximum diversity based on the Shannon index. The Shannon index is maximized when the total number of individuals in a sample is evenly distributed among the species represented in a sample. The converse of evenness, dominance is another way of looking at diversity. The Berger-Parker index is a sample measure of dominance and is defined as the inverse of the proportion of the sample occupied by most abundant species.

3.3. ANALYSIS OF MORPHOLOGICAL DATA

Three approaches of were employed for analyzing morphological data. The first one was analysis for the whole population without splitting the data obtained for all the taxonomic species. Secondly, analysis was done for tetraploids together. In the third case, one of the dominant taxonomic species *T. turgidum* ssp. *durum* was treated alone. Frequencies of the phenotypic classes of each character within population, altitude and region were calculated. These frequencies were used to compute the Shannon-Weaver diversity index (H') in order the phenotypic diversities for each phenotypic character, population estimate, altitudinal class and regions. The analysis of H' was made by using SPSS (1998) for windows. The altitude was arbitrarily classified into six classes.

In the case of phenotypic study, eight qualitative traits namely glume hairiness, glume color, awnedness, beak awn, awn color, seed color, spike density and awn length were recorded. The scoring of these qualitative traits was based on IPGR's wheat descriptor's list (IPGRI, 1994). Among these traits awnedness was found to be monomorphic and fixed in all the

populations included in the study. Belay (1997) states that these traits are little affected by the environment, which makes them reliable markers for characterisation of wheat germplasm.

Each trait was classified into specific subclass as follows: glume hairiness into two subclasses hairy and nonhairy; seed and glume color as white-yellow, purple-black and red-brown; awnedness as awned and awnless; awn color as black and non-black; awn length as short, intermediate and long; beak awn as acuminate, pointed and awned; and purple-black; spike density as lax, intermediate, dense and very dense.

The phenotypic frequency data for seven characters scored, each in two, three or four classes, were analyzed by the Shannon-Weaver diversity index (H) as defined by Jain *et al.* (1975):

$$H = -\sum_{i=1}^{n} P_i \ln P_i$$

Where n is the number of phenotypic classes for a character and Pi is the genotype frequency or the proportion of the total number of entries in the i^{th} class

Since different numbers of phenotypic classes were recognized for the seven characters, H was standardized by converting it to the relative index, H' as by dividing it with $H_{max} = \log_e (n)$ as in the following:

$$H = -\sum_{i=1}^{n} P_i \ln P_i / H_{max}$$

The non-normalized values of H' were used in the one-way analysis of variance of diversity for individual characters across altitudinal classes and regions.

The analysis of variance (ANOVA) was carried out for each of the qualitative traits by region and altitude. Moreover, hierarchical ANOVA pooled over traits was also performed to estimate the contribution of the different variance components to the level of diversity by using MINITAB (1998) software

3. 4. ISOZYME STUDY

The protocol of Chamberlain (1998) was followed for running the electrophoresis. Seeds were germinated under laboratory conditions at room temperature from 3 to 4 days. Enzymes were extracted from the shoot of the seedlings in two drops of extraction buffer (0.1M tris-HCl pH = 8.5, 0.14 M beta-mercaptoethanol) by placing into round-bottomed extracting plate. The plate was kept cool by putting it in an ice bucket. Fresh extractions were then used for electrophoresis.

Isozyme analysis was made on 14 landrace populations of *T. turgidum* in which 20 individual plants represented each of these landraces. The starch gel used was 13.3%. Moreover, 300-mm trays were employed. The gel was sliced vertically across a width of 3-3.5cm from the cathodal edge of the gel tray. Enzyme extracts absorbed on filter paper wicks were inserted vertically 1.5 to 2 mm apart, leaving a little space on each side of the wicks. The electrophoresis was run at 295 v and 60mA for 4 to 5 hours in a cooling chamber kept at a temperature of 4 °C. Each gel was cut into three slices whereby the middle slices were used for the assays.

The enzyme systems assayed were Aspartate aminotransferase (AAT), Estrase (EST) and Leucine amino peptidase (LAP). After electrophoresis, the gel was removed and trimmed along the edges. Then the gel slices were removed, placed in a staining box and stained with either of these three enzyme systems. The gel slices were then incubated at 37°C for about 30 minutes. Fixation was made with 50% glycerol and incubated for overnight at 4-10°C so that a clear band would appear.

During scoring, where more than one locus was detected on the zymogram, the loci were designated numerically taking the name of the enzyme system as prefix based upon their migration distance from the wick insertion point starting from the fast migration point.

Computation of isozyme data was made using BIOSYS-1 (Swafford and Selander, 1981). Allelic frequencies in populations, genetic similarity and distance coefficient, cluster analysis, F-statistics for individual alleles and summary F-statistics at all loci were calculated. The Nei index of genetic similarity, I, which is a measure of the proportion of electrophoretically identical proteins in a pair of populations (Nei, 1978) was analysed. Genetic variability at the loci observed was also calculated. The dendrograms based on allele frequencies were compared and contrasted (Nei, 1978).

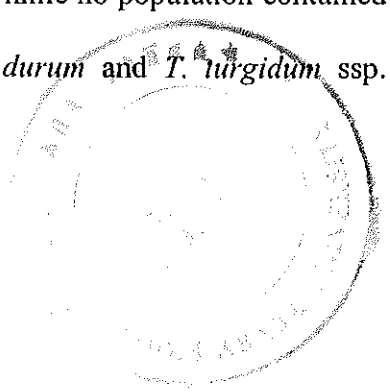
4. RESULTS

4. 1. BIOLOGICAL DIVERSITY OF TAXONOMIC SPECIES

4. 1. 1. SPECIES COMPOSITION WITHIN POPULATIONS

The percentage proportion in individual populations of the different taxonomic species is presented in Table 3. When the entire collection was considered, two populations originating from Bale region were found to be purely *T. turgidum* ssp. *aethiopicum* while two other populations exclusively represented *T. turgidum* ssp. *durum*. The highest number of taxonomic species recorded in landraces was found to be four. This was observed in only one population and four of these species were *T. turgidum* ssp. *durum, T. turgidum, T. turgidum* ssp. *aethiopicum* and *T. aestivum*. Moreover, two populations from Wello region were exclusively represented by *T. turgidum* ssp. *durum*. *T. turgidum* ssp. *durum* took the highest share (67.32 %) followed by *T. turgidum* ssp. *aethiopicum* (23.85%) and the next most abundant was *T. turgidum* ssp. *turgidum* (6.54%). *T. aestivum* (1.91%) was also recorded in small proportion. Species such as *T. turgidum* ssp. *polonicum* (0.14%), *T. turgidum* ssp. *pyramidale* (0.06%) and *T. turgidum* ssp. *dicoccum* (0.18%) were rarely planted in mixed forms with the predominant species.

T. turgidum ssp. *turgidum* was more frequent in Wello than in Bale. *T. turgidum* ssp. *dicoccum* was not recorded in Wello region. The hexaploid species, *T. aestivum*, was found in nine of the populations and its frequency reached upto 35.5% whhile no population contained hexaploid species from Bale. In addition, *T. turgidum* ssp. *durum* and *T. turgidum* ssp.



aethopicum were predominant (>50%) in 25 and seven of the remaining populations, respectively. That means no one taxonomic species was predominant in any of the populations. However, *T. turgidum* ssp. *aethiopicum* was rare in the Wello collections.

Separate analysis of the proportion of these landrace populations was made to know the proportions of tetraploid wheats, excluding both *T. turgidum* ssp. *dicoccum* and *T. aestivum* (Figure 1). Similarly, the first rank of the species composition was given for *T. turgidum* ssp. *durum* followed by *T. turgidum* ssp. *aethiopicum.*

4.1.2. ALTITUDINAL DISTRIBUTION OF SPECIES

The frequency of the different taxonomic species in various altitudinal classes is presented in Figure 2. Only two species, *T. turgidum* ssp. *durum* and *T. turgidum* ssp. *aethopicum,* occurred at altitudes below 2300 masl. However, *T. turgidum* ssp. *turgidum* was frequent between 2501-2700 masl while *T. turgidum* ssp. *aethiopicum* appeared more frequently at altitudes below 2100 masl than in any other altitudinal class. *T. turgidum* ssp. *polonicum* and *T. turgidum* ssp. *pyramidale* were more frequent in intermediate altitudinal classes. Above an altitude 2900 masl the only two species *T. turgidum* ssp. *durum* and *T. turgidum* ssp. *turgidum* were observed.

Table 3. Percentage frequency of the occurrence of taxonomic species of wheat landrace populations from two regions of Ethiopia; both tetraploid and hexaploid wheats treated together.

Region	Popn	TDU	TTR	TPO	TPY	TAE	TDI	TAS
Wello								
	1	97.2	0	0	1.9	0	0	0.9
	2	79.6	20.4	0	0	0	0	0
	3	58.2	6.4	0	0	0	0	35.5
	4	83.0	14.2	0	0	0.9	0	1.9
	5	79.1	20.0	0	0	0	0	0.9
	6	81.7	0	0	0	0.9	0	17.4
	7	100.0	0	0	0	0	0	0
	8	96.4	0	2.7	0	0	0	0.9
	9	99.1	0	0	0	0	0	0.9
	10	96.4	1.8	0	0	0	0	1.8
	11	100.0	0	0	0	0	0	0
	12	68.2	31.8	0	0	0	0	0
	13	99.1	0	0	0	0	0	0.9
	14	70.9	29.1	0	0	0	0	0
	15	53.2	46.8	0	0	0	0	0
	16	64.5	35.5	0	0	0	0	0
mean		**82.9**	**12.9**	**0.2**	**0.1**	**0.1**	**0**	**3.8**
Bale	17	1.6	0	0	0	96.7	1.6	0
	18	74.6	0	1.7	0	23.7	0	0
	19	88.4	0	0	0	11.6	0	0
	20	20.8	0	0	0	75.0	4.2	0
	21	20.0	0	0	0	80.0	0	0
	22	83.3	1.7	0	0	15.0	0	0
	23	91.7	0	0	0	8.3	0	0
	24	20.0	1.7	0	0	78.3	0	0
	25	21.7	0	0	0	78.3	0	0
	26	100.0	0	0	0	0	0	0
	27	0	0	0	0	100.0	0	0
	28	0	0	0	0	100.0	0	0
	29	62.2	0	0	0	37.8	0	0
	30	100.0	0	0	0	0	0	0
	31	66.7	0	0	0	33.3	0	0
	32	76.7	0	0	0	23.3	0	0
mean		**51.7**	**0.2**	**0.1**	**0**	**47.6**	**0.4**	**0**
Total		**67.3**	**6.5**	**0.1**	**0.1**	**23.9**	**0.2**	**1.9**

TDU, *T.durum;* TTR, *T. turgidum;* TPO, *T. turgidum* ssp. *polonicum;* TPY, *T. turgidum* ssp. *pyramidale;* TAE, *T.aethopicum;* TDI, *T. turgidum* ssp. *dicoccum;* TAS, *T. aestivum*

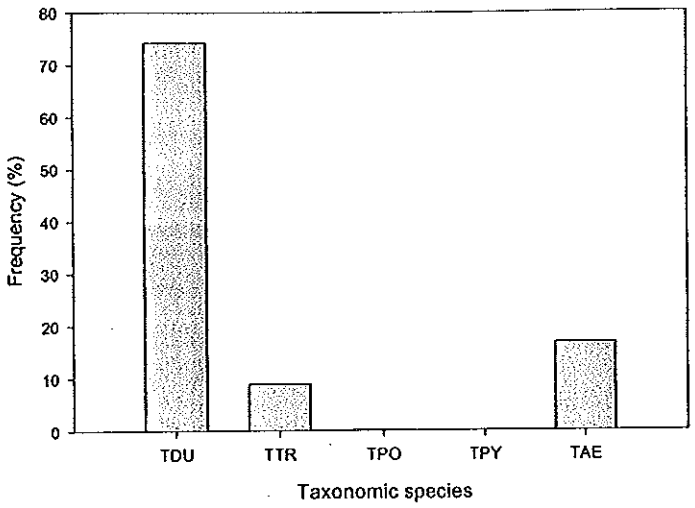


Figure 1. Abundance (in percent) of taxonomic species in tetraploid wheat landrace populations

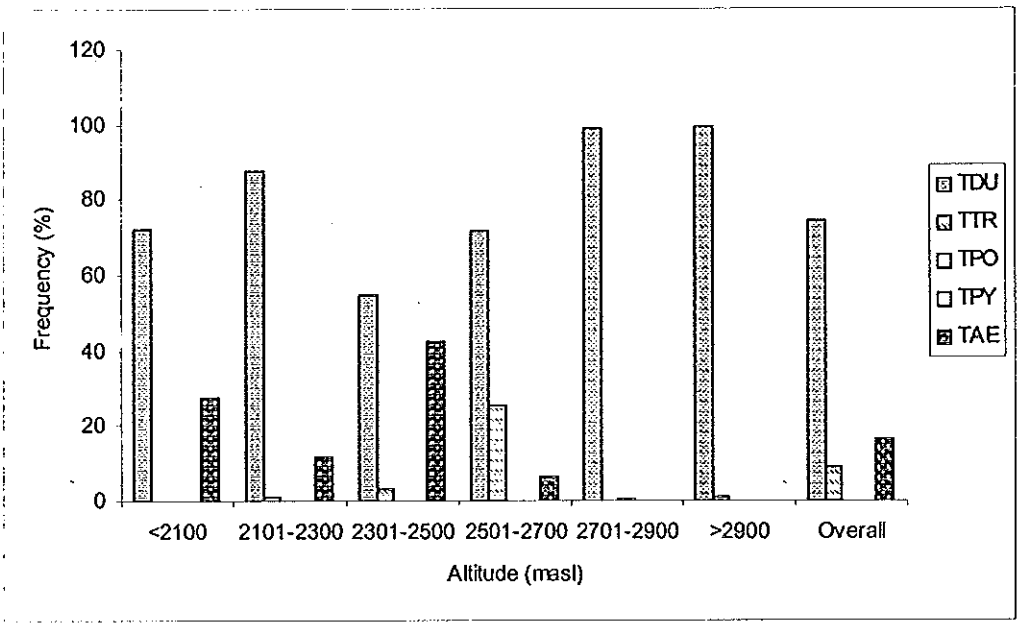


Figure 2. The frequency of occurrence of different taxonomic species in tetraploid wheats across various altitudinal gradients

4.1.3. CLUSTER ANALYSIS

Seven groups or clusters were obtained through analysis conducted on the frequencies of phenotypic classes of seven qualitative traits in 32 landrace populations of tetraploid wheat (Figure 3). Populations from Wello region were grouped in different clusters from those of Bale landraces, indicating variations in phenotypic characters that were used in the clustering analysis. Clusters A, B, C and D entirely contained landraces from Wello region whereas

three other clusters (E, F and G) contained entirely Bale collections, implying that populations from the two regions were clustered in different groups.

