ADDIS ABABA UNIVERSITY

SCHOOL OF GRADUATE STUDIES

GENETIC DIVERSITY AND ASSOCIATION OF CHARACTERS IN RELEASED VARIETIES OF TEF [*ERAGROSTIS TEF* (ZUCC.) TROTTER]

A Thesis presented to the School of Graduate Studies of Addis Ababa University in Partial Fulfillment of the Requirements for the Degree of Master of Science in Biology (Applied Genetics)

BY

HABTE JIFAR

JULY 2008

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ABBREVIATIONS

AFLP	Amplified Fragment Length Polymorphism
ANOVA	Analysis of Variance
ANCOVA	Analysis of Covariance
CA	Cluster Analysis
CSA	Central Statistics Agency
CV	Coefficient of variation
DAP	Diamonium Phosphate
DZARC	Debre Zeit Agricultural Research Center
EIAR	Ethiopian Institute of Agricultural Research
GA	Genetic Advance
GCV	Genotypic Coefficient of Variation
HARC	Holetta Agricultural Research Center
IAR	Institute of Agricultural Research
ISSR	Inter Simple Sequence Repeats
JARC	Jimma Agricultural Research Center
PCA	Principal Component Analysis
PCs	Principal Components
PCV	Phenotypic Coefficient of Variation
QTL	Quantitative Traits Loci
RAPD	Random Amplified Polymorphic DNA
RCBD	Randomized Completely Block Design
MoARD	Ministry of Agriculture and Rural Development

ABSTRACT

Nineteen released varieties and two local landraces of tef from Jimma area were planted in quadruplicated completely randomized block design at Jimma Agricultural Research Center during the 2007 main cropping season to assess the extent of genetic diversity and association among different traits of tef. Data were collected on 19 quantitative traits including days to heading and to maturity, grain filling period, plant height, panicle length, culm length, number of fertile tillers per plant, number of spikelet and panicle branches per main panicle, first and second basal culm diameters, harvest index, single plant phytomass, grain and straw yield, thousand seed weight, head smudge disease incidence and severity, and lodging index. Similarly, qualitative trait data were recorded on panicle form, and seed coat and lemma color. The analysis of variance showed highly significant ($P \leq 0.01$) genotype differences for all quantitative traits and at ($P \leq 0.05$) for traits such as culm length and number of fertile tillers per plant which depicted merely significant differences among the test genotypes. The range computed for all of the traits revealed wide range of phenotypic variation in the genotypes studied. The estimated values for phenotypic variance were higher than genotypic variance for all the traits. Likewise, the phenotypic (PCV) and genotypic coefficients of variability (GCV) showed wide variation among the different traits. The GCV ranged from 2.87 to 31.97 % and the PCV ranged from 4.53 to 38.74 %. The highest and lowest heritability estimate was observed for single plant straw yield (93.13%) and number of fertile tillers per plant (16.87%), respectively. Similarly, expected genetic advance ranged from 0.029 for harvest index to as high as 48.04 for number of spiklets per panicle. On the other hand, GA as percent of the mean ranged from 3.09% for days to heading to 54.35 % for lodging index. Single plant grain yield showed positive and significant correlation with all traits except days to grain filling period, harvest index, head smudge disease incidence and severity, and lodging index at both phenotypic and genotypic level and number of fertile tillers per plant at genotypic level. Lodging index showed negative phenotypic and genotypic correlation with all traits except number of fertile tiller per plant, harvest index and disease severity and incidence. Disease index similarly showed significant correlation with about 60% of the quantitative traits of tef under consideration. The cluster analysis grouped the tef genotypes into four clusters of one to 13 genotypes per cluster at about 60% similarity level. The first five principal components with eigenvalue greater than one accounted for 85.2% of the entire genetic variation in the tef genotypes used in this study. Moreover, the contribution of each of the first five principal components is 43.9%, 20.9%, 8.4%, 6.2%, and 5.0%, respectively. Overall, the study revealed variation among the tef genotypes with respect to phenotypic traits. However, future research in this area should focus on data supported by DNA analysis in order to augment the results based on morphological data. As the two landraces used in this study are a mixed population, they should be purified using appropriate breeding procedure based on their data on qualitative traits. DZ-01-974 was the best performing one with respect to most important traits considered in this study. Therefore, an adaptation trial should be conducted on this variety to recommend it for the area if it repeats its good performance.

Key words: Tef, genotypes, varieties, landraces, cluster, principal components, quantitative

traits, qualitative traits, phenotypic level and genotypic level.

1. INTRODUCTION

Tef (*Eragrostis tef* [Zucc.] Trotter) is an allotetraploid plant with chromosome number (2*n* =4*x* =40) (Jones *et al*., 1978; Ponti, 1978; Tavassoli, 1986) and is a cereal crop grown primarily in Ethiopia (Amanda and Doyle, 2003). It is the only cereal cultivated in the genus *Eragrostis* which consists of 350 species (Tefera and Ketema, 2001; Tefera et al, 2003).

Tef is a crop for which Ethiopia is the center of origin and diversity (Vavilov, 1951). The domestication of tef is one of the contributions of the Ethiopian farmers to our world. Its domestication was made by pre Semitic people before the birth of Christ and Ethiopia is the only country where its major diversity exists (Ketema, 1997). Forty-four of the 350 *Eragrostis* species are found in Ethiopia (Philips, 1995).

As compared to other cereals grown in Ethiopia, tef is the most preferred cereal by urban consumers as well as its producers. The reasons for its preferences include source of best quality human food and animal feed, tolerance to both high and low moisture stresses, high price for its grain and straw, low-post harvest pest and disease problems and high longevity of the grain even under farmers' traditional storage conditions (Ketema, 1993, 1997; Assefa et al, 2001a). Annually, over two million hectares of land is being devoted for tef production (Tefera *et al.*, 2003). For instance, 2.25 million hectares of land were under the production of tef in 2005/6 cropping year (CSA, 2006). It covers 27.8% of the total area under cereals and more than 18.7% of the total grain production in the country (CSA, 2006). This makes tef a leading cereal in area coverage and second to maize in total annual grain production.