When the nature of populations in individual clusters is considered, Cluster A contains 10 populations most of which were mainly collected from two altitudinal classes with relatively high elevation i.e., altitudes ranging between 2501-2700 masl and 2701-2900 masl. Cluster B contains only one population and it is collected from the fourth altitude class (2501-2700 masl). This population is characterized by having relatively high proportion of short awn length (91.7%), hairy glume (62.4%) and reasonably high percentage frequency of black awn color as compared to other populations. This particular population also had very high diversity index value for traits such as seed color (H' = 1.00), awn color (H' = 1.00), glume hairiness (H' = 0.96) and glume color (H' = 0.90) while very low value of H' (monomorphic) (H' = 0.10) for glume color as compared to most populations. Cluster C consisted two populations (1 and 11) from two different classes (the first from 2501-2700 masl while the second from elevation >2900 masl). Cluster D has three populations (3, 10 and 13) each from different altitude groups. In Cluster E three populations originating from Bale were not grouped together with those obtained from Wello. Clusters F and G contain exclusively materials from Bale region, both of which were clustered under one common node.

Six clusters were delineated among 30 populations of *T. turgidum* ssp. *durum* whereby ten landrace populations were grouped in cluster A, two in Cluster B, three in cluster C, one in cluster D, four in cluster E and ten in Cluster F (Figure 4). Most of the landraces that were grouped in the same cluster had a high morphological similarity that is close to 100%.

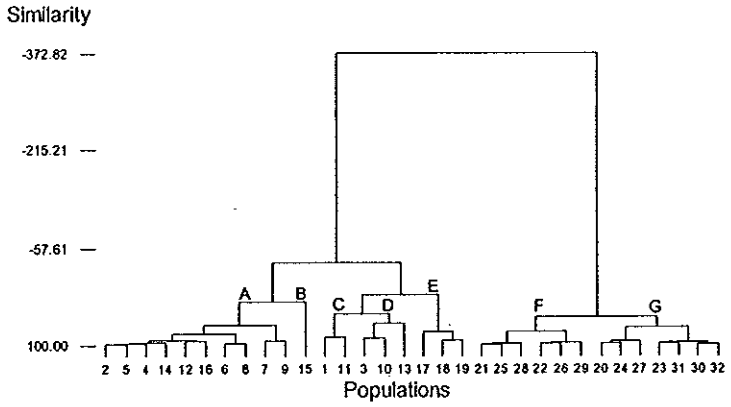


Figure 3. Dendrogram of phenotypic similarities among 32 populations of tetraploid wheat landraces (frequencies of phenotypic classes were used as a grouping variable)

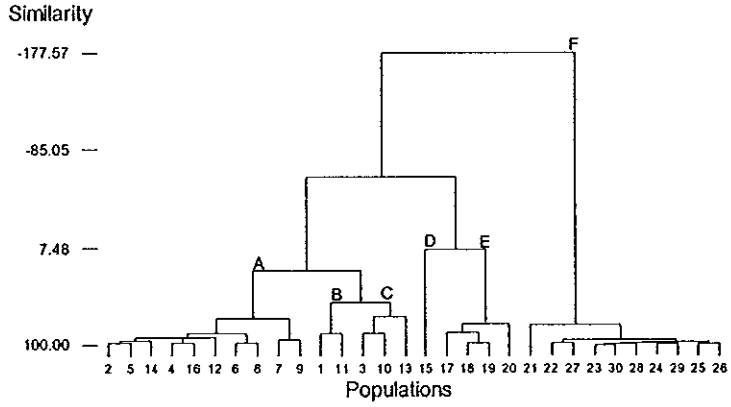


Figure 4. Dendrogram of phenotypic similarities among 30 populations of *T. turgidum* ssp. *durum* landraces (frequencies of phenotypic classes were used as a grouping variable)

4.1.4. DISCRIMINANT ANALYSIS

The summary of discriminant analysis resulting from the frequencies of phenotypic classes as a classifying variable is given in Table 4. The result indicated that about 91.5% of originally grouped taxonomic classes were correctly classified as belonging to their actual taxonomic species.

The contribution of each trait for classifying each taxonomic species in its own group is presented in Table 5. Characters such as beak awn followed by awn length; seed color and awn color had significant importance than the other characters in classifying species into different taxonomic classes. This is evident from the three dimensional representation of intercluster distances of the first canonical function (Figure 5). This implies that variation due to these traits is significantly high among species of wheat as compared to the variability observed due to the rest of the characters.

Standardized canonical discriminant function (correlation) coefficients, eigenvalues, percent of total and cumulative variances of seven qualitative traits are given in Table 5. The first three canonical variable accounted for 99.4% of the total morphological variation, being 63.3% of the proportion of the variance explained by CAN-1 alone. This axis which maximized the differentiation among the landraces was closely related to beak awn (shape) and awn length, showing correction coefficients of 0.665 and 0.590, respectively. The second

function was responsible for 32.3% whereas the third was for 3.8% of the variation. The cumulative variance at CAN-3 was 99.4%.

Table 4. Summary of discriminant analysis indicating how much percent of each taxonomic species is correctly put into its own respective groups[a]

Species[a]	TDU	TTR	TPO	TPY	TAE	TDI	TAS	Total
TDU	94.6	1.9	0.0	0.1	1.3	0.0	2.1	100.0
TTR	11.5	84.1	0.0	0.0	0.4	0.0	4.0	100.0
TPO	25.0	0.0	0.0	75.0	0.0	0.0	0.0	100.0
TPY	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0
TAE	7.5	0.0	0.0	0.0	92.3	0.0	0.2	100.0
TDI	0.0	0.0	0.0	0.0	0.0	100.0	0.0	100.0
TAS	49.3	16.4	0.0	0.0	0.0	0.0	34.3	100.0

a 91.5% of original grouped cases correctly classified.

Table 5. Standardized canonical Discriminant function (correlation) coefficients, eigenvalue, and percent of total variance and cumulative variance of seven qualitative traits

Traits	CAN1	CAN2	CAN3
Beak awn	0.665**	-0.033	0.417
Awn length	0.590*	0.519	-0.415
Seed color	0.347	-0.713*	-0.362
Awn color	0.208	-0.053	0.514*
Glume hairiness	0.080	-0.132	0.297
Glume color	0.366	-0.234	0.261
Spike density	0.041	0.470	-0.074
Eigenvalue	1.295	0.661	0.078
% total variance	63.30	32.30	3.80
% Cumulative variance	63.30	95.60	99.40

*Largest absolute correlation between each variable and any discriminant function

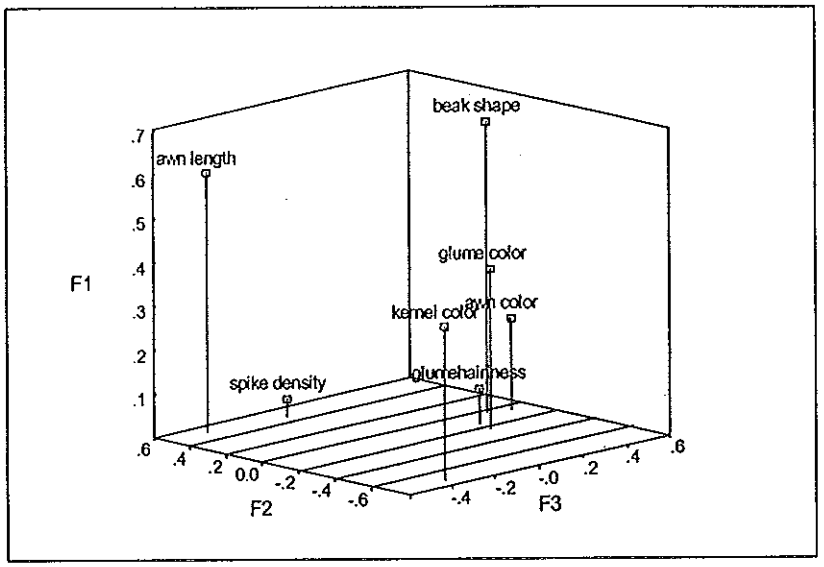


Figure 5. Three-dimensional representation of intercluster distances resulting from the first three canonical components used in clustering of taxonomic species by the frequency of each class in seven qualitative traits

4. 2. ANALYSIS OF INDICES OF SPECIES DIVERSITY

Several of the numerous diversity indices are employed in the present study. Tables 6, 7 and 8, respectively, indicate values of indicators of species diversity for each population, among populations across altitudinal classes and across regions of collection.

4. 2. 1. SPECIES DIVERSITY ACROSS POPULATIONS

At population level various levels of species diversity were observed (Table 6). Margalef index, which is an indicator of species richness, ranged from 0.00 to 0.64, while the level of

species dominance ranged from 1.00 to 1.88. Those populations with a dominance index of 1.00 correspondingly had zero values for richness, evenness, Simpson and Shannon-Weaver diversity indices.

Table 6. Analysis of different diversity indices for populations of landraces of wheat originating from Bale and Wello regions (tetraploid and hexaploid)

No.	Richness	Dominance	Shannon Evenness	Simpson	Shannon-Weaver index
1	0.43	1.03	0.06	0.05	0.07
2	0.21	1.26	0.38	0.32	0.26
3	0.43	1.72	0.40	0.53	0.44
4	0.64	1.20	0.20	0.29	0.28
5	0.43	1.26	0.25	0.33	0.28
6	0.43	1.22	0.24	0.30	0.26
7	0.00	1.00	0.00	0.00	0.00
8	0.43	1.04	0.08	0.07	0.09
9	0.21	1.09	0.02	0.02	0.03
10	0.43	1.04	0.05	0.07	0.09
11	0.00	1.00	0.00	0.00	0.00
12	0.21	1.47	0.16	0.43	0.32
13	0.21	1.01	0.02	0.02	0.03
14	0.21	1.41	0.16	0.41	0.31
15	0.21	1.88	0.19	0.50	0.36
16	0.21	1.55	0.17	0.46	0.33
17	0.49	1.03	0.04	0.06	0.08
18	0.49	1.34	0.17	0.39	0.33
19	0.27	1.13	0.09	0.10	0.18
20	0.52	1.33	0.15	0.39	0.35
21	0.24	1.25	0.13	0.32	0.26
22	0.49	1.20	0.13	0.28	0.26
23	0.24	1.09	0.06	0.15	0.11
24	0.49	1.28	0.15	0.35	0.30
25	0.24	1.28	0.14	0.34	0.27
26	0.00	1.00	0.00	0.00	0.00
27	0.00	1.00	0.00	0.00	0.00
28	0.00	1.00	0.00	0.00	0.00
29	0.26	1.61	0.17	0.47	0.34
30	0.00	1.00	0.00	0.00	0.00
31	0.26	1.50	0.17	0.44	0.33
32	0.24	1.30	0.14	0.36	0.28
Total	0.76	1.39	0.23	0.43	0.44

4. 2. 2. SPECIES DIVERSITY ACROSS ALTITUDINAL CLASSES

Table 7 shows biological diversity indices of landraces across gradients of altitudinal classes. Relatively large Margalef index (richness) was observed at altitude range between 2301-2500 masl. The least was observed at altitude below 2100 masl. Other altitudinal classes had the values ranging between 0.37 and 0.73. The value for dominance index was also large (D=1.9) in the altitudinal class between 2301-2500 masl.

The largest Shannon evenness index was recorded at lower altitudes below 2100 masl (SI=0.43) while the smallest value at altitudes between 2301-2500 masl. The maximum value for Simpson index was recorded between 2701-2900 masl. Small values of Simpson index indicate larger diversity. Shannon-Weaver diversity index was small in all altitudinal classes. But relatively large value (H'=0.40) was obtained in altitudinal class ranging between 2501-2700 masl.

Table 7. Estimates of diversity indices for the species composition of landrace populations along gradients of altitudinal classes

Altitude (masl)	Richness	Dominance	Evenness	Simpson	Shannon-Weaver index
<2100	0.21	1.40	0.43	0.40	0.30
2001-2300	0.42	1.10	0.19	0.22	0.21
2301-2500	0.75	1.90	0.04	0.57	0.07
2501-2700	0.73	1.40	0.22	0.44	0.40
2701-2900	0.49	1.10	0.09	0.89	0.13
>2900	0.37	1.00	0.05	0.04	0.05
Total	0.76	1.39	0.23	0.43	0.44

4.2.3. REGIONAL SPECIES DIVERSITY

On the basis of region, landrace populations originating from Wello region had larger Margalef index (MR=0.67) as compared to those from Bale region (MR=0.59) (Table 8). Conversely, the former region had smaller Berger Parker index (small dominance value), while the latter had larger Berger-Parker (dominance) index. The value of Shannon evenness is also large for the same region, indicating a more even distribution of species composition in the former region. The smaller Simpson index and larger diversity index relative to the former region further support the more even distribution of the species composition. The overall analysis of biological diversity of landrace populations of wheat collected from the two regions showed that landrace populations from Wello region have more diverse species composition than those from Bale region.

Table 8. Species richness, dominance, evenness in distribution, Simpson index and Shannon Weaver diversity index by region

Region	Richness	Dominance	Evenness	Simpson	Shannon-Weaver index
Wello	0.67	1.21	0.16	0.29	0.29
Bale	0.59	1.96	0.06	0.51	0.01
Total	0.76	1.39	0.23	0.43	0.44

4.3. MORPHOLOGICAL STUDY

4. 3.1. PHENOTYPIC DISTRIBUTION OF CHARACTERS

4.3.1.1. DISTRIBUTION OF PHENOTYPIC CHARACTERS ACROSS POPULATIONS

The frequencies of each phenotypic class for each of the populations are presented in Table 9 (for tetraploid species) and in Table 10 (for *T. turgidum* ssp. *durum).*

Awn color

Black awn color was not observed in wheat populations originating from Bale except in one population with a frequency of 16.3% (Table 9). This character has been found in all landraces of Wello collection. The frequency ranged between 1.8% and 68.5% for Wello region. Non-black awn color was predominant in all populations except two from Wello (populations #10 and #13). Similar trend of occurrence was observed in the analysis of *T. turgidum ssp. urum* as in the case of tetraploids (Table, 10).

Glume color

Purple to black type of glume color was not present in two landraces of Bale region (Table 9). The maximum frequency of occurrence for this character was found to be 100% and it was recorded in two landraces of this region. Moreover, red–brown glume color was absent in fourteen landraces and similarly white-yellow glume color was not recorded in two landrace

populations. There was high percentage frequency of white-yellow glume color in Wello materials than in Bale. However, purple-black glume color was more frequent in Bale materials than Wello materials.

Awn length

Most of the landraces had high frequency for long awn length while short and intermediate awn length had low frequency of occurrence in tetraploid species treated as a whole (Table, 9). But the frequency of occurrence for short awn length ranged from 0% (in four landraces) to 91.7% (in one landrace). The majority of the landraces were with the percentage frequencies of less than 20%. The intermediate awn length was also with low percent frequency of occurrence though it has more frequently been observed than the short awn length.

Beak shape

Observations made for beak shape showed that most of the tetraploid wheats that were collected from Bale region are awned and the acuminate and pointed types are rarely observed in this region. Belay *et al.* (1997) also reported the frequent occurrence of awned types of tetraploid wheats for this particular character.

Spike density

Lax and very dense spike types were rarely recorded whereas dense and intermediate ones dominated all the landraces investigated here in this study. Lax spike types had a frequency ranging from 0% to 19.1% while very dense spike type had 0% to 45% (occurred in only five landraces from Wello region).

Glume pubescence

Non-hairy types (glabrous glumes) were more frequent in Bale materials as opposed to that of Wello. The overall frequency of occurrence indicates that over 90% is shared by non-hairy types.

Kernel color

This character showed wide and relatively uniform distribution in most landraces. However, white-yellow kernel color types were absent in eleven landraces most of which were from Bale collections. Purple-black kernel color is abundant in Bale region than Wello region.

Table 9. Phenotypic frequencies for individual characters as percentages of the number of observations in each population of tetraploid wheat landraces

Pop	GH		AC		AL			BA			GC			SC				SD		
	H	NH	B	NB	S	I	L	A	P	AW	W-Y	R-B	P-B	W-Y	R-B	P-B	LA	ID	D	VD
1	65.4	34.6	4.7	95.3	0.0	0.0	100.0	0.0	4.7	95.3	87.9	9.4	2.8	1.9	98.1	0.0	0.0	0.0	98.1	1.9
2	1.9	98.1	7.4	92.6	18.5	1.9	78.6	13.9	80.6	5.6	65.7	30.6	3.7	5.6	71.3	23.2	10.2	34.3	55.6	0.0
3	0	100.0	7.0	93.0	8.5	0.0	91.6	7.0	88.7	4.2	23.9	66.2	9.9	42.7	51.8	5.4	4.2	15.5	80.3	0.0
4	1.9	98.1	26.9	73.1	14.4	7.7	77.9	13.5	85.6	0.9	58.7	29.8	11.5	26.4	64.2	9.4	1.0	23.1	76.0	0.0
5	2.8	97.2	20.2	79.8	20.2	0.9	78.9	20.2	79.8	0.0	69.7	11.0	19.3	8.2	60.0	31.8	7.3	38.5	54.1	0.0
6	1.1	98.9	16.7	83.3	1.1	26.7	67.32	0.0	98.9	1.1	42.2	20.0	37.8	18.3	72.5	9.2	3.3	32.2	64.4	0.0
7	0	100	1.8	98.2	2.7	59.1	38.2	1.8	83.6	14.6	45.5	24.6	30.0	1.8	56.4	41.8	0.9	17.3	81.8	0.0
8	11.9	88.1	15.6	84.4	3.7	40.4	56.0	16.5	78.9	4.6	41.3	13.8	45.0	19.1	73.6	7.3	0.0	22.9	64.2	12.8
9	0	100	1.8	98.2	2.8	50.5	46.8	28.4	63.3	8.3	72.5	8.3	19.3	0.0	25.5	74.5	1.8	33.0	65.1	0.0
10	8.3	91.7	50.0	50.0	7.4	6.5	86.1	30.6	42.6	26.9	41.7	55.6	2.8	44.4	42.6	13.0	1.9	0.9	96.3	0.9
11	30.0	70.0	5.5	94.6	0.0	1.8	98.2	16.4	22.7	60.9	71.8	22.7	5.5	37.3	55.5	7.3	2.7	14.6	60.0	22.7
12	11.8	88.2	32.7	67.3	35.5	0.0	64.6	38.2	57.3	4.6	82.7	10.0	7.3	0.9	79.1	20.0	19.1	47.3	33.6	0.0
13	0	100	68.5	31.5	0.9	1.9	97.2	1.9	9.3	88.9	79.6	1.9	18.5	74.0	24.7	1.3	0.0	4.6	95.4	0.0
14	0	100.0	12.7	87.3	30.0	7.3	62.7	33.6	65.5	0.9	70.0	25.5	4.6	0.0	50.0	50.0	3.6	43.6	52.7	0.0
15	62.4	37.6	41.3	58.7	91.7	0.0	8.3	45.9	3.2	0.9	98.2	0.0	1.8	46.8	53.2	0.0	11.9	33.0	10.1	45.0
16	10	90	26.4	73.6	37.3	1.8	60.9	33.6	66.4	0.0	77.3	12.7	10.0	15.4	77.3	7.3	5.5	12.7	81.8	0.0
Wm	13.0	87.0	21.2	78.8	17.2	12.9	69.6	18.8	58.2	19.9	64.3	21.4	14.4	21.4	59.7	18.9	4.6	23.3	66.8	5.2
17	0	100	0.0	100	23.3	13.3	63.3	0.0	0.0	100	96.7	3.3	0.0	3.3	6.5	90.2	3.3	76.7	20.0	0.0
18	8.5	91.5	0.0	100	8.5	15.3	76.3	25.4	1.7	72.9	91.6	0.0	8.5	74.6	1.7	23.7	0.0	67.8	32.2	0.0
19	4.7	95.3	16.3	83.7	16.3	16.3	67.4	37.2	0.0	62.8	100	0.0	0.0	83.7	2.3	14.0	0.0	46.5	53.5	0.0
20	0	100	0.0	100	2.2	23.9	73.9	2.2	0.0	97.8	6.5	0.0	93.5	25.0	0.0	75.0	0.0	93.5	6.5	0.0
21	0	100	0.0	100	6.7	10.0	83.3	10.0	1.7	88.3	15.0	0.0	85.0	0.0	21.7	78.3	0.0	70.0	30.0	0.0
22	0	100	0.0	100	10.0	21.7	68.3	10.0	0.0	90.0	33.3	3.3	63.3	0.0	86.7	13.3	0.0	80.0	20.0	0.0
23	0	100	0.0	100	16.7	5.0	78.3	0.0	0.0	100	21.7	1.7	76.7	0.0	91.7	8.3	0.0	76.7	23.3	0.0
24	0	100	0.0	100	8.3	20.0	71.7	0.0	0.0	100	8.3	0.0	91.7	0.0	21.7	78.3	0.0	83.3	16.7	0.0
25	0	100	0.0	100	0.0	15.0	85.0	0.0	0.0	100	6.7	0.0	93.3	0.0	28.3	71.7	6.7	76.7	16.7	0.0
26	0	100	0.0	100	10.2	10.2	79.6	0.0	0.0	100	8.2	0.0	91.8	0.0	100	0.0	0.0	80.0	20.0	0.0
27	0	100	0.0	100	10.0	10.0	80.0	0.0	0.0	100	0.0	0.0	100	0.0	0.0	100.0	0.0	53.3	46.7	0.0
28	0	100	0.0	100	1.7	18.3	80.0	0.0	0.0	100	0.0	0.0	100	0.0	0.0	100.0	0.0	57.8	37.8	0.0
29	0	100	0.0	100	0.0	28.9	71.1	0.0	0.0	100	24.4	0.0	75.6	0.0	62.2	37.8	4.4	65.0	35.0	0.0
30	0	100	0.0	100	13.3	15.0	71.7	0.0	0.0	100	25.0	0.0	75.0	21.7	78.3	0.0	0.0	62.2	37.8	0.0
31	0	100	0.0	100	2.2	20.0	77.8	0.0	0.0	100	13.3	0.0	86.7	0.0	66.7	33.3	0.0	68.3	30.0	0.0
32	0	100	0.0	100	13.3	5.0	81.7	1.7	0.0	98.3	15.0	0.0	85.0	5.0	68.3	26.7	1.7	40.0	53.1	0.0
Bm	**0.8**	**99.2**	**1.0**	**99.0**	**8.9**	**15.5**	**75.6**	**5.4**	**0.2**	**94.4**	**29.1**	**0.5**	**70.4**	**13.3**	**39.5**	**47.2**	**1.0**	**68.6**	**30.0**	**0.0**
Tt	**9.1**	**90.9**	**14.4**	**85.6**	**14.7**	**13.8**	**71.5**	**14.7**	**39.8**	**45.5**	**53.0**	**13.6**	**33.5**	**18.1**	**52.8**	**29.2**	**3.1**	**45.9**	**48.4**	**2.6**

GH= glume hairiness, H=hairy, NH=nonhairy, AC=awn color, B=black, NB=nonblack, AL=awnlength,, S=short, I=intermediate, L=long, BA=Beak awn, A= acuminate, P=pointed AW=awned, GC=glume color, W-Y=yellow-white, R-B=red-brown, P-B=purple-black, SC=seed color, SD=spike density, LA=lax, ID=intermediate dense, D=dense, VD=very dense Wm= Wello mean, Bm=Bale mean

Table 10. Percentage frequencies of individual phenotypic characters in *T. turgidum* ssp.*durum* landrace populations

Pop	GH		AC		AL			BA			GC			SC			SD			
	H	NH	B	NB	S	I	L	A	P	AW	W-Y	R-B	P-B	W-Y	R-B	P-B	LA	ID	D	VD
1	64 8	35 2	2.9	97.1	0.0	0.0	100.0	0.0	4.8	95.2	87.6	9 5	2.9	0.0	100.0	0 0	0 0	0.0	100 0	0 0
2	0 0	100.0	0.0	100.0	2.3	2.3	95.3	0.0	93 0	7.0	58.1	38.4	3.5	7.0	74.4	18 6	4 7	33.7	61 6	0 0
3	0 0	100.0	4.7	95.3	0.0	0.0	100.0	3.1	93.8	3.1	15.6	73.4	10.9	68.8	26.6	4.7	1.6	12.5	85 9	0 0
4	0 0	100.0	27.3	72.7	1 1	9.1	89.8	0.0	98.9	1.1	51.1	35.2	13.6	30.7	63.6	5 7	0.0	22.7	77 3	0 0
5	1 2	98.8	19.8	80.2	0.0	1.2	98.8	0.0	100.0	0.0	62.8	14.0	23.3	9.3	66.3	24.4	3.5	33.7	62 8	0 0
6	1 1	98.9	16.9	83.1	1 1	27.0	71.9	0.0	98.9	1.1	41.6	20.2	38.2	5.6	85.4	9.0	2.2	32.6	65 2	0 0
7	0.0	100.0	1.8	98.2	2.7	59.1	38.2	1.8	83.6	14.5	45.5	24.5	30.0	1.8	56.4	41 8	0.9	17.3	81 8	0 0
8	12 3	87.7	16.0	84.0	1.0	41.5	57.5	17.0	78.3	4.7	40.6	14.2	45.3	16.0	76.4	7.5	0.0	23.6	63 2	13 2
9	0 0	100.0	1.8	98.2	2.8	50.5	46.8	28.4	63.3	8.3	72.5	8.3	19.3	0.0	24.8	75 2	1 8	33.0	65 1	0 0
10	6 6	93.4	50.8	49 1	5.7	6.6	87.7	29.2	43.4	27.4	40.6	56.6	2.8	45.3	41.5	13.2	1 9	0.9	97 2	0 0
11	30 0	70.0	5.5	94.5	0 0	1.8	98.2	16.4	22.7	60.9	71.8	22.7	5.5	37.3	55.5	7.3	2 7	14.5	60 0	22 7
12	13.0	62.0	33.3	66.7	9.3	0.0	90.7	12.0	81.3	6.7	80.0	14.7	5.3	0.0	76.0	24 0	9.3	49.3	41.3	0 0
13	0.0	100.0	68.5	31.5	0.9	1.9	97.2	1.9	9.2	88.9	79.6	1.9	18.5	75.0	24.1	0.9	0.0	4.6	95.4	0.0
14	0.0	100.0	12.8	87.2	8.0	9.0	82.1	12.8	85.9	1.3	61.5	32.1	6.4	0.0	42.3	57.7	3.8	39.7	56.4	0.0
15	89.7	10.3	3.4	96.6	86.2	0.0	13.8	1.7	98.3	0.0	100.0	0.0	0.0	84.5	15.0	0.5	1.7	12.1	1.7	84.5
16	7.0	93.0	28.2	71.8	14.1	1.4	84.5	9.9	90.1	0.0	67.6	19.7	12.7	7.0	84.5	8.5	0.0	9.9	90.1	0.0
Wm	**14.1**	**84.3**	**18.4**	**81.6**	**8.5**	**13.2**	**78.3**	**8.4**	**71.6**	**20.0**	**61.0**	**24.1**	**14.9**	**24.3**	**57.1**	**18.7**	**2.1**	**21.3**	**69.1**	**7.5**
17	0.0	100.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	100.0	100.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0
18	11.4	88.6	0.0	100.0	6.8	15.9	77.3	25.0	2.3	72.7	95.5	0.0	4.5	97.7	2.3	0.0	0.0	56.8	43 2	0.0
19	5 3	94.7	18.4	81.6	13.2	13.2	73.7	42.1	0.0	57.9	100.0	0.0	0.0	94.7	2.6	2.6	0.0	39.5	60 5	0 0
20	0.0	100.0	0.0	100.0	0.0	40.0	60.0	0.0	0.0	100.0	30.0	0.0	70.0	100.0	0.0	0.0	0.0	90.0	10 0	0 0
21	0.0	100.0	0.0	100.0	16.7	8.3	75.0	50.0	8.3	41.7	66.7	0.0	33.3	0.0	100.0	0.0	0.0	66.7	33.3	0.0
22	0.0	100.0	0.0	100.0	12.0	24.0	64.0	12.0	0.0	88.0	34.0	2.0	64.0	0.0	100.0	0.0	0.0	76.0	24.0	0.0
23	0.0	100.0	0.0	100.0	16.4	5.5	78.2	0.0	0.0	100.0	23.6	1.8	74.5	0.0	100.0	0.0	0.0	74.5	25.5	0.0
24	0.0	100.0	0.0	100.0	16.7	8.3	75.0	8.3	8.3	83.3	8.3	0.0	91.7	0.0	100.0	0.0	0.0	66.7	33.3	0.0
25	0.0	100.0	0.0	100.0	0.0	7.7	92.3	0.0	0.0	100.0	0.0	0.0	100.0	0.0	100.0	0.0	7.7	84.6	7.7	0.0
26	0.0	100.0	0.0	100.0	10.2	10.2	79.6	0.0	0.0	100.0	8.2	0.0	91.8	0.0	100.0	0.0	0.0	83.7	16.3	0.0
27	0.0	100.0	0.0	100.0	0.0	21.4	78.6	0.0	0.0	100.0	39.3	0.0	60.7	0.0	100.0	0.0	3.6	53.6	42.9	0.0
28	0.0	100.0	0.0	100.0	13.3	15.0	71.7	0.0	0.0	100.0	25.0	0.0	75.0	21.7	78.3	0.0	0.0	65.0	35.0	0.0
29	0 0	100.0	0.0	100.0	3.3	23.3	73.3	0.0	0.0	100.0	6.7	0.0	93.0	0.0	100.0	0.0	0.0	66.7	33 3	0 0
30	0 0	100.0	0.0	100.0	13.0	6.5	80.4	2.2	0.0	97.8	17.4	0.0	82.6	6.5	89.1	4.3	2.2	71.7	26.1	0.0
Bm	**1.2**	**98.8**	**1.3**	**98.7**	**8.7**	**14.2**	**77.1**	**10.0**	**1.4**	**88.7**	**39.6**	**0.3**	**60.1**	**30.0**	**69.5**	**0.5**	**1.0**	**71.1**	**27.9**	**0.0**
Tt	**10.5**	**89.5**	**14.8**	**85.2**	**7.3**	**14.9**	**77.8**	**9.1**	**51.8**	**39.1**	**55.1**	**18.0**	**26.9**	**23.1**	**61.9**	**15.0**	**1.7**	**31.8**	**61.9**	**4.6**