Tef adapts to a wide range of environmental conditions and fits to different cropping systems, patterns and sequences. It can be grown from sea level up to an altitude of 2800m above sea level and under various rainfall, temperature and soil regimes (Ketema, 1993). According to Assefa *et al* (2001a), tef is characterized by a versatile adaptation and grows in 11 of the 18 major agroecological zones of Ethiopia. They also noted that tef often exhibits high level of phenotypic plasticity in phenology, morphology and agronomic performance depending on the environment in which it is grown. Generally, it is the most resilient crop that can grow with low risk of failure than other cereals grown in the country (Tefera *et al*., 2003a). Nevertheless, both the quality and yield of tef are affected by the climate and soils under which it is grown (Ketema, 1993).

Despite the preferences by the urban consumer community and the largest area coverage of tef, its national average yield is very low as compared to other cereals. The national average grain yield for the country is estimated to be 0.96 tones per hectare (t/ha) and below 0.5 t/ha for southwestern Ethiopia (CSA, 2006). With improved varieties and management practices; however, a yield of 1.7-2.5 t/ ha and up to 3.4 t/ha on farmers field and an experimental plot, respectively can be obtained (Tefera and Ketema, 2001). Limited number of improved released varieties for the area, and the problems of lodging and diseases are the major causes for yield reduction of tef. The extent of the problem of low productivity due to these constraints varies from place to place within the country. For instance, the problem of disease is aggravated in the south western parts of Ethiopia where there is high rainfall, and hot and humid climate. The National Tef Improvement Program has so far released about 20 tef varieties (MoARD, 2006). Most of these varieties were released based on their national average performance and they may

or may not perform equally at all the test locations. This implies the presence of possibility of ignoring a genotype which may perform better at some specific locations while the one performing poorly at that location is released nationally. In Jimma area for instance, there are two prominent tef landraces that are being widely cultivated by the farming communities around there. These local materials, most of the times, perform comparable to or in some cases even better than that of the improved nationally released tef varieties when being used as a local check (personal observation). Knowing the genetic variation existing among these landrace materials and released varieties and assessing the association between their different morpho-agronomic characters will enable us to utilize their potential for further breeding works. Consequently, conducting genetic diversity study of the nationally released tef varieties together with these most widely cultivated landraces at Jimma area and comparing their overall performances is quite essential. This study was, therefore, designed to assess the variation based on measurements of pheno-morphological traits.

2. LITERATURE REVIEW

2.1. Origin and Evolution of tef

Understanding the origins of crop plants can provide valuable information for plant breeders who are interested in introgressing agronomically desirable traits from wild relatives of the cultivated species (Ponti, 1978, Tavassoli, 1986; Amanda and Doyle, 2003). A number of investigators have suggested on the origin of tef using morphological, cytological, and biochemical characters and have suggested 14 wild *Eragrostis* species as potential progenitors of the crop (Amanda and Doyle, 2003). According to these authors, the current general consensus among the different studies on investigating the progenitor of tef indicated that *Eragrostis pilosa* is the most likely candidate wild progenitor of *Eragrostis tef*.

2.2. Methods of assessing genetic diversity in crop plant

Genetic diversity in crop plants may be assessed at different levels: individual genotypes such as inbred lines or clones, populations, germplasm accessions, and species (Mohammadi and Prasma, 2003). Such genetic diversity study of crop varieties and landraces can be done using different techniques including the use of morphological, biochemical and molecular (DNA) markers.

Morphological markers are the earliest markers utilized in the assessment of genetic diversity within and between populations. They are simple and direct measure of phenotypes and cheap for characterizing germplasm accessions. However, compared to molecular markers they have low polymorphism, heritability and expression, and are vulnerable to environmental influences (Smith and Smith, 1992).

Molecular (DNA) markers, on the other hand, can reveal immense number of genetic loci and are mostly neutral, not growth stage specific and not subjected to environmental effect (Bai *et al.,* 1999). However, this does not mean that they are free of any problem. Some of the problems of using molecular markers include the need for complex laboratories and procedure as well as relatively high cost and technical know how. Taking these difficulties of using molecular markers into account, the present study was focused on studying the genetic variation of released varieties and local landraces of tef based on pheno-morphological traits.

2.3. Genetic diversity in tef

Several studies have been conducted to measure the genetic diversity in tef by using most of the markers. These include studies on phenomorphic traits, on leaf and seed proteins (biochemicals), grain chemical composition, diversity at DNA level and QTL studies. A few among these studies are variations in morphological traits (Ebba, 1975; Tefera*,* 1988; Ketema, 1993, 1997; Bekele, 1996; Teklu, 1998; Assefa et al, 1999, 2000, 2001a&b, 2002, 2003a; Assefa, 2003; Kefyalew, *et al.,* 2000; Adenew, 2002; Tefera, *et al.,* 2003; Tefera and Teklu, 2005), in seed protein (Bekele, 1995) and grain chemical composition (Hundera, 1998); Bekele and Lester (1981). Similarly, variation at DNA level using molecular markers such as RAPD (Bai *et al.,* 2000), AFLP (Ayelle *et al.*, 1999; Bai *et al.,* 1999; Ayelle and Nugyen, 2000), and ISSR (Assefa *et al.,* 2003b) were also reported. Most recently, expressed sequence tag Analysis (Yu *et al.,* 2006) and QTL studies on agronomic traits of tef (Yu et al., 2007) were conducted on tef.