GH= glume hairiness, H=hairy, NH=nonhairy, AC=awn color, B=black, NB=nonblack, AL=awnlength,, S=short, I=intermediate, L=long, BA=Beak awn, A= acuminate, P=pointed AW=awned, GC=glume color, W-Y=yellow-white, R-B=red-brown, P-B=purple-black, SC=seed color, SD=spike density, LA=lax, ID=intermediate dense, D=dense, VD=very dense Wm= Wello mean, Bm=Bale mean; *pulationsNo. 27 and 28 didn't contain *T. turgidum* ssp. *durum*

4.3.1.2. ALTITUDINAL DISTRIBUTION OF CHARACTERS

The distribution of traits such as awn color, awn length, beak awn, glume color, seed color, spike density and glume hairiness across a range of altitudes is presented in Figure 6. Black type of awn color was not recorded below 2500 masl. As in the case of hairy glume the maximum proportion for this character was recorded in altitudes above 2900 masl. High frequency was recorded for long awn length in most of the six-altitudinal classes. This phenotypic class had nearly equal proportion with intermediate type of awn length at altitudes ranging between 2701-2900 masl. At altitudes between 2501-2700 masl short awn length is more frequent compared to intermediate type. In other altitudinal classes, however, the two had similar proportion.

An awned type of beak awn (shape) is the most frequent than acuminate and pointed types at altitudes below 2500 masl. Pointed type of beak awn was frequently recorded at altitudinal ranges between 2101-2300 masl and below 2100 masl.

Relatively higher frequencies of purple-black type of glume color were obtained at low altitudes. The frequency for this phenotypic class increased with a decrease in altitude though this trend was not uniform in some altitudinal classes. The frequency of red-brown type of glume color uniformly increased with the rise in elevation.

When seed color is considered red-brown types were the most abundant in all altitudinal classes, except at elevations ranging from 2301-2500 masl where purple-black types are more

frequent than other types. The intermediate dense types are most frequent at lower elevations while the dense types at higher elevations. Glume hairiness was monomorphic for non-hairy type in altitudes below 2300–masl. Hairy glumes were observed in all other four-altitudinal classes but with relatively large proportion at elevations above 2900 masl.

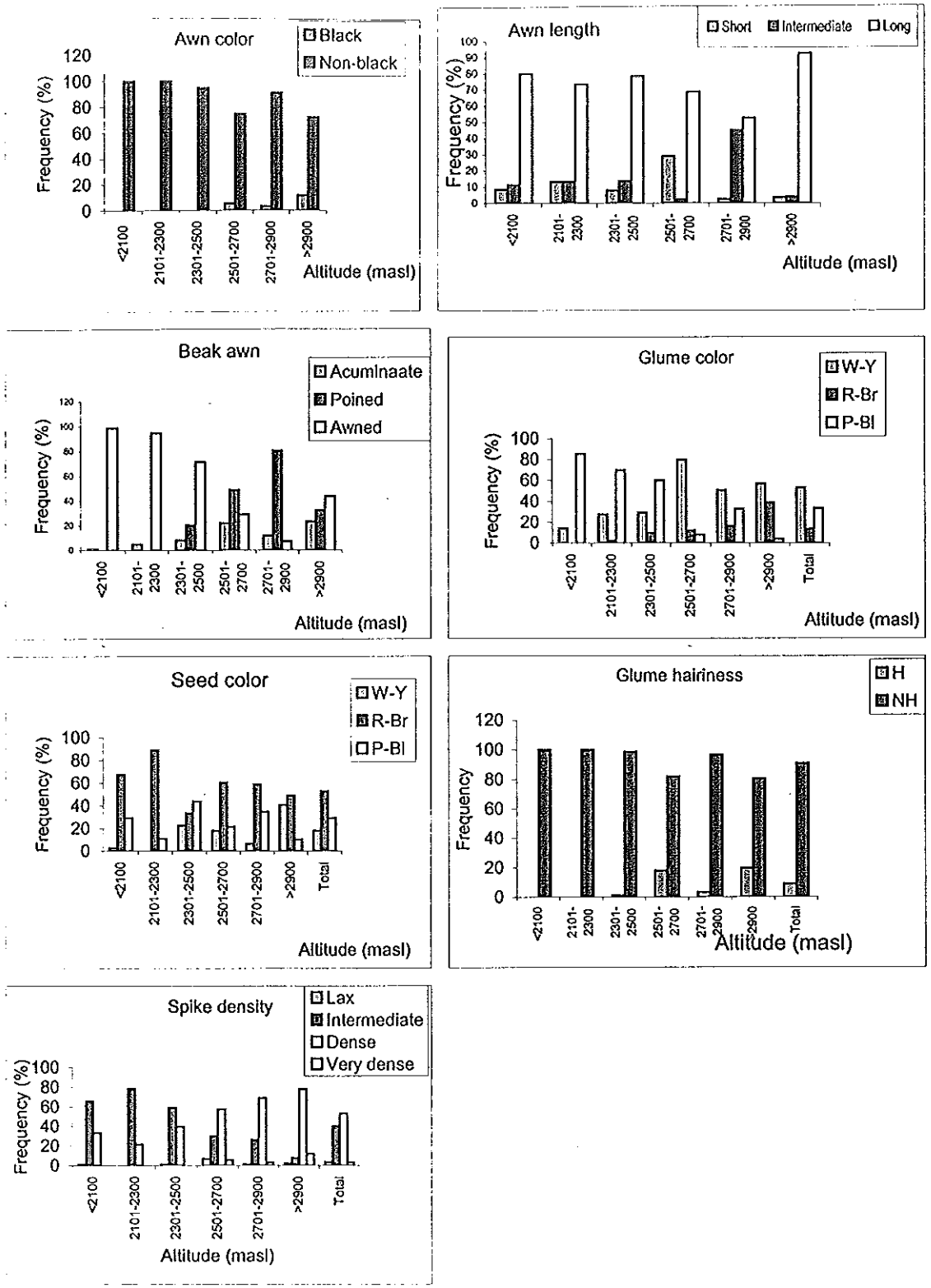


Figure 6. Frequencies of each phenotypic class for awn color, awn length, beak awn, glume color, seed color, glume hairiness and spike density in landrace populations of tetraploid wheats by altitude

4.3.1.3. REGIONAL DISTRIBUTION OF CHARACTERS

Figure 7 shows the regional distribution of awn length, beak awn, glume color, seed color, spike density, glume hairiness and awn color. Long awn length is frequently observed in both regions. But short type of awn length is the next frequent phenotypic class in Wello region while the intermediate type for Bale region. Black awn color is a rare class for both regions.

Pointed types of beak awn dominated landrace populations originating from Wello region while awned types dominated those from Bale region. Acuminate and awned types had similar proportion for Wello region while awned ones are more frequent than acuminate for Bale region. When glume color is considered white–yellow types were more abundant in Wello while purple-black in Bale region. Red-brown glume colors were rarely recorded in Bale materials but it was widely observed in landraces from Wello region.

Red-brown types of seed color were the most abundant in both Bale and Wello landrace populations. While relatively high proportions of purple-black seed color types were observed in Bale region.

Dense types of spike density are dominant in Wello region while the intermediate types are more abundant in Bale region. Overall the regions the dense types are more frequent. The proportion hairy type of glume color is much larger in Wello region as compared to Bale materials. Bale materials are almost exclusively non-hairy types. Similarly black type of awn

color is rarely found in Bale region. The regional distribution of each phenotypic class in *T. turgidum* ssp. *durum* shows similar trend of occurrence with that of tetraploids (Table 11). Black awn is rare in Bale region while purple glume color is dominant. Purple-black seeded type of durum is also rare but it occurred with about equal proportion with white-yellow types in Wello region.

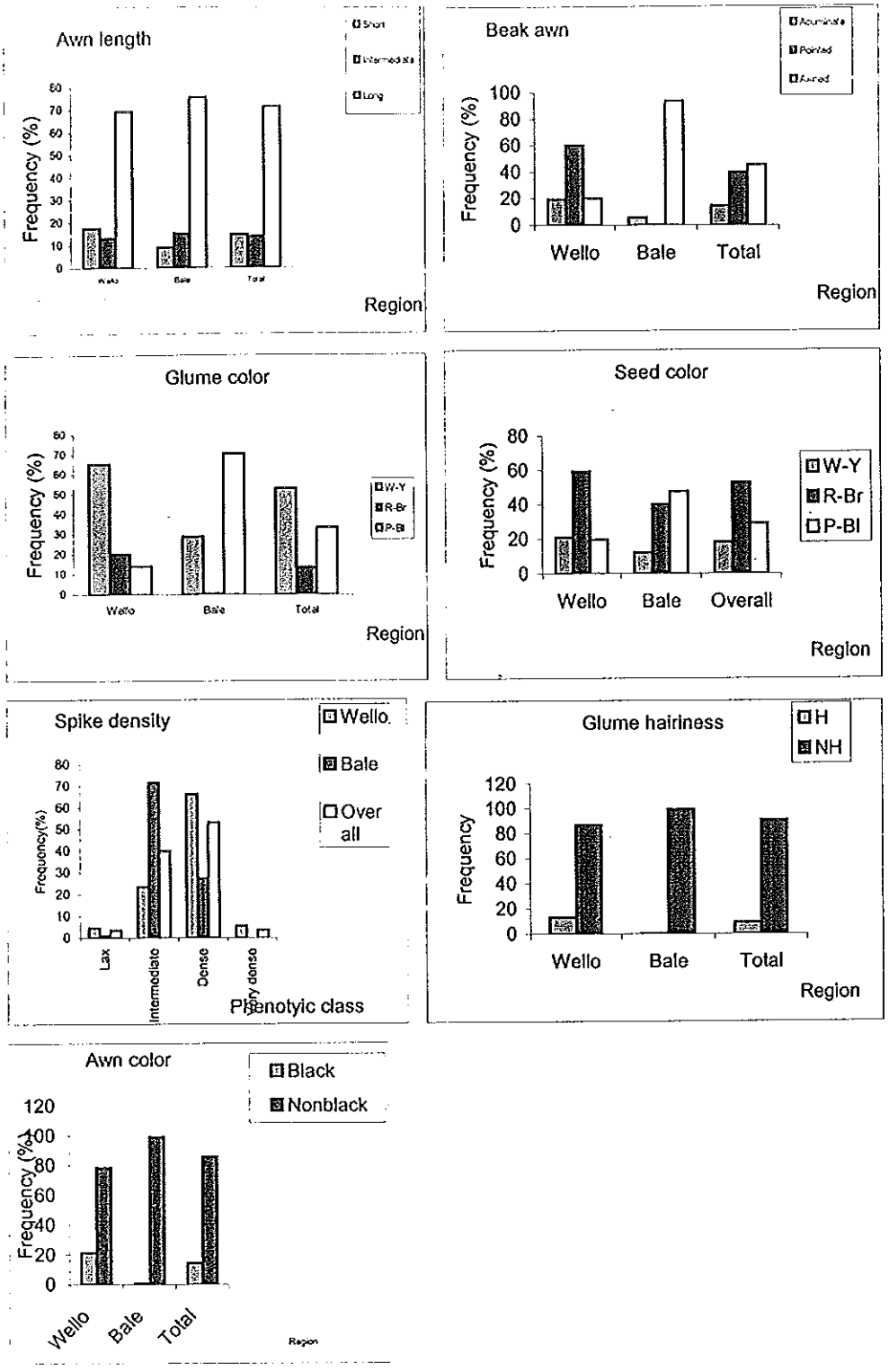


Figure 7. Frequencies of each phenotypic class for awn length, beak awn, glume color, seed color, spike density, awn color and glume hairiness in landrace populations of tetraploid wheats by region

Table 11. Percentage frequencies of each phenotypic class of different qualitative traits in *T. turgidum* ssp. *durum* landraces

Region	AC		AL			BA			GC			GH		KC			SD			
	B	NB	S	I	L	A	P	AW	W-Y	R-B	P-B	H	NH	W-Y	R-B	P-B	LA	ID	D	VD
Wello	18.9	81.1	6.3	15.0	78.6	9.0	67.6	23.3	60.9	23.4	15.7	13.3	86.7	23.0	57.6	19.4	2.0	20.6	71.3	6.1
Bale	1.6	98.4	10.5	14.3	75.2	9.2	0.7	90.2	36.4	0.4	63.2	1.6	98.4	23.7	75.7	0.7	0.70	67.9	31.5	0
Total	**14.8**	**85.2**	**7.3**	**14.9**	**77.8**	**9.1**	**51.8**	**39.1**	**55.1**	**18.0**	**26.9**	**10.5**	**89.5**	**23.1**	**61.9**	**15.0**	**1.7**	**31.8**	**61.9**	**4.6**

GH= glume hairiness, H=hairy, NH=nonhairy, AC=awn color, B=black, NB=nonblack, AL=awnlength,, S=short, I=intermediate, L=long, BA=Beak awn, A= acuminate, P=pointed AW=awned, GC=glume color, W-Y=yellow-white, R-B=red-brown, P-B=purple-black, SC=seed color, SD=spike density, LA=lax, ID=intermediate dense, D=dense, VD=very dense

4. 3.2. ESTIMATES OF DIVERSITY INDICES

Estimates of the Shannon-Weaver diversity index (H') for each character, population, altitude, region and means pooled over characters were computed from the frequencies of each phenotypic class. Analysis was made by considering ploidy level and species type.