A study on variations of morpho-agronomic characters and grain chemical composition of released tef varieties, revealed the presence of highly significant differences among the varieties

for days to maturity, plant height, culm and panicle length and number of tillers per plant while substantial difference were not observed for grain yield (Hundera, 1998). The variation noted in culm length, diameter of the first and second basal culm internodes indicate the prospect for combating lodging problem which is a major production bottleneck in tef (Hundera, 1998; Assefa *et al.,* 2000). Hundera (1998) indicated that the coefficient of variation varies from 2% for days to maturity to 23% for lodging index. On top of this, tef varieties also showed variations in chemical composition in the grain such that, the estimated values for total nitrogen and protein content of the grains was found to range from 1.5% to 2.04% and 9.38% to 12.75%, respectively (Hundera, 1998). Besides, the study of Hundera (1998) also indicated the presence of considerable amount of some fatty acid compositions in the caryopsis of tef varieties.

Studies on phenotypic and molecular diversity indicated the presence of high diversity for the different set of tef varieties and landraces tested (Assefa, 2003). According to Assefa *et al.* (2001a), tef generally takes 25-81 days for heading, 60-140 days to mature and 29-76 days for grain filling. Different studies reported a range value of 20 and 24 days (Assefa *et al.,* 2000) and 14 and 14 days (Assefa *et al.,* 2001a), respectively for days to heading and maturity. Likewise, Assefa *et al*. (2002) also noted a range value of 17, 23 and 22 days for days to heading, maturity and grain filling, in that order. This existence of wide range of variation for each of the phenological traits enables breeders to undergo selection for different maturity groups as well as adaptation to different agro-ecologies (Assefa *et al*., 2002).

Tefera (1988) studied the variability of characters in 35 tef cultivars described by Ebba (1975) and reported the existence of wide range of phenotypic variability in grain yield and all the other

grain yield component and grain yield related characters considered. This study further revealed high genotypic coefficient of variability and heritability for traits such as spiklet per main panicle, grains per main panicle, kernel weight per main panicle, productive tillers per plant and panicle length. Moreover, the presence of wide variation was also seen in tef varieties and landraces with respect to lodging susceptibility and lodging related traits such as plant height, culm length, and thickness of the culm internodes (Assefa *et al.,* 2001a, 2003b).

Differences in panicle form, seed and lemma color are other indicators of variation existing in tef genotypes. Based on productivity and panicle form, Tefera (1988) identified 15 top yielders out of the 35 tef cultivars described by Ebba (1975). These 15 identified top yielders according to Tefera (1988) were represented by very loose (66.7%), fairly loose (26.7 %) and semi compact (6.6 %) panicle form cultivars. The presence of a very high potential for progress through selection for grain yield from within the very loose, fairly loose and semi compact was noted. The high yielding and widely adapted released varieties of tef, for instance, are among the cultivars having very loose types of panicle.

Similarly, study on cluster and principal component analysis also showed the existence of variation in the Ethiopian germplasm of tef (Assefa *et al.,* 2000, 2001a, 2003a; Adenew, 2002; Adenew *et al.,* 2005) and sorghum (Ayana and Bekele, 1999; Ayana, 2001). For instance, cluster and principal component analysis of the various sets of tef germplasm confirmed that tef is a very diverse crop species (Assefa *et al.,* 2003a). According to Assefa *et al.* (2000), the first five principal components (PCs) with eigenvalue greater than one extracted about 71% of the entire variation of 320 germplasm lines. Likewise, Adenew *et al.* (2005) reported that the first five PCs with latent value greater than one accounted for about 80.6% of the variability existing in 144

heterogeneous tef germplasm. Likewise in sorghum, Ayana and Bekele (1999) and Ayana (2001) reported that 79% of the phenotypic variance was explained by the first five principal components. On the other hand, hierarchical cluster analysis at 75%, 65% and 50% level of similarity grouped 320 tef germplasm lines into 161, 44 and six major groups, respectively (Assefa *et al.,* 2000). Similarly, 144 tef germplam accessions were clustered in to eight genetically distinct classes with one to 78 members in the smallest and largest clusters, respectively (Adenew *et al.,* 2005).

As to the contribution of each component, Assefa *et al.* (2000) reported that about 28% of the total variance explained by the first PC in 320 tef lines evaluated for 17 traits was due to variation in the main shoot internodes, grain yield per plant, and peduncle length. However, the first principal component according to Adenew *et al.* (2005) constituted 55% of the variability mainly from almost equal contribution of 10 quantitative traits.

In addition to the above investigations, study on biochemical assessment involving chromatography of leaf protein and electrophoresis of seed proteins also showed the presence of complex pattern of variation among tef cultivars (Bekele and Lester, 1981).

2.4. Inception and progress of tef improvement research in Ethiopia

Research on tef was started in 1956 with the general objectives of increasing the productivity of the crop through genetic improvement and appropriate cultural practices (Hundera, 1998). Since then, several germplasm accessions have been collected, characterized and evaluated to identify superior or high yielding cultivars resistant to lodging, diseases and pests, and adaptable to

different agroecological zones of the country. Until today, tef breeding has passed through three main phases. The first phase, 1960-1974, was the period when the research work largely focused on mass selection from farmers' varieties. The second phase, 1975-1995, was the period of discovery of floral biology of tef that enabled the developing of varieties through trait recombination. The third, since 1995, was the time when molecular breeding approaches were considered to augment the conventional breeding (Tefera *et al.*, 2001). Up to now, over 20 varieties of tef were officially released for large scale production (MoARD, 2006). The varieties released before 1995 were evaluated for different morphological and agronomic characters (Teklu, 1998; Teklu and Tefera; 2005) and chemical composition (Hundera, 1998). However, the recent releases covering over 50 % of the total number of released tef varieties have yet not been evaluated together for such characters. Efficient utilization of the tef genetic resources still requires comprehensive and systematic collection, evaluation and characterization (Assefa *et al.,* 2003). This indicates the importance of conducting genetic diversity studies including the recent released varieties.