4.3.3. ANALYSIS OF DIVERSITY INDEX FOR TETRAPLOID WHEAT SPECIES

4.3.3.1. DIVERSITY INDEX WITHIN AND ACROSS POPULATIONS

At population level, the Shannon–Weaver diversity index ranged from completely monomorphic for some traits to highly polymorphic level in others (Table 12). High diversity indices (H' > 0.60) pooled over characters were obtained in eight populations the majority of which were collected from Wello region. Intermediate mean H' (0.40 ≤H' ≤0.60) pooled over characters were obtained in fourteen populations. Low mean H' (0.10 ≤H' ≤0.40) was observed in the rest ten populations. When mean H' of each trait is considered, the highest value (H'=0.68) was calculated for spike density while the smallest value (H' = 0.19) for glume hairiness. Comparison of total diversity index of each trait indicates that seed color and beak awn showed the highest value of H' (0.92).

The pooled mean H' over characters ranged from 0.19 ± 0.12 to 0.73 ± 0.08. The total H' for the characters ranged from intermediate for awn color (H' = 0.59) to very high H' (H' = 0.92) in two traits, seed color and beak awn. The overall diversity index was found to be high

(H'=0.81±0.05). The highest mean H' (H' = 0.73 ± 0.08) pooled over traits was obtained in two populations originating from Wello region while the smallest value of mean H' (H' = 0.19 ± 0.12) pooled over traits was observed in landrace population collected from Bale region.

4.3.3.2. ALTITUDINAL AND REGIONAL INDEX OF DIVERSITY

Estimates of mean H' by altitude were presented in Figures 9 and 10 for tetraploid species. Seed color, spike density and beak awn exhibited high diversity index at most of the altitude classes while the other traits showed varying degrees of variability. Though the pattern was not uniform the mean diversity index of seed color and beak awn increased with altitude. However, the other traits did not show any clear relationship with altitude.

On regional bases, except glume hairiness, which had, low H' value (H' = 0.34) all the other seven traits had intermediate (H' = 0.56 for awn length) to a high level (H' = 0.71 for seed color) for landrace collected from Wello region (Table 12). This value has ranged from monomorphic (for awn color and glume hairiness) and low diversity (in beak awn) to intermediate high diversity for Bale region.

Table 12. Diversity index (H') estimates for each character in landrace populations (tetraploids)

Region	Popn	GH	AC	AL	BA	GC	SC	SD	Mean ± S.E.
Wello	1	0.93	0.3	0.0	0.3	0.4	0.1	0.1	0.30±012
	2	0.4	0.4	0.5	0.6	0.7	0.7	0.8	0.59±0.06
	3	0	0.4	0.4	0.4	0.8	0.8	0.6	0.49±0.11
	4	0.14	0.8	0.6	0.4	0.8	0.8	0.4	0.56±0.10
	5	0.18	0.5	0.5	0.7	0.7	0.8	0.8	0.60±0.08
	6	0.09	0.4	0.6	0.1	1.0	0.5	0.7	0.48±0.12
	7	0	0.1	0.7	0.5	1.0	0.7	0.5	0.50±0.13
	8	0.53	0.6	0.7	0.6	0.9	0.7	0.8	0.69±0.05
	9	0	0.1	1.0	0.8	0.7	0.8	0.7	0.59±0.14
	10	0.41	1.0	0.6	1.0	0.7	0.9	0.1	0.67±0.13
	11	.88	0.3	0.8	0.9	0.7	0.8	0.7	0.73±0.08
	12	0.52	0.9	0.9	0.9	0.5	0.5	0.9	0.73±0.08
	13	0	0.9	0.1	0.4	0.5	0.6	0.3	0.40±0.12
	14	0	0.6	0.5	0.4	0.7	1.0	0.8	0.57±0.12
	15	0.96	1.0	0.4	0.7	0.1	1.0	0.9	0.72±0.13
	16	0.47	0.8	0.7	0.9	0.6	0.6	0.5	0.65±0.06
Mean		**0.34**	**0.57**	**0.56**	**0.60**	**0.68**	**0.71**	**0.60**	**0.58±0.12**
Bale	17	0	0.0	0.8	0.0	0.2	0.1	0.6	0.24±0.12
	18	0.42	0.0	0.6	0.6	0.4	0.6	0.9	0.50±0.10
	19	0.27	0.6	0.8	1.0	0.0	0.5	1.0	0.60±0.14
	20	0	0.0	0.6	0.2	0.2	0.8	0.4	0.31±0.11
	21	0	0.0	0.5	0.4	0.9	0.8	0.8	0.49±0.14
	22	0	0.0	0.8	0.5	0.7	0.6	0.7	0.47±0.13
	23	0	0.0	0.6	0.0	0.6	0.4	0.8	0.34±0.12
	24	0	0.0	0.7	0.4	0.4	0.8	0.7	0.43±0.14
	25	0	0.0	0.6	0.0	0.4	0.9	0.6	0.36±0.11
	26	0	0.0	0.6	0.0	0.4	0.0	0.6	0.23±0.12
	27	0	0.0	0.6	0.0	0.0	0.0	0.7	0.19±0.12
	28	0	0.0	0.5	0.0	0.0	0.0	1.0	0.21±0.15
	29	0	0.0	0.9	0.0	0.8	1.0	0.8	0.50±0.18
	30	0	0.0	0.7	0.0	0.8	0.8	0.9	0.46±0.16
	31	0	0.0	0.6	0.0	0.6	0.6	1.0	0.40±0.15
	32	0	0.0	0.5	0.1	0.6	0.7	0.6	0.36±0.12
Mean		**0.04**	**0.04**	**0.65**	**0.20**	**0.44**	**0.54**	**0.76**	**0.38±0.29**
Overall mean		**0.89**	**0.59**	**0.72**	**0.92**	**0.89**	**0.92**	**0.71**	**0.81±0.05**

GH= glume hairiness; AC=awn color; AL=awnlength; BA=Beak awn; GC=glume color; SC=seed color; SD=spike density

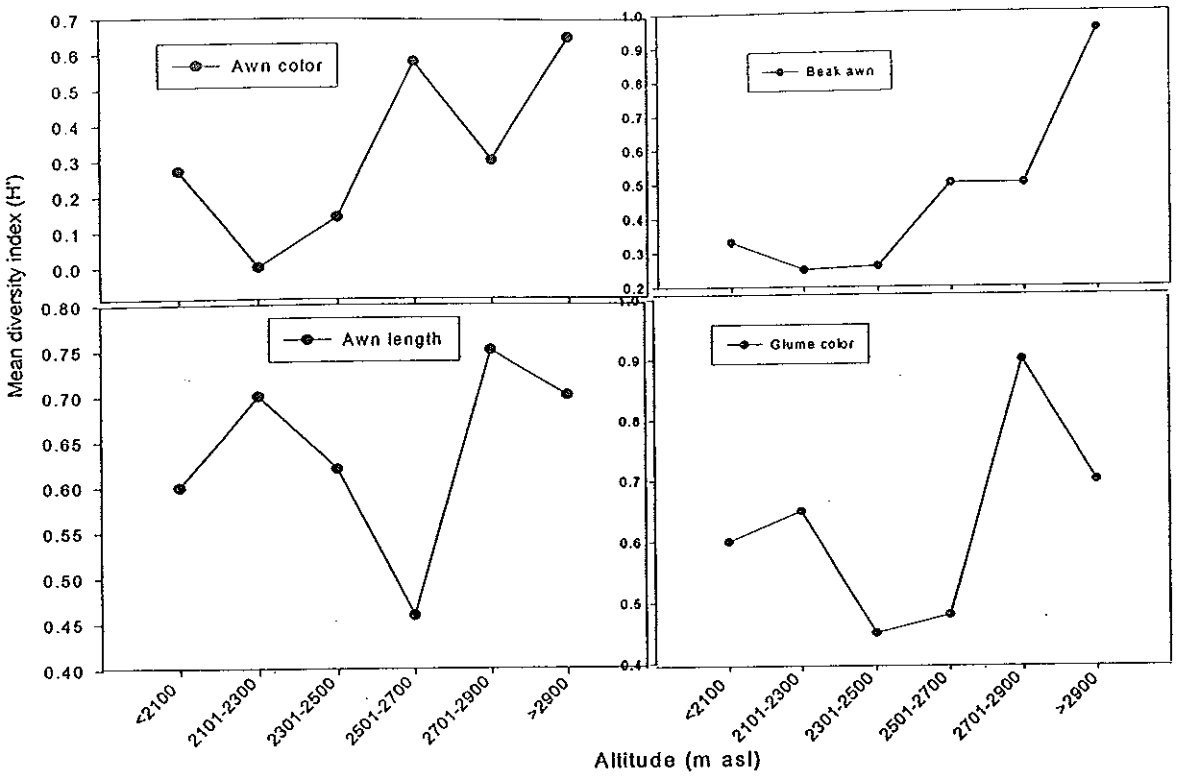


Figure 8. Mean diversity index of awn color, beak awn, awn length and glume color by altitude (tetraploids)

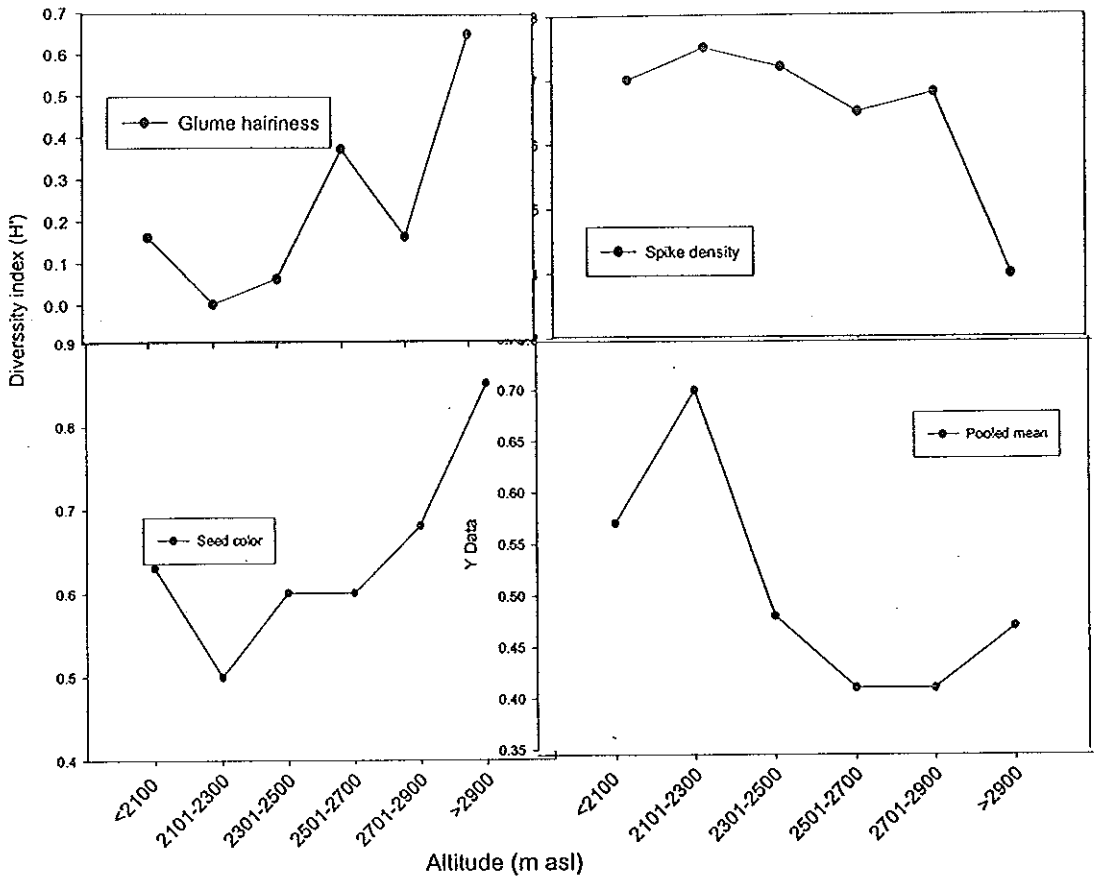


Figure 9. Diversity index of glume hairiness, spike density, seed color and pooled mean diversity index in tetraploid wheats

4.3.4. ESTIMATES OF DIVERSITY INDEX IN *T. TURGIDUM* SSP. *DURUM*

4.3.4.1. DIVERSITY INDEX WITHIN AND OVER POPULATIONS

Estimates of H' of each trait for each population, mean H' pooled across all traits and the overall diversity index of *T. turgidum* ssp. *durum* were given in Table 13. At population level as it is observed in the mixed populations of tetraploid species, H' varied from completely monomorphic (H' = 0.00) for glume color, beak awn and awn color to polymorphic states. Monomorphism was more commonly observable in Bale materials than in Wello collections.

Mean H' of each trait computed over population had low (H' = 0.01 ± 0.01) to high (H' = 0.64 ± 0.13) level H' values. The overall diversity index for durum was found to be 0.63±0.08.

Regional analysis of mean diversity index of each trait indicated that except awn length and spike in larger value for Wello region than Bale region (Table 13). The diversity index pooled over all the traits was 0.66 ± 0.07 for landraces collected from Wello while it was a bit smaller for 0.46 ± 0.11 for Bale region.

4.3.4. 2. ALTITUDINAL INDEX OF DIVERSITY

Estimates of diversity index across range of altitudinal are presented in Table 14. Glume color and awn color showed monomorphism in the first two-altitudinal classes. Seed color was found to be monomorphic at altitudes ranging between 2101-2300 masl. On the other hand, the largest H' value (H' = 0.95) was observed in glume color. High mean H' pooled over all

the traits was observed in the second altitudinal class (H' = 0.70 ± 0.09) while small (H' = 0.3±0.1) was for elevations below 2100 masl.

4.3.5. ANALYSIS OF VARIANCE OF THE DIVERSITY INDEX

One-way analysis of variance (ANOVA) was computed by the use of the non-normalized values of diversity indices to partition the differences observed due to altitudinal and regional classes for *T. turgidum* ssp. *durum* (Table 15). The variance was mainly due to the within populations variation for some traits rather than due to between regions and altitudinal classes. However, awn color, glume color and seed color showed highly significant variation ($p < 0.01$) between region components whereas awn length showed significant difference ($p < 0.05$) between regions. For glume hairiness, beak awn and spike density most of the variances were due to the within region component.

Beak awn, glume hairiness and spike density showed high variation within populations. Significant ($p < 0.05$) between altitude variation was observed for awn length, beak awn, glume hairiness and seed color, while awn color, glume color and spike density showed significant variation between populations within regions and altitude.

For characters such as awn length, beak awn, glume hairiness and seed color most of the variance was due to the between altitude component. Awn length, and seed color are the only two traits that showed statistically significant differences both between regions and between altitudes simultaneously.

The analysis of variance for traits in tetraploid wheats also showed highly significant differences between regions ($p<0.05$) for awn color, beak awn, glume color and seed color

(Table 16). ANOVA of traits against altitudinal classes also indicated that the 'between altitude' variations were observed for beak awn and glume color. The variation was mainly due to the variance between the region component for awn color, beak awn, glume hairiness and glume color. This was also true for beak awn, glume hairiness and glume color when altitude was used as a classifying variable. Awn length, seed color and spike density, however, showed statistically significant differences between within populations.

Hierarchical analysis of variance was used to partition the within regions and altitudinal class variances (Table 17). Highly significant ($p<0.01$) and significant variations ($p<0.05$), respectively, were observed between regions and altitudinal classes. Much of the variation was also because of the differences in the level of the different characters within populations. However, there were no statistically significant differences ($p<0.05$) between populations within altitudes and regions.

Table 13. Diversity index of each of seven characters, mean and standard errors of H' in *T. durum* landraces

Region	Popn	GC	GH	BA	AL	AC	SC	SD	Mean ± S.E.
Wello	1	0.4	0.9	0.2	0.0	0.2	0.0	0.0	0.24±012
	2	0.7	0.0	0.2	0.2	0.0	0.7	0.6	0.34±0.12
	3	0.7	0.0	0.3	0.0	0.3	0.7	0.3	0.33±0.11
	4	0.9	0.0	0.1	0.1	0.3	0.7	0.4	0.36±0.13
	5	0.8	0.1	0.0	0.1	0.7	0.8	0.6	0.44±0.14
	6	0.3	0.1	0.1	0.6	0.7	0.5	0.5	0.40±0.09
	7	1.0	0.0	0.5	0.7	0.0	0.7	0.4	0.47±0.14
	8	0.9	0.6	0.6	0.7	0.6	0.6	0.7	0.67±0.04
	9	0.7	0.0	0.8	0.7	0.2	0.5	0.5	0.49±0.11
	10	0.7	0.4	1.0	0.4	1.0	0.9	0.1	0.64±0.13
	11	0.7	0.9	0.9	0.1	0.3	0.8	0.7	0.63±0.12
	12	0.6	0.7	0.6	0.3	0.9	0.5	0.7	0.61±0.07
	13	0.5	0.0	0.1	0.1	0.9	0.6	0.1	0.33±0.13
	14	0.8	0.0	0.4	0.5	0.6	0.6	0.6	0.50±0.10
	15	0.0	0.5	0.1	0.4	0.2	0.4	0.4	0.29±0.07
	16	0.8	0.2	0.3	0.4	0.9	0.5	0.2	0.47±0.11
Mean		**0.85**	**0.57**	**0.75**	**0.59**	**0.35**	**0.89**	**0.59**	0.66±0.07
Bale	17	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.01±0.01
	18	0.2	0.3	0.6	0.6	0.0	0.2	0.5	0.34±0.09
	19	0.0	0.2	0.6	0.7	0.5	0.0	0.5	0.36±0.11
	20	0.2	0.0	0.0	0.6	0.0	0.0	0.2	0.14±0.08
	21	0.6	0.0	0.3	0.7	0.0	0.0	0.5	0.30±0.12
	22	0.7	0.0	0.1	0.8	0.0	0.0	0.4	0.29±0.13
	23	0.6	0.0	0.0	0.6	0.0	0.0	0.4	0.23±0.11
	24	0.3	0.0	0.5	0.7	0.0	0.0	0.5	0.29±0.11
	25	0.0	0.0	0.0	0.3	0.0	0.0	0.4	0.10±0.07
	26	0.3	0.0	0.0	0.6	0.0	0.0	0.3	0.17±0.09
	27	0.6	0.0	0.0	0.5	0.0	0.0	0.6	0.24±0.12
	28	0.5	0.0	0.0	0.7	0.0	0.5	0.4	0.30±0.11
	29	0.2	0.0	0.0	0.6	0.0	0.0	0.5	0.24±0.10
	30	0.4	0.0	0.1	0.4	0.0	0.4	0.5	0.26±0.08
Mean		**0.62**	**0.12**	**0.32**	**0.66**	**0.06**	**0.84**	**0.63**	**0.46±0.11**
Overall mean		**0.9**	**0.48**	**0.84**	**0.61**	**0.60**	**0.84**	**0.63**	**0.63±0.08**

GH= glume hairiness; AC=awn color; AL=awnlength; BA=Beak awn; GC=glume color; SC=seed color; SD=spike density

Table 14. Mean estimates of H' of each trait and standard error by altitude in *T. turgidum* ssp. *durum*

Altitude	GH	AC	AL	BA	GC	SC	SD	Mean ± S.E.
<2100	0	0	0.62	0.06	0.36	0.56	0.48	0.30±0.10
2101-2300	0	0	0.22	0.20	0.62	0	0.40	0.72±0.55
2301-2500	0.12	0.12	0.52	0.82	0.95	0.70	0.53	0.54±0.12
2501-2700	0.74	0.77	0.11	0.71	0.67	0.84	0.57	0.63±0.09
2701-2900	0.21	0.43	0.70	0.57	0.92	0.77	0.53	0.59±0.09
>2900	0.69	0.51	0.27	0.97	0.75	0.86	0.53	0.70±0.09

GH= glume hairiness; AC=awn color; AL=awnlength; BA=Beak awn; GC=glume color; SC=seed color; SD=spike density

Table 15. Mean squares of index of diversity of regions and altitudinal classes from the analysis of variance of H' for individual characters in *T. turgidum* ssp. *durum*

Character	Between		Between populations within	
	Region (df=1)	Altitude (df=5)	Region (df=28)	Altitude (df=24)
Awn color	0.69**	0.09	0.04	0.05
Awn length	0.42*	0.22*	0.07	0.05
Beak awn	0.37	0.3*	0.10	0.06
Glume hairiness	0.09	0.07*	0.03	0.02
Glume color	0.99**	0.11	0.07	0.10
Seed color	2.28**	0.31*	0.04	0.08
Spike density	0.01	0.02	0.07	0.07

df = degrees of freedom, *P<0.05, **p<0.01, ns = non-significant

Table 16. Mean squares of diversity index of regions and altitudinal classes from the analysis of variance of H' for individual characters in tetraploids

Character	Between		Between populations within	
	Region (df=1)	Altitude (df=5)	Region (df=30)	Altitude (df=26)
Awn color	1.1**	0.1	0.0	0.0
Awn length	0.1	0.1	0.0	0.0
Beak awn	1.3**	0.3*	0.1	0.1
Glume hairiness	0.73*	0.19*	0.07	0.07
Glume color	1.3**	0.2*	0.1	0.1
Seed color	0.6	0.1	0.1	0.1
Spike density	0.1	0.0	0.1	0.1

df = degrees of freedom, *P<0.05, **p<0.01, ns = non-significant

Table 17. Hierarchical analysis of variance of diversity index across traits

Sources of variation	Df	Mean square	*F-ratio*
Between			
- Regions	1	2.224	21.557**
- Populations within regions	30	0.1032	1.007^{ns}
- Altitude	5	0.2993	2.92*
- Populations within altitude	26	0.1470	1.434^{ns}
Characters within population	192	0.1025	

df = degrees of freedom, *P<0.05, **p<0.01, ns = non-significant

4.4. ISOZYME STUDY

A total of five isozyme loci were detected by the three enzyme systems EST, AAT and LAP. Table 18 shows the allele frequencies of these five isozyme loci in fourteen landrace populations of tetraploid wheats. All of the loci displayed varying levels of polymorphism. The allelic composition of the populations appeared to be similar with similar allele frequencies except for few landraces. Variations in allele frequencies were observed in eight of the fourteen populations for EST-2, which is designated as a slow moving locus. At the Estrase locus the slower allele was more frequent in many of the population even in the group where it showed monomorphism.

The genetic variability at 5 loci in all populations is presented in Table 19. The mean number of alleles per locus ranged from 1.4 to 2.2. The commonest mean number of alleles in the populations was 1.8. The percentage of polymorphic loci also ranged from 40% to 80%. Fourty-three percent of the total population included in the isozyme assay showed high value of polymorphism. The smallest value for the average heterozygosity was 0.40, which was observed in about 79% of the population.

The matrix of genetic similarity and/or distance coefficients expressed in genetic identity and unbiased minimum distance (Nei, 1978) is given in Table 20. A pair-wise comparison of populations over five isozyme loci indicated that the unbiased genetic identity ranged from 0.904 to 1.00, whereby the genetic distance ranged from 0.00 and 0.053 indicating the existence of little variation among populations. The values for genetic distance are close to zero in all the populations indicating the similarity nature of the landraces. Moreover, this

could also be shown by values that are indicated in genetic identity, which is either 1.00 or close to one for most of the populations compared based on the isozyme data.

A summary of F-statistics at all loci is presented in Table 21. Ranges of variability were observed among populations. It has ranged between 0 and 0.233 whereby the degree of differentiation (Fst) of individual loci showed a variation amounting between these two values. The average variation among populations was low whereby relatively high total variability was observed for EST-2.

Cluster analysis

Clustering made based on the allelic frequency of isozyme data is indicated in Figure 10. Fourteen of the populations were grouped into five clusters/groups. The first cluster (A) comprised of four populations all of which originated from Wello region. The second cluster (B) also comprised four other populations, while the third cluster (C) had two populations. Following these clusters are found one out-lier and three other populations are put in cluster E.

Table 18. Summary of allele frequencies for five polymorphic loci among populations tetraploid wheat*

Locus	1	4	8	9	12	13	15	16	21	24	25	26	27	31
AAT1-A	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500
-B	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500
AAT2-A	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500
-B	.500	.400	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500	.500
-C	.000	.100	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000	.000
LAP1-A	1.000	1.000	1.000	.900	.950	.700	.900	1.000	1.000	1.000	1.000	1.000	1.000	1.000
-B	.000	.000	.000	.100	.050	.000	.100	.000	.000	.000	.000	.000	.000	.000
-C	.000	.000	.000	.000	.000	.300	.000	.000	.000	.000	.000	.000	.000	.000
EST1-A	1.000	1.000	1.000	1.000	.950	1.000	1.000	.950	.800	.950	1.000	1.000	1.000	1.000
-B	.000	.000	.000	.000	.000	.000	.000	.050	.100	.050	.000	.000	.000	.000
-C	.000	.000	.000	.000	.050	.000	.000	.000	.100	.000	.000	.000	.000	.000
EST2-A	1.000	.900	1.000	.900	1.000	1.000	.875	.900	.850	.750	.525	.500	1.000	.675
-B	.000	.100	.000	.100	.000	.000	.125	.100	.050	.150	.000	.000	.000	.000
-C	.000	.000	.000	.000	.000	.000	.000	.000	.100	.100	.475	.500	.000	.325

* see appendix 8 for the description of the code

Table 19. Measure of genetic variability at 5 loci in all populations (standard errors in parentheses)

Population*	Mean no. of alleles per locus	Percentage of loci polymorphic**	Mean heterozygosity	
			Observed	Estimated (HdyWbg)
1	1.4(0.2)	40.0	0.400	0.211(0.129)
4	1.8(0.4)	60.0	0.400	0.265(0.129)
8	1.4(0.2)	40.0	0.400	0.211(0.129)
9	1.8(0.2)	80.0	0.400	0.286(0.104)
12	1.8(0.2)	80.0	0.420	0.244(0.111)
13	1.6(0.2)	60.0	0.400	0.299(0.123)
15	1.8(0.2)	80.0	0.450	0.287(0.100)
16	1.8(0.2)	80.0	0.400	0.262(0.1107
21	2.2(0.4)	80.0	0.400	0.329(0.095)
24	2.0(0.3)	80.0	0.400	0.308(0.108)
25	1.6(0.2)	60.0	0.590	0.307(0.126)
26	1.6(0.2)	60.0	0.600	0.316(0.129)
27	1.4(0.2)	40.0	0.400	0.211(0.129)
31	1.6(0.2)	60.0	0.530	0.295(0.129)
	1.5	64.3	0.442	0.274(0.121)

* see appendix 8 for the description of the code
** A locus is considered polymorphic if more than one allele was detected ** Unbiased estimate (see Nei, 1978)

Table 20. Matrix of genetic similarity and/or distance coefficients

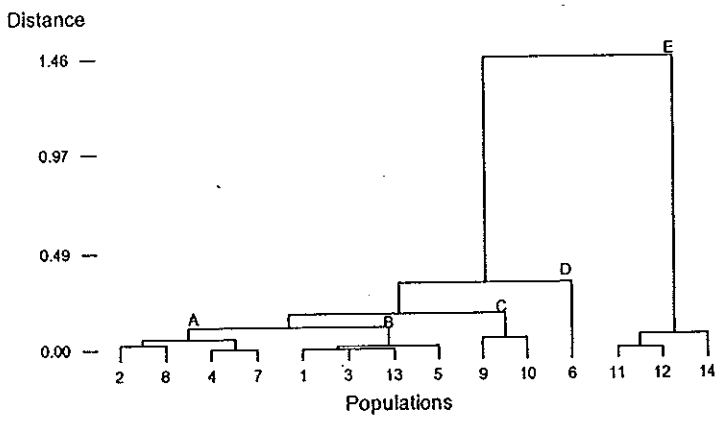
Population*	1	4	8	9	12	13	15	16	21	24	25	26	27	31
1	*****	.995	1.000	.996	.999	.978	.995	.997	.990	.989	.942	.935	1.000	.974
4	.000	*****	.995	.995	.993	.970	.995	.997	.988	.992	.946	.940	.995	.975
8	.000	.000	*****	.996	.999	.978	.995	.997	.990	.989	.942	.935	1.000	.974
9	.000	.000	.000	*****	.996	.978	1.000	.997	.987	.992	.945	.939	.996	.974
12	.000	.000	.000	.000	*****	.979	.995	.996	.991	.987	.938	.931	.999	.971
13	.005	.008	.005	.001	.005	*****	.976	.972	.961	.961	.911	.904	.978	.945
15	.000	.000	.000	.000	.000	.006	*****	.997	.987	.993	.946	.940	.995	.975
16	.000	.000	.000	.000	.000	.010	.000	*****	.994	.996	.948	.942	.997	.977
21	.000	.000	.000	.000	.000	.016	.002	.000	*****	.992	.955	.950	.990	.980
24	.001	.000	.001	.000	.004	.017	.000	.000	.000	*****	.969	.964	.989	.988
25	.036	.029	.036	.029	.039	.052	.031	.031	.023	.014	*****	1.000	.942	.994
26	.037	.029	.037	.029	.040	.053	.031	.031	.022	.013	.000	*****	.935	.991
27	.000	.000	.000	.000	.000	.005	.000	.000	.000	.001	.036	.037	*****	.974
31	.012	.008	.012	.008	.015	.028	.011	.010	.007	.001	.000	.000	.012	*****

* see appendix for the description of the code
Below diagonal: unbiased minimum distance
Above diagonal: genetic identity

Table 21. Summary of F-statistics at all loci.