According to Teklu and Tefera (2005), grain yield gain from tef breeding from 1970-1995 had been linear with an average annual increase of 0.8%. Improved biomass yield, plant height, panicle length, spiklet per panicle and yield per panicle were reported to be characteristics of the modern tef genotypes. On top of this, varieties developed through hybridization produced 9% higher yield than those developed through direct selection from germplasm accessions. However, no change had occurred in harvest index and 100-kernel weights while a general similarity for days to physiological maturity for both old and modern varieties was reported (Teklu and Tefera, 2005).

2.5. Phenotypic and genotypic variance and coefficients of variability

Compared to simple coefficient of variation, phenotypic and genotypic coefficients of variation are better measures of the comparative diversity of traits since the latter are based on partitioning of the total phenotypic variance into components due to genetic and non-genetic (environmental) factors (Assefa *et al.,* 2001b). Tefera (1988) found wide range of phenotypic variation for grain yield per plant, 100 Kernel weight, grain per main panicle, productive tillers per plant, plant height, panicle length, number of spiklet per panicle, days to heading and maturity and number of kernel weight per panicle. He also noted the presence of high phenotypic coefficient of variability for characters like spiklet per panicle, grain per main panicle, kernel weight per main panicle and productive tillers per plant. Moreover, Tefera (1988) concluded that the variability observed in phenotype for different characters has been more of genetic than non genetic as the estimate of genotypic variance was higher than that of the error variance. On the other hand, Assefa *et al.* (2001b) reported the lowest (3%) and highest (28%) phenotypic coefficients of variability values for days to maturity and for grain yield, respectively while genotypic coefficient of variation ranged from less than 2% for days to maturity to 15% for number of fertile tillers per plant. Besides, Chanyalew (2007) reported a genotypic coefficient of variability ranging from 1% for days to maturity to 39.3% for number of tillers per plant while phenotypic coefficient of variation ranged from 2.29% for days to maturity to 46.48% for tiller numbers per plant at Debre Zeit. However, at Melkassa, he obtained GCV values ranging from 0.02% for shoot biomass to 13.20% for grain yield while the PCV ranged from 6.44 % for days to maturity to 44.68% for grain yield. In most cases, the lowest phenotypic and genotypic coefficient variation values were observed for days to maturity (Assefa *et al.,* 2001; Chanyalew, 2007). In another study, a relatively high simple coefficient of

variation was reported for flag leaf area (52%), single plant grain yield (48%) and straw yield (39%) while it was relatively low (about 8%) for days to maturity (Ketema, 1993).

2.6. Heritability and genetic advance

Heritability can be of two kinds: broad sense heritability and narrow sense heritability. Broad sense heritability is the ratio of genotypic variance to the total phenotypic variance (Burton and Devane, 1953). It comprises of both the additive and dominant effect of a given gene plus environment.

High estimates of heritability values accompanied by relatively high genetic advance value serve as an indicator for the efficiency of the phenotype-based selection (Assefa *et al.,* 2001a). On top of this, if heritability of a character is very high (>80 %), selection for such character would be fairly easy as there is close correspondence between genotype and phenotype due to the relatively small contribution of the environmental effect to the phenotype (Singh and Ceccerelli, 1995). Assefa *et al.* (2001a) reported that panicle length and number of fertile florets per spikelets had a combination of relatively high heritability and genetic advance while they reported a relatively low heritability and GA estimates for most lodging related traits such as culm length, and length and diameter of the culm internodes.

A study on heritability and genetic advance in recombinant inbred lines of tef by Tefera *et al.* (2003) indicated a comparatively high heritability for days to heading (31%) followed by panicle length (25%) and grain yield (23%) while moderate amounts of heritability values were obtained for panicle weight and yield per panicle. On the other hand, other tef studies showed heritability

values ranging from less than 1% for second basal culm diameter to 71% for panicle length (Assefa *et al*., 2000) and from 17 % for single plant phytomass to 73% for days to heading (Assefa *et al.,* 2001a). Similarly, Chanyalew (2007) observed heritability value ranging from 4% for panicle seed weight to 72% for number of tillers per plant at Debre Zeit and from 2% for plant height to 29 % for days to heading at Melkassa.

Likewise, estimates of GA as percent of mean noted in various tef studies ranged from less than 1 % for second basal culm diameter to 21 % for number of fertile tiller per plant (Assefa *et al*., 2000) from less than 2 % for days to maturity to 23 % for number of fertile tiller per plant (Assefa *et al.,* 2001), and from 2.22% for harvest index to 68 % for number of tillers per plant (Chanyalew, 2007).

2.7. Associations among different traits of tef

Phenotypic and genotypic correlations are the key genetic parameters in the selection of superior genotypes and to evaluate breeding strategies to be utilized (Falconer, 1989). Correlation analysis provides a measure of the degree of association between the variables or the goodness of fit of a prescribed relationship to the data at hand (Gomez and Gomez, 1984). Phenotypic correlation measures how different traits covary across phenotypes while genotypic correlation measures the degree to which different traits are controlled by the same genes or genes that are closely linked (Balcha *et al.*, 2003). Genotypic correlation coefficient, on the other hand, provides a measure of genetic association between traits that enable us to identify important traits to be considered for improvement program.

Tefera (1988) noted that traits such as panicle form (loose panicle), panicle length, panicle weight, tiller number and biomass yield are highly associated with grain yield of tef. To this end, Assefa *et al.* (2003a) showed the presence of significant and positive correlation of grain yield per plant with that of panicle length. Teklu and Tefera (2005), on the other hand, reported that grain yield depicted no significant (p=0.05) association with all phenological traits, while it was significantly and positively associated with number of spikelet per panicle. Nevertheless, Tefera *et al.* (2003) indicated the presence of a strong positive association (r = 0.26–0.70) between grain yield and traits such as shoot biomass, lodging index, panicle length, plant height, panicle weight and yield per panicle. Likewise, positive and significant correlation was observed between grain yield and kernel weight per main panicle and hence, the latter character and numbers of productive tillers are considered as the major constituents of grain yield in tef cultivars (Tefera, 1988).

2.8. Distance Analysis

D^2 statistics or Mahalanobis generalized distance is an important tool in discriminating the population based on morphological measures (Rao, 1952). It is being used by plant breeders to qualify the genetic divergence between and within populations of crop plants. Adenew *et al.* (2005) reported that pair wise generalized inter-cluster distances for 144 germplasm accessions studied for 18 quantitative traits grouped the tef germplasm in that study into eight distinct classes. Furthermore, the presence of a highly significant distance for most of the cluster pairs was reported (Adenew *et al.,* 2005). Keneni *et al.* (2005a & b) reported significant genetic distances among most of the clusters in studying the extent and pattern of genetic diversity for morpho-agronomic traits in both field peas and faba beans.

3. OBJECTIVES:

3.1. General Objective:

- To assess the extent of genetic variation and level of trait association among released tef varieties and some landraces from Jimma area in Ethiopia.

3.2. Specific objectives:

- To determine and compare the extent of genetic variations and agronomic performances among released varieties and landraces of tef
- To assess the level of associations among the different traits
- To classify the released varieties and landraces into similarity groups
- To identify traits accounting for the gross diversity of the varieties and landraces

4. MATERIALS AND METHODS

4.1. Description of the study area, experimental materials and Design

4.1.1. Description of the study area

The study was carried out at Jimma Agricultural Research Centre (JARC) during the 2007 main cropping season (July to December). JARC is located at 7^0 46' N and 36^0 E at a distance of 364 killo meters (Km) and 8km South West of Addis Ababa and Jimma town, respectively. It is situated at an altitude of 1753 m above sea level. The soil type of the experimental site is Eutric Nitosol (Reddish brown) with a pH of around 5.2. The long term annual average rainfall of the area is 1536 mm with maximum and minimum temperature of 25.9^o C and 11.2 ^{o} C, respectively (IAR, 1997). The monthly rainfall distribution, number of rainy days, temperature and humidity during the crop growing season in relation to the previous two years has been summarized and presented (Table 1).

Table 1. The rainfall distribution, number of rainy days, relative humidity and temperature of the study area (2005-2007).

Weather parameters		Year	Months						
			June	July	August	September	October	November	December
amount of Rainfall (mm)		2005	257.6	134.7	200.7	215.8	121.3	43.6	0.00
		2006	163.9	321.6	275.3	138.7	110.6	86.6	121.8
		2007	185.9	205.6	210.4	250.2	63.3	12.1	0.00
Number of rainy days		2005	24.0	19.0	25.0	21.0	13.0	8.0.0	9.0
		2006	17.0	27.0	26.0	23.0	12.0	10.0	12.0
		2007	18.0	23.0	21.0	25.0	8.0	6.0	0.00
Humidity (%)		2005	76.0	80.0	78.0	76.0	70.0	64.0	53.0
		2006	72.0	80.0	82.0	79.0	73.0	67.0	70.0
		2007	75.0	78.0	80.0	76.0	65.0	57.0	51.0
Temp.(0_C)		2005	14.9	15.2	15.0	15.2	13.6	10.4	7.3
		2006	14.9	15.5	15.5	15.8	15.9	14.1	13.8
	Min.	2007	15.9	15.8	15.8	15.4	12.4	11.4	8.9
		2005	24.0	25.4	25.0	25.5	26.8	26.6	27.7
		2006	25.4	24.4	23.2	24.8	26.7	26.9	26.7
	Max.	2007	24.9	23.9	23.6	24.8	27.0	28.5	28.8

4.1.2. Experimental materials

A total of 21 tef genotypes consisting of 19 released varieties and two locally known and widely cultivated landraces in Jimma area (Dalasso and Koche) were used for the study. The description of released varieties and landraces used in this study is presented (Table-2).

Table 2. Description of tef genotypes used in the study

No.	Name of Varieties/ landraces	Year of release	Seed color	Adaptation zone (altitude) (meter above sea level)
1	DZ-01-354 (Enatit)	1970	Pale white	1600-2400
2	DZ-01-99	1970	Brown	1600-2400
3	DZ-01-196 (Magna)	1970	Very white	1800-2400
4	DZ-01-787	1978	Pale White	1600-2400
5	DZ-Cr-44	1982	White	1800-2500
6	DZ-Cr-82	1982	Pale white	1700-2000
7	DZ-Cr-37 (Tseday)	1984	White	1600-2400
8	DZ-Cr-255 (Gibe)	1993	White	1700-2000
9	DZ-Cr-358 (Ziquala)	1995	White	1400-2400
10	DZ-01-974 (Dukem)	1995	White	1400-2400
11	DZ-01-2053(Holeta Key)**	1999	Brown	1900-2700
12	DZ-01-1278(Ambo-Toke)**	2000	White	2200-2400
13	DZ-01-1281(Gerado)	2002	White	1850
14	DZ-01-1285 (Koye)	2002	White	1900-2200
15	DZ-01-1681(Key Tena)	2002	Brown	1600-1900
16	DZ-01-2675 (Dega Tef)	2005	White	1800-2500
17	DZ-01-899 (Gimbichu)	2005	White	2000-2500
18	Ho -Cr-136 (Amarach)	2006	White	Low moisture areas of rift valley
19	DZ-Cr-387 (Quncho)	2006	Very white	1800-2400
20	Jimma local-1(Dalasso)*	-	Mixed	Jimma area
21	Jimma local-2 (Koche)*	-	Mixed	Jimma area

**Only the last two are landraces and the rest are released varieties*

***The two varieties released by Holetta Agricultural Research Center (HARC) while the rest were released by Debre Zeit Agricultural Research Center(DZARC).*