Locus	F(IS)	F(IT)	F(ST)
AAT-1	-1.000	-1.000	.000
AAT-2	-.977	-.972	.003
LAP-1	1.000	1.000	.180
EST-1	.840	.854	.090
EST-2	.006	.238	.233
Mean	**-.678**	**-.580**	**.058**

F (IS) = variability within populations
F (IT) = total genetic variability
F (ST)= variability among populations



*Numbers bound by brackets are used to represent population numbers whereas those outside of brackets are codes for each population: 1(1), 2(4), 3(8), 4(9), 5(12), 6(13), 7(15), 8(16), 9(21), 10(24), 11(25), 12(26), 13(27), 14(31)

Figure 10. Dendrogram of fourteen tetraploid wheat species as clustered using the genetic distance by allele frequencies of isozyme data

5. DISCUSSION

5.1. BIOLOGICAL DIVERSITY OF TAXONOMIC SPECIES

The boundaries between wheat species are hard to define. Firstly, because of high genetic variability and the occurrence of crossability and hybrid viability within the groups of different ploidy levels, and secondly, due to the fact that genus *Triticum* is a young unit (Mac Key, 1966 quoted in Bekele, 1984b). This problem of unambiguous taxonomic treatment is exacerbated in Ethiopian tetraploid wheat landraces due to the presence of continuous variation in the Ethiopian wheats (Porceddu *et al.*, 1973; Bekele, 1984b; Tesemma *et al.* 1991). Nevertheless, with accumulated experience it is possible to classify Ethiopian wheats to their respective taxonomic species to a large degree of certainty (Belay and Furuta, 2001). This can be evidenced from the discriminant analysis that showed 91.5% correct classification of the taxonomic classes.

Six tetraploid and one hexaploid wheat species were recorded in the presently studied landrace populations from Bale and Wello. These species include *T. turgidum* ssp. *durum, T. turgidum* ssp. *aethiopicum, T. turgidum* ssp. *turgidum, T. aestivum, T. turgidum* ssp. *polonicum, T. turgidum* ssp. *pyramidale* and *T. turgidum* ssp. *dicoccum* in that order. Proceddu *et.al.* (1973) reported that Ethiopian wheats belong to *T. turgidum* ssp. *dicoccum, T. turgidum* ssp. *durum, T. turgidum, T. turgidum* ssp. *polonicum, T. aestivum, T. compactum* and *T. abysinicum* (syn. , *T. turgidum* ssp. *aethiopicum*).

The findings of Mekbib and Habtemariam (1990) meet the result of the present study and they reported that *T. turgidum* ssp. *durum* and *T. turgidum* ssp. *aethiopicum* were the two major tetraploid wheats. Tsegaye (1997), however, indicated that *T. turgidum* and *T. dicoccum* account mainly for the bulk of the Ethiopian tetraploid wheat germplasm.

The predominance of *T. turgidum* ssp. *durum* in most of the landrace populations may be attributed to its tolerance to stress environments (Tesemma *et al.,* 1991). Artificial selection pressures are also responsible for the frequent appearance of one species over others. Local farmers in Ethiopia deliberately, and unconsciously too, grow several varietal forms together to add variety to their diet, to reduce the risk of economic loss due to biotic or abiotic stresses (Bekele, 1984b). Human preferences for specialized traditional consumption might have played the major role for the persistence of *T. turgidum* ssp. *aethopicum*; in most cases it consists of purple–grained wheats which are preferred for 'Areke' preparation (Belay *et al.*, 1995).

T. turgidum ssp. *polonicum* is distinct but has never and/or very rarely been found in the field in its own, perhaps it could be a mutant and this conforms well with treating it as a mutant with the *Turgidum* groups rather than giving it a species rank (Bekele, 1984b). On the other hand, *T. turgidum* ssp. *dicoccum* is rarely found in mixtures, but is grown as pure stand. Therefore, the results should not be misinterpreted, as this particular species is a rare species.

The maximum number of taxonomic species recorded in a single landrace was four. Mekbib and Habtemariam (1990) noted that Ethiopian wheat accessions collected in the same locality in a single sampling could have mixtures of two; three or more species with different

botanical forms. This could possibly contribute to the overall genetic diversity of the populations of tetraploid wheats, as there is no reproduction barrier among different taxonomic species (Bekele, 1984b; Tesemma and Belay, 1991).

The occurrence of species in varying degrees at different altitude classes may be attributed to the growing condition. For instance, it was observed that only two species, *T. turgidum* ssp. *durum* and *T. turgidum* ssp. *aethiopicum,* occurred at altitudes below 2300 masl. According to Demissie (1991) Ethiopian wheats also have forms that are adapted to elevations as low as 1200-msal and as high as 3300-msal. *T. turgidum* ssp. *turgidum* was frequent at intermediate altitudes (2501-2700 masl), *T. turgidum* ssp. *aethiopicum* appeared more frequently at altitudes between 23001-2500 masl. *T. turgidum* ssp. *polonicum* and *T. turgidum* ssp. *pyramidale* were obtained in intermediate altitudinal classes. At altitudes higher than 2900 masl, the only two species observed were *T. turgidum* ssp. *durum* and *T. turgidum* ssp. *turgidum.* However, tetraploid wheats are mainly grown in the altitudinal range of 1800-2800 msal (Tesemma and Belay, 1991).

Populations from Wello region were grouped in different clusters from those of Bale landraces, indicating the presence of high phenotypic variation of the characters used in the clustering analysis. This also implies that populations with contrasting agro-ecological conditions were clustered in different groups. The reason for this could be, firstly, due to the possibility of germplasm exchange, and, secondly, due to the peculiar geographic and climatic features of their sites of origin relative to others in the region (Pecetti and Damania, 1996).

In discriminant analysis traits such as beak awn, seed color and awn length played a significant role for classifying different taxonomic species, indicating the presence of large amount of variation in each character among populations. It also follows that the first canonical function was responsible for 63% of the total variation, the second for 32.3% and the third for 3.8% of the total variation giving a cumulative variance of 99.4%.

5.2. MORPHOLOGICAL STUDY

5. 2.1. PHENOTYPIC DISTRIBUTION OF CHARACTERS

All the phenotypic characters used in this study (including seed color, glume color, awn color, spike density, awn length, beak awn and glume hairiness) showed different levels of variation among populations. However, awnedness was found to be monomorphic and fixed for the presence of awn in all the landraces. This is in conformity with most of other previous studies (e.g. Jain *et al.*, 1975; Bekele 1984b; Tesemma *et al.* 1991; Bechere *et al.*, 1996; Belay *et al* 1997) except Negassa (1986) who reported the presence of non-awned types though the awned types are predominant in all the provinces. He found that a large amount of awn tissue is concentrated in the Arussi-Bale Highlands.

The dominant nature of long awn in most of the landraces and the low frequency of occurrence of short and intermediate awn length in tetraploid wheat species is in agreement with the findings of Tamiru (1999). Tesemma *et al.* (1991) observed monomorphism in awn length in many of the tetraploid wheat populations collected from four districts (Ambo, Kotu,

Chefe Donsa and Bichena) of their study sites. They also found polymorphism in varying degrees for glume color, awn color, beak length, spike density and seed color.

Observations made on beak awn showed that most of the tetraploid wheats that were collected from Bale region are awned, whereas the acuminate and pointed types are rarely observed in this region. Belay *et al.* (1997) also reported the frequent occurrence of awned types in tetraploid wheats. Bechere *et al.* (1996) reported monomorphism in many of the populations for long beak in landraces originating from Wello, Tigray, Gondar, Gojam and North Shewa regions.

Lax and very dense spike types were rarely recorded whereas dense and intermediate types dominated all the landraces. Lax type of spike density is a rare character and only reached 2% in the higher altitudinal class (Kibebew *et al.*, 2001) and this trait is associated with high rainfall and temperature (Belay, 1997). Bechere *et al.* (1996) in their study obtained that dense-spike types predominate in all the regions. According to Negassa (1986), lax and dense spike types occurred all over the study sites, while the compact type was mainly restricted to the Centeral Plateau from where it moved out to the north and south.

Bekele (1984b) states that glume hairiness is more polymorphic in tetraploids than hexaploids. Non-hairy (glabrous) glumes are more frequent and fixed than hairy glumes whereby the overall frequency of occurrence was over 90% for glabrous glumes. Previous studies also indicate that glabrous glumes are more frequent than the alternate variant, hairy (pubescent) glume (Bechere *et al.*, 1996; Belay, 1997). Tesmma *et al.* (1991) also observed

monomorphism for glume pubescence. Bechere *et al.*, (1996) reported monomorphism in many of the populations for glabrous glume in landraces originating from Wello, Tigray, Gondar, Gojam and North Shewa regions. The adaptive nature of glabrous glume is not clear (Jain *et al.*, 1975), even though its role in controlling seed diseases and insects has been speculated (Warham, 1988).

Black awn color was rarely observed in wheat populations originating from Bale collection though relatively greater diversity was observed in Wello collections. Bekele (1984b) found that white awn color is the most frequent, while black awn color the least frequent in Ethiopian tetraploid wheats. As it was indicated by Jain *et al.* (1975), black awn predominates in Southwest Europe and North Africa, whereas nonblack is more frequent in the remaining regions including Ethiopia. Purple to black type of glume color was fixed in few populations while it was also absent in others particularly in Bale collections. These color types were more frequent in Bale materials than in Wello materials. White-yellow glume color types were more abundant in Wello collections than in Bale collections. Negassa (1986) observed that the white glume color occurs at intermediate frequency along with red color while Bekele (1984b) reported that glume color is mostly white. Red–brown glume color was absent in fourteen landraces and similarly white-yellow glume color was not recorded in two landrace populations. Significant differences among altitude groups were detected only for the glume color (Bechere *et al.*, 1996).

Seed colors showed wide and relatively uniform distribution in most landraces. Kibebew *et al.* (2001) reported that except the brown seed color groups, the other variants, white and purple, showed more or lees even distribution in all altitudinal classes. Belay (1997) also

reported that the frequency of the purple seed color increases with increasing altitude. The absence of white-yellow kernel color types in many populations particularly from Bale collections is in agreement with the reports made by Bechere *et al.* (1996) and by Bekele (1984b) in which brown seed colors were predominant. They found that three different color groups were found in similar proportions in their collection but with considerable regional differences. Ethiopian tetraploid wheats with purple grain color were given the scientific name *T. turgidum* ssp. *aethiopicum* (Belay, 2001, Pers. Comm.). According to Zeven (1991), purple seeds in cultivated tetraploid wheats are endemic to Ethiopia.

Relatively high frequencies of purple-black type of glume color were found at low altitudes. The white glume color occurs at intermediate frequency all over the regions along with the red glume color (Negassa, 1986). Jain *et al.* (1975) found that black glume colors are rare in Ethiopian durum wheats. The frequency for this phenotypic class increased with a decrease in altitude though this trend was not clear in some altitudinal classes. Kibebew *et al.* (2001) observed white glume color to dominate at lower altitudes (<2300 msal), while brown glume at higher altitudes (>2300 msal). Three durum wheat varieties recommended for production to higher altitude condition of Ethiopia were also found to contain brown glume (Belay, 1997). The frequency of red-brown type of glume color uniformly increased with the rise in elevation. Moreover, red-brown seed color types were the most predominant in all altitudinal classes, except at elevations ranging from 2301-2500 masl, where purple-black types are more frequent than other types.

In general, variability among traits in Ethiopian wheats belonging to different geographic regions was reported by various authors (Bekele 1984b; Negassa, 1986; Belay, 1997).

Similarly this particular study also revealed considerable amount of variation among the characters considered. The degree of variation also varied among region of collections of landraces. This can be substantiated by the fact that some traits are fixed in some localities and exhibit polymorphism in other areas. For instance, landraces originating from Bale region are entirely glabrous types whereas hairy types of glumes are also observable in Wello collections. Similarly, black type of awn color is rarely found in Bale region as opposed to landraces from Wello region. The regional distribution of each phenotypic class in *T. turgidum* ssp. *durum* followed a similar trend of occurrence with that of tetraploids.

5. 2.2. ESTIMATES OF DIVERSITY INDEX

The findings of this study indicated that there is a considerable amount of genetic diversity in Ethiopian tetraploid wheats, in general and in durum wheats, in particular. A survey of literature was made on the diversity indices of different traits in Ethiopian wheats so that inference is made on the rates of genetic erosion that has possibly occurred through time. As it is indicated in Table 22, the relative contribution of each of the seven qualitative traits to the total diversity, H', varied considerably; high variations were due to seed color (H' = 0.92), beak awn (H' = 0.92), and glume color (H' = 0.89). Kibebew *et al.* (2001) reported high variation for beak length (H' = 0.99), seed color (H'= 0.92) and glume hairiness (H'= 0.84). Negassa (1986) observed intermediate level of diversity for awn presence and head color.

As stated by Jain *et al.* (1975), the Shannon-Weaver diversity index (H') which they used to examine overall genetic divergence on country and regional basis of world collections of durum wheats indicated that Ethiopia and Portugal had the greatest diversity (H' = 0.87 and

0.86, respectively), and Turkey, Bulgaria, and USA had significantly low diversity index (H' = 0.50, 0.41, and 0.39, respectively). From their findings they pointed out that the centers of diversity seem to be Ethiopia, the Mediterranean region, and India. Tesemma *et al.* (1991) observed the lowest diversity for glume pubescence, an intermediate level of diversity for awn color and spike density and a high level of diversity for glume color, beak length and seed color.

High diversity indices (H' > 0.60) pooled over populations and regions of collection was observed for each of the seven characters except for awn color (H' = 0.59) which showed intermediate level of diversity in tetraploid wheat species. Comparison of total diversity index of each trait indicates that seed color and beak awn both with H' values of 0.92 contributed much of the diversity than other characters. In *T. turgidum* ssp. *durum,* however, glume hairiness attained smaller H' (0.48) as compared to the other traits which had larger H' (>0.60).