4.1.3. Experimental design and crop management practices

The design employed for this study was randomized complete block design (RCBD) with four replications. Each experimental genotype was grown on a plot area of 1m x 1m with spacing of 0.5m between plots within replication and two meters between replications. Land was prepared and ploughed five times to get a fine seedbed that enhances better germination. Each experimental plot was divided in to six rows having an inter row spacing of 20 centimeters. Planting was made on 22nd of July and seeds of each material was broadcasted uniformly along the six rows in each plot at a seed rate of 30 kg/ha. The experimental plots were fertilized at the rate of 40 Kg N and 60 Kg P_2O_5 per hectare in the form of Diammonium Phosphate (DAP) (18%N and 46% P_2O_5) at planting and top dressing of the remaining N in the form of Urea at tillering stage. The plants in each row were thinned to five centimeter intra-row spacing four weeks after planting; and thus, leaving only 20 plants per row. Hand weeding was made four times during the crop growth stage. Five random samples of plants from the central rows of each plot were tagged on the main shoots at early tillering, and all individual plant related data were collected on these five random samples of plants.

4.2. Data collection

Data were taken on 19 quantitative and three qualitative traits of tef described below.

4.2.1. Quantitative traits evaluation

1. **Days to heading:** The number of days from sowing up to the emergence of the tips of the panicles from the flag leaf sheath in 50% of the plot stands.
2. **Days to maturity:** The number of days from sowing up to 50% of the plants in the plot reaching phonological maturity stage (as judged visually of the plant stands when the

color is changed from green to color of straw).

3. Grain filling period (days): It is the number of days from 50% heading to 50% maturity of the stands in each plot.

4. Plant height (cm): Measured as the distance in centimeter from the base of the stem of the main tiller to the tip of the panicle at maturity and recorded as the average of five plants per plot.

5. Panicle length (cm): The length in centimeter from the node where the first panicle branch starts up to the tip of the main panicle at maturity, recorded as the average of five plants per plot.

6. Culm length (cm): The length of the main shoot culm from the ground level up to the point of emergence of the panicle branches on five random sample of plants per plot.

7. Fertile tillers per plant: It is the record of the number of branch bearing tillers produced per plant assessed as the mean of five random plants per plot.

8. Number of spikelets per panicle: It is the number of spiklets on the main shoot panicle taken on the mean of the mean of five random plants per plot.

9. Number of primary branches per main panicle: It is the number of primary branches that emerged from the rachis of the main panicle.

10. First basal culm diameter (mm): the girth of the stem of the first internode from the ground level taken as the average of five sample plants.

11. Second basal culm diameter (mm): the girth of the stem of the second internodes from the ground level taken as the average of five sample plants.

12. Single plant phytomass (g): The weight of single plant including tillers harvested at the level of the ground.

13. Grain yield per plant (g): the weight of grain for a single plant including all tillers yield.

14. Straw yield per plant (g): The weight of straw plus chaff for a single plant including that of all tillers yield.

15. Thousand Seed weight (mg): It is the weight of thousand seeds at 12.5% moisture content.

16. Harvest Index (HI): It is the value computed as the ratio of grain yield to the shoot biomass.

17. Lodging Index: it is the value recorded following the method of Caldicott and Nuttall (1979) who defined lodging index as the sum of product of each scale or degree of lodging (0-5) and their respective percentage divided by five.

18. Disease incidence (percentage): It is the ratio of the total infected plants to total plants in the row times hundred.

19. Disease severity: It is the value which is obtained by the summation of the corresponding scale (0-9) multiplied the number of each plant having infected tillers and then divided by the maximum scale (9) multiplied by total number of infected plants having tillers.

4.2.2. Qualitative traits evaluation

Qualitative traits data such as panicle form, seed and lemma color were recorded on individual plant bases from five sample plants in each plot. These qualitative traits are described below.

1. Seed color: visual classification of the seed coat color after threshing all the panicles. It was recorded as very white (1), white (2), blurred white, (3), brown 4).

3. Lemma colour: Visual classification of the panicles color taken after flowering. It was recorded as yellowish white (1), variegated (2), red (3) and purple (4).

4. Panicle form: Visual scoring of the panicle appearance taken after flowering. It was

recorded as very loose (1), loose (2), fairly loose (3), semi compact (4) and compact (5)

4.3. Data Analysis

The data collected for all the 19 quantitative traits were subjected to analysis of variance (ANOVA) as per the procedure suggested by Gomez and Gomez (1984). The statistical software packages used for analysis were MSTATC microcomputer statistical programs (Michigan State University, 1989), SAS (SAS Institute, 2001) and MINTAB (MINTAB, 2003).

4.3.1. Descriptive Statistics

The mean, range and standard error of the mean for the different traits were computed using the following furmula.

a) **Mean = $\sum$X/n**

Where; n is the number of genotypes, X is the value of each observation for the different traits

b) The standard error of the mean is designated as: σ_M. It is the standard deviation of the sampling distribution of the mean. The formula for the standard error of the mean is:

$$\sigma_M = \sigma/\sqrt{N}$$

Where σ is the standard deviation of the original distribution and N is the sample size (the number of scores each mean is based upon).

c) Range is simple the difference between the highest and the lowest values for each trait.

Range= H-L

Where; H and L are the highest and lowest score for the trait, respectively.

4.3.2. Analysis of variance and Covariance

4.3.2.1. Analysis of variance

The analysis of quantitative trait data in this experiment was done by using the following model (Singh and Ceccarelli, 1995).

$Yij = \mu + gi + rj + eij$

Where: **Yij**= the response of trait Y from the i^{th} genotype grown in the j^{th} replication.

μ = General mean

gi= The effect of the i^{th} genotype

ri = The effect of the j^{th} replication

eij = experimental error

Table 3. Summary of the analysis of variance model

Source	Degree of Freedom	Mean square	Expected mean Square
Replication	(r-1)	MSr	
Varieties and landraces	(g-1)	MSg	$\sigma^2e + r\sigma^2g$
Error	(r-1) (g-1)	MSe	σ^2e

r= number of replications; MSr =replication mean square; σ^2e= error variance; g= number of genotypes; MSg= genotype mean square; MSe= error mean square; and σ^2g = genotypes variance

4.3.2.2. Analysis of covariance

Genotypic and Phenotypic covariance analysis for the different traits were computed manually using the formula suggested by (Singh and Chaudhury, 1996) as follows.

Genotypic covariance analysis ($Covg_{xy}$)

$Covg_{xy} = (MSP_{gxy} - MSP_{exy})/r$

Where, $Covg_{xy}$ =genotypic covariance between traits x and y.

MSP_{gxy} = Mean sum of product of genotype for traits x and y

$MSP_{exy)}$ = Mean sum of product of environment for traits x and y

r = number of replications

Table 4. Summary of the analysis of covariance model

Source	DF	MSP	Expected MSP
Replication	(r-1)	MSPrxy	
Genotype	(g-1)	MSPgxy	$\sigma^2exy + r\sigma^2gxy$
Error	(r-1) (g-1)	MSPexy	σ^2exy

MSPrxy= Mean sum of product of replication for traits x and y; σ^2g = genotypic covariance for traits x &y; MSPgxy= Mean sum of product of genotype for traits x and y; σ^2exy = error covariance for traits x and y; and MSPexy= Mean sum of product of error for traits x and y

4.3.3. Estimation of Variance & Coefficient of Variability Components, Heritability and Genetic Advance

The total observed variance obtained from the analysis of variance for each of the 19 quantitative traits was partitioned into components due to genetic and non genetic (environmental) effects. Consequently, estimates for phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability, genetic advance (GA) and GA (as % mean) were computed according to the method suggested by Burton and de Vane (1953) as follows:

4.3.3.1. Estimation of phenotypic and genotypic variances

The total phenotypic variance of each of the traits was partitioned into contributions due to genetic and non genetic factors using the analysis of variance components method suggested by Singh and Chaudhury (1996).

a) $\boldsymbol{\sigma^2p = \sigma^2g + \sigma^2e}$

Where: $\boldsymbol{\sigma^2p}$ = Phenotypic variance

$\boldsymbol{\sigma^2g}$ = Genotypic variance

σ^2e = Environmental variance

b) σ^2g = (MSt - MSe)/r

Where: MSt = Mean square of varieties and landraces

MSe = Mean square of error (environmental variance)

r = Number of replications

4.3.3.2. Estimation of phenotypic and genotypic coefficient of variation

a) Phenotypic coefficient of variation (PCV)

PCV= ($\sqrt{\sigma^2}$p /X) *100

Where: PCV= Phenotypic coefficient of variation

X= the grand mean for the trait considered

b) Genotypic coefficient of variation (GCV)

GCV= ($\sqrt{\sigma^2}$g /X)* 100

Where: GCV= genotypic coefficient of variation.

σ^2g= the genotypic variance, and

X= the grand mean for the trait considered

4.3.3.3. Estimates of heritability, genetic advance (GA) and GA as % of mean

Heritability in broad sense, genetic advance (GA) and GA as % of mean were computed as suggested by Allard (1960).

a) Heritability (h^2) = σ^2g/σ^2p*100

Where: h^2 =Heritability in broad sense

σ^2p= Phenotypic variance

σ^2g =Genotypic variance

b) GA= K ($\sqrt{\sigma^2 p}$) (h^2)

c) GA (as % of mean) = (GA/grand mean)*100

Where: GA= Genetic advance

K= A constant which at selection intensity of 5% is about 2.06;

$\sqrt{\sigma^2 p}$= Square root of phenotypic variance

h^2 = Heritability in broad sense

4.3.4. Phenotypic and genotypic correlation analysis

Phenotypic correlation is the observable correlation between two variables and it includes both genotypes and environmental components between two variables. The total correlation coefficients were partitioned into these two components and the phenotypic and genotypic correlation coefficients were computed using the formula suggested by Singh and Chaudhury, (1996).

a) Phenotypic coefficient of correlation (r_P)

r_p= Pcovxy/ $\sqrt{(\sigma^2 px . \sigma^2 py)}$

b) Genotypic coefficient of correlation (r_g)

r_g= Gcovxy/ $\sqrt{(\sigma^2 gx . \sigma^2 gy)}$

Where: rp = Phenotypic correlation coefficient

rg = Genotypic correlation coefficient

Pcovxy = Phenotypic covariance between variables x and y

Gcovxy = Genotypic covariance between variables x and y

$\sigma^2 g$ x=Genotypic variance for trait X

σ^2g y=Genotypic variance for trait Y

σ^2px=Phenotypic variance for trait X

σ^2py=Phenotypic variance for trait Y

4.3.5. Multivariate analysis

Multivariate analysis has proved useful for characterization and classification of plant genetic resources evaluated for several phenol-morphic and agronomic traits (Assefa *et al.,* 2003a). The data collected for 19 quantitative traits of the 19 21 tef genotypes was subjected to multivariate statistical analysis methods such as cluster analysis (CA) using SPSS version 13.0 (SPSS, 2004) and principal component analysis (PCA) using the MINTAB statistical computer package, version 14.00 (MINITAB, 2003). Pair-wise comparisons of clusters means for the 19 quantitative traits were made using t-test.

4.3.6. Distance analysis

Genetic distance between clusters was computed using the generalized Mahalanobis's D^2 statistics formula as suggested in Singh and Chaudhary (1996).

$D^2_p = (X_i-X_j)' S^{-1} (X_i-X_j)$

Where, $D^2_p =$ total generalized distance based on p characters.

X_i and X_j are the p mean vectors of 21 test genotypes **i** and **j**, respectively.

S = p x p pooled error variance and covariance matrix.