The overall H' was found to be high (H' = 0.81 ± 0.07) for tetraploids and it was relatively small for durum alone (H'= 0.63 ± 0.08). Other authors (Table 22) also reported similar results. High diversity index values for seed color have also been reported in world collections of Ethiopian tetraploid wheats (Jain *et al.*, 1975), in collection from centeral highlands of Ethiopia (Tesemma *et al.*, 1991), and in collections from North and North centeral regions of Ethiopia (Bechere *et al.*, 1996). Considering all traits, Belay *et al.* (1997) in their study of the diversity of tetraploid wheats found that the over all diversity, H', for Ethiopia was 0.77 ± 0.09. These authors also indicated that H' was high and reached maximum under relatively favorable climatic conditions. Moreover, they stated that most

traits were not conspicuously unique to any single region or altitude group, but glume color and spike density may be considered varietal features for specific localities. In conclusion, this study did not clearly indicate the trend of genetic erosion. After comparing H' value for wheat landrace collections made in 1970 (Pecetti and Damania, 1996) from Tigray with that of their collections in 1994, Belay *et al.* (1997) have also concluded that genetic erosion could not be evidenced.

Table 22. Summary of diversity indices reported by various authors on Ethiopian tetraploid wheats

GC	GH	BA	AL	AC	SC	SD	Mean	Source
0.79	0.88	0.50	-	-	0.99	0.24	-	Bechere *et al.* (1996)
0.60	0.74	0.96	-	0.50	0.97	0.94	0.79±0.08	Tamiru (1999)
0.86	0.78	0.80	-	0.80	0.98	0.43	0.77±0.09	Belay *et. al* (1997)
0.49	0.72	-	-	0.98	1.30	-	0.87±0.04	Jain *et al.* (1975)
0.71	0.47	-	-	-	-	0.91	0.81±0.03	Negassa, *et. al.* (1986)
0.76	0.84	0.99	-	-	0.92	0.54	0.81±0.01	Kibebew *et al.* (2001)
0.90	0.48	0.84	0.61	0.60	0.84	0.63	0.63±0.08	Present study (durum wheat)
0.89	0.89	0.92	0.72	0.59	0.92	0.71	0.81±0.07	Present study (tetraploid wheat)

5.2.3. ANALYSIS OF VARIANCE OF THE DIVERSITY INDEX

In this particular study, awn length, seed color and spike density showed statistically significant within ($p < 0.05$) population variations. However, statistically significant differences ($p < 0.05$) were observed for the between region variance for awn color, beak awn, glume hairiness and glume color in tetraploids. Similar results were also obtained for traits such as beak awn, glume hairiness and glume color when altitude was used as a classifying variable.

Hierarchical analysis of variance indicated statistically highly significant ($p < 0.01$) variation between regions and significant variation ($p < 0.05$) between altitudinal classes. Variations were, however, mainly because of the differences in the level of the different characters within populations whereby non-significant ($p < 0.05$) differences were observed between populations within altitudes and regions. Tesemma *et al.* (1991) indicated that most of the variations observed between landraces were due to differences among districts rather than among populations within districts. Based on this they suggested that future collections would better cover more different areas than having more samples from similar areas. Contrary to what Tesemma *et al.* (1991) reported, the study made by Bechere *et al.* (1996) showed that much of the variance was among populations within region and within altitude group but not among regions or altitude groups. Bekele (1984b) and Tsegaye *et al.* (1996b) also reported similar results. Tsegaye *et al.* (1996b) also suggested taking more samples within a locality or population would be a better approach to capture the range of variation in the landrace populations of the central highlands of Ethiopia. Bekele (1994b) reports that the total variation of Ethiopian durum and bread wheat accessions varied from character to character and that the total phenotypic variation was highest within populations followed by differences among populations within a region, and the least among regions.

Belay (1997) reported that spike density showed significant variation for the 'between region' and 'between altitude' groups. Tamiru (1999) also reported that most of variance was due to the 'within altitudinal group' components in seed color, beak length, spike density and awn color except for glume color and glume pubescence. Contrary to what Belay (1997) reported, this study revealed that spike density had high variance for the between populations within

regions and altitudes. Pecetti and Damania (1996) observed that when the total phenotypic variance was partitioned among hierarchical components (between and within provinces, and within populations) that with no exception the highest contribution to the variation was one due to the component of lowest order, viz. among agrotypes within populations. Bekele (1984b) also found the same order of magnitude, partitioning the total variance for morphological characters in Ethiopian wheat tetraploid landraces: within populations > among populations > among regions. According to him, this was reasonably due to the fact that landraces are highly heterogeneous plant communities including a number of genotypes differing from morpho-agronomic features.

5.3. ISOZYME VARIATION

In the present study, the isozyme data showed various levels of polymorphism in the landraces of tetraploid wheats. Five isozyme loci, two of which were from the enzyme system AAT, two other loci from EST and one locus from LAP showed bands after staining. The populations differed in allelic frequencies.

The mean number of alleles per locus ranged from 1.4 to 2.2. The commonest mean number of alleles in the populations was 1.8. Though they used a different enzyme system, a study made by Tsegaye *et al.* (1997) to investigate the genetic variation between brown, purple and white seeded durum wheat landraces by isozyme analysis at six highly polymorphic loci showed that the mean number of alleles per locus was 1.95. They further indicated that the brown and white seeded types had very high genetic identity and the genetic identity values

between seed color groups were only slightly smaller and concluded that agrotypes of different seed colors cannot be treated as genetically separate and distinct groups.

The percentage of polymorphic loci ranged from 40% to 80%. Fourty-three percent of the total population included in the isozyme assay showed high value of polymorphism. The smallest value for the average heterozygosity was 0.40, which was observed in about 79% of the population. Comparison of two populations over five isozyme loci indicates very high genetic identity between populations whereas the genetic distance between populations ranged from 0.00 to 0.053. Bekele (1983b) indicated that genetic distance, is not related to geographical distance as two populations could be very far apart from each other but genetically similar owing to common selection pressure.

A summary of F-statistics showed the presence of ranges of variability among populations that varied from 0 to 0.233. The mean of the variation among populations was low whereby relatively high total variability was observed for EST-2.

The relationships discerned among the populations were more of a similarity nature that could be ascribed to sharing a common ancestral population and/or adaptation to similar climatic conditions. As it is observed from this study, the divergence of the pattern of genetic variation appeared to be independent of geographic region, since the isozyme data indicates the highest genetic distance was obtained between two landraces both originating from the same (Bale) region. Contrary to this, however, the analysis of the phenotypic data showed that the phenotypic diversity index of Wello region is higher than that of Bale region. This may help guide germplasm curators to decide from where to take more samples of landrace populations.

6. CONCLUSION

This study has been undertaken in order to investigate the phenotypic and isozyme genetic diversity of tetraploid wheats from Bale and Wello regions of Ethiopia. Furthermore, the study was also aimed at estimating the rate of genetic erosion that occurred in the landraces with time by comparing the result of the present study to those of the previous studies.

The analysis of biological (species) diversity revealed that farmers commonly (about 87.5%) grow more than two species of wheat in mixed forms. The commonest species observed was *T. turgidum* ssp. *durum*. This species is widely grown at all sites of collection except at two sites of Bale region, where *T. turgidum* ssp. *aethiopicum* is a sole crop. The next abundant species for Bale collection was *T. turgidum* ssp. *aethiopicum*, while *T. turgidum* ssp. *turgidum* was the next common species for Wello region. A hexaploid *T. aestivum* was frequently observed in Bale materials. Other tetraploid species such as *T. turgidum* ssp. *polonicum*, *T. turgidum* ssp. *pyramidale* and *T. turgidum* ssp. *dicoccum* were rarely observed. In general, the landrace populations collected from Wello could be considered as species rich when compared to those of Bale collections.

The distribution of phenotypic classes in seven qualitative traits showed variations between populations, altitudinal classes and between regions of collection. Classifications of the landraces based on these phenotypic classes for durum and tetraploid wheats, respectively,

resulted into six and seven groups of clusters. However, Bale materials were grouped into different cluster from Wello materials.

At character basis, the analysis of variance showed that awn color, beak awn, glume color and glume hairiness showed significant differences ($p < 0.05$) between regions in tetraploid species. Moreover, beak awn, glume hairiness, and glume color showed significant differences ($p < 0.05$) at altitude bases. Contrary to the absence of significant variation observed for seed color between altitude classes and between regions in tetraploid species, this particular trait showed significant difference ($p < 0.05$) for durum wheat. Variations were largely due to the differences in the level of the different characters within populations.

Allelic polymorphism was detected in all the fourteen populations included in the isozyme assay. However, the genetic variability revealed by the three enzyme systems (EST, AAT and LAP) was estimated to be low implying that the expected variation between each taxonomic species was not detected by these enzyme systems used. Moreover, a comparison between the levels of phenotypic diversity index of tetraploids and *T. turgidum* ssp. *durum* treated alone pooled across all the traits indicates that tetraploids have higher diversity index ($H' = 0.81 \pm 0.05$) than the diversity index of *T. turgidum* ssp. *durum* ($H' = 0.63 \pm 0.08$).

A review of the literature made on the diversity indices previously reported by various authors in order to estimate the level of genetic erosion in Ethiopian tetraploid wheats indicated that there is no clear indication of the loss of genetic diversity. The value of the Shannon-Weaver diversity index computed in the current study is not significantly different from the diversity indices that were reported on Ethiopian tetraploid wheats. Since the enzyme systems used for

isozyme study did not reveal genetic variability that was expected to exist among taxonomic species in tetraploid wheats further study is suggested by using as many enzyme systems as possible. Finally, it can be concluded that the study on morphological data showed very high diversity among different landraces originating from Bale and Wello regions of Ethiopia.

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8. APPENDIX

Appendix 1. List of wheat landraces used for this study with description of their sites of collection

P No.	Col. No.	Local/ var. name	Region	District	Village	Altitude m a.s.l.
	Wello collection					
1	BCST-001	Shasho	Welo	Debresina	Betaso	2600
2	BCST-002	Kusit	Welo	Debresina	Betaso	2550
3	BCST-003	Gojame	Welo	Debresina	Islam amba	2500
4	BCST-004	Tikur sinde	Welo	Debresina	Islamamba	2500
5	BCST-005	Kurshit	Welo	Debresina	Mehaldenbi	2560
6	BCST-006	Tikursinde	Welo	Tenta	Tedat	2800
7	BCST-007	Tikursinde	Welo	Tenta	Tedat	2800
8	BCST-008	Bani	Welo	Tenta	Sostiye	2840
9	BCST-009	Kindibe tikur	Welo	Tenta	Sostiye	2840
10	BCST-010	Enat sinde	Welo	Tenta	Metekiya	2950
11	BCST-011	Enat sinde	Welo	Tenta	Amume	2950
12	BCST-012	Aminge	Welo	Jama	Guye	2640
13	BCST-013	Wotiye	Welo	Jama	Gendashine	2680
14	BCST-014	Jiru sinde	Welo	Jama	Gagure	2680
15	BCST-015	Kerkere/ayalfush	Welo	Jama	GebreGuracha	2600
16	BCST-016	Yabesha Sinde	Welo	Were Ilu	Tulu Sereto	2650
	Bale collection					
17	ANS-067-Br	Kemedi	Bale	Goro	Addisalemna	1900
18	ADS-041-Fa	-	Bale	Agarfa	Waiewagarge	2400
19	ADS-056-Br	Kemedi	Bale	Jara	Woffe	2350
20	ADS-047-Fa	Kemediguracha	Bale	Agarfa	H. ganat	2400
21	ADS-047-Br	-	Bale	Agarfa	Wafie wagarre	2400
22	ADS-04??-Br	Kemediguracha	Bale	Sinanadinsho	Temosuleman	2400
23	ADS-041-Fa	Kemediguracha	Bale	Sinana	Miarbene	2270
24	ADS-067-??	Kemedi	Bale	Goro	Addisalemna	1900
25	ANS-056-??	Kemedi	Bale	Jara	Wotte	2350
26	ADS-047-BDI	Kemediguracha	Bale	Agarfa	H. ganat	2400
27	ADS-046-??	-	Bale	Agarfa	W. garge	2400
28	ADS-041-??	Kemediguracha	Bale	Sinana	Mirrabene	2270
29	ADS-040-BDI	Kemediguracha	Bale	Sinanadinsho	Temosuleman	2400
30	ADS-002-BDI	Inglizii	Bale	Adaba	Konsho	2420
31	ADS-0609-BDI	-	Bale	Adaba	Konsho	2650
32	ADS-0018-BDI	-	Bale	Adaba	Garadillo	2360

Appendix 2. Classification of collection sites into six altitudinal groups

Altitudinal class m a.s.l.	Code for the class
1900-2100	1
2101-2300	2
2301-2500	3
2501-2700	4
2701-2900	5
>2900	6

Appendix 3. Codes for description of collection sites of landraces (Total no. entries = 2559).

No.	Region	District	District code	Village	Village code	Altitudinal class code	No. of entries
1	Welo	Debresina	1	Betaso	1	4	107
2	Welo	Debresina	1	Betaso	1	4	108
3	Welo	Debresina	1	Islam amba	2	3	71
4	Welo	Debresina	1	Islamamba	2	3	104
5	Welo	Debresina	1	Mehaldenbi	3	4	109
6	Welo	Tenta	2	Tedat	4	5	90
7	Welo	Tenta	2	Tedat	4	5	110
8	Welo	Tenta	2	Sostiye	5	5	109
9	Welo	Tenta	2	Sostiye	5	5	109
10	Welo	Tenta	2	Metekiya	6	6	108
11	Welo	Tenta	2	Amume	7	6	110
12	Welo	Jama	3	Guye	8	4	110
13	Welo	Jama	3	Gendashine	9	4	108
14	Welo	Jama	3	Gagure	10	4	110
15	Welo	Jama	3	Gebre Guracha	11	4	109
16	Welo	Were Ilu	4	Tulu Sereto	12	1	110
17	Bale	Adaba	5	Garadillo	13	4	60
18	Bale	Adaba	6	Garadillo	14	3	59
19	Bale	Adaba	6	Konsho	15	3	49
20	Bale	Sinanadinsho	7	Temosuleman	16	3	46
21	Bale	Sinanadinsho	7	Temosuleman	16	3	60
22	Bale	Sinana	8	Mirrabene	17	2	60
23	Bale	Sinana	8	Mirrabene	17	2	60
24	Bale	Agarfa	9	Woie wagarge	18	3	60
25	Bale	Agarfa	9	Wofie	19	3	60
26	Bale	Agarfa	9	Wofie	19	3	49
27	Bale	Agarfa	9	Hasanogenet	20	3	50
28	Bale	Agarfa	9	Hasanogenet	20	3	60
29	Bale	Jara	10	Woffe	21	3	45
30	Bale	Goro	10	Wofie	21	3	60
31	Bale	Goro	11	Addisalemina	22	1	45
32	Bale	Goro	11	Addisalemina	22	1	60