The D^2 value obtained for pairs of clusters were considered as the calculated value of Chi-squire (χ^2) and were tested for significance at 5% and 1% level of probability against the tabulated values of χ^2 at 19 degrees of freedom.

4.3.7. Analysis of qualitative traits of the tef genotypes

The phenotypic diversity among the varieties and landraces was assessed for the three qualitative traits including panicle form, seed coat and lemma color. The rating and recording of data were made based on visual observations. The comparisons between the different genotypes were computed by using mean proportion values for each trait.

5. RESULTS AND DISCUSSION

5.1. Descriptive statistics of quantitative traits

The result of this investigation showed the presence of a wide range of variation for all the quantitative traits considered (Table 5). The genotype mean values for the three phenological traits, days to heading and to maturity and grain filling period were 46-56, 87-101 and 41-47 days, respectively. Similarly, the mean values for the other traits also varied from 51-77 cm for plant height, 24-37cm for panicle length, 28-41 cm for culm length, and 1.09-1.79 for number of fertile tillers per plant. DZ-01-974 was the variety with maximum mean performance for seven of the 19 quantitative traits considered in this study. On the other hand, Ho-Cr-136 showed the maximum values for both disease and lodging index. This implies that this variety the most susceptible for both disease and lodging. The probable reason could be its ecological adaptation as it was released to fit for the low land, low moisture areas of the central rift valley areas. The detail genotypes mean values for all the 19 quantitative traits are presented along with their respective standard error (Table 5). The genotypes mean values of phenological traits days to heading and to maturity is not different from that of Assefa *et al.* (2001). However, the range values obtained for days to heading (10), days to maturity (15) and for days to grain filling period (6 days) in this investigation were low compared to what have earlier been reported by Assefa *et al.,* (2000, 2001a, 2002). Likewise, the range values for culm and panicle length, grain yield per plant, single plant phytomass and harvest index were 13.99 cm, 12.81 cm, 0.67g, 2.53g and 0.11, respectively. The range values for all these five traits, except grain yield per plant are again relatively low as compared to that of Assefa *et al.,* (2000, 2001a, 2002). The probable reason for the low value of range in this investigation could be the culmination of rainfall early in the season, beginning from the early reproductive growth phase of the tef crop stands at

Jimma. As such the impacts of the terminal moisture stress had presumably been more so pronounced especially on the late than the early maturing tef genotypes. The values of simple coefficient of variation in this investigation ranged from 2.94% for days to heading to 21.89 % for lodging index. This is in agreement with simple coefficient of variability values ranging from 6 % to 28% reported by Assefa *et al.* (2002) on tef germplasm population.

5.2. Analysis of Variance

The results of the analysis of variance revealed the presence of significant variations among the tef genotypes tested for all of the quantitative traits considered in this study. Except two traits, culm length and fertile tillers per plant, which showed significant genotype difference at ($p<0.05$), all the other traits depicted highly significant ($p<0.01$) genotypic effects (Table 6). The findings of the present study are in line with the previous results of Mengesha (1965); Tefera (1988); Hundera (1998); Adenew (2002) who reported the presence of significant genotypic variations for most of these traits.

5.3. Estimation of variance components and other parameters of variability

5.3.1 Estimation of phenotypic and genotypic variances

The estimates of the variance components for each of the 19 traits of tef under consideration were obtained by partitioning the variance resulting from the analysis of variance (ANOVA). The values obtained for these components were subsequently used to estimate the phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) and heritability percentage (Table 7). Since genetic variance was greater than environmental variance, we can say that all of the variabilities observed in this study for phenotypes of the different traits were due chiefly to genetic

than the non genetic factors. These findings are in agreement with the results formerly reported by Tefera (1988).

5.3.2. Estimation of phenotypic and genotypic coefficient of variability

The phenotypic and genotypic coefficients of variability estimates for the different traits in this study are given (Table 8). The GCV values ranged from 2.87% for days from heading to grain filling to 31.97% for lodging index. High values of GCV were detected for lodging index (31.97%), single plant straw yield (26.96 %) and head smudge disease severity (25.36%); while relatively low values were obtained for days from heading to grain filling (2.87 %), days to maturity (4.12 %) and culm length (6.95 %), respectively. On the other hand, previous studies of Assefa *et al.* (2001a) showed low GCV values ranging from less than 2% for days to maturity to 15% for number of fertile tiller per plant. However, the current results are comparable to what Chanyalew (2007) has reported for study conducted at Debre Zeit while that of Melkassa was still as low as that reported by Assefa *et al.* (2001a).

The lowest and highest PCV values were obtained for days to maturity (4.53%) and for lodging index (38.74 %), respectively. Other traits with relatively high PCV were head smudge disease severity (31.25 %) and single plant straw yield (27.89 %) while the phenological traits days to maturity (4.53 %), days from heading to grain filling (5.50 %) and days to heading (7.20 %) were the three traits with lower PCV values in that order. On the other hand, Assefa *et al.* (2003) reported PCV values ranging from 3% for days to maturity to 28% for grain yield of plants. On top of this, Chanyalew (2007) reported PCV values ranging from 2.29% for days to maturity to 46.48% for number of tillers at Debre Zeit and 6.44% for days to maturity to 44.68% for grain

yield at Melkassa. In most cases, the PCV values obtained in this investigation were not as such different from Assefa *et al.* (2001a) and Chanyalew (2007). The highest PCV (38.74%) and GCV (31.94%) values obtained for the current investigation, however, were by far greater than those reported by Assefa *et al.* (2001).

5.3.3. Estimation of broad sense heritability

The broad sense heritability estimates are presented in Table 8. The values ranged from 16.87 % for number of fertile tillers per plant to 93.43 % for single plant straw yield. The heritability percentage values detected in the current study are higher than those previously reported by Assefa *et al. (*2000, 2001). Single plant straw yield (93.43 %), single plant phytomass (90.76 %) and thousand seed weight (87.88 %), days to heading (83.29%) and days to maturity (82.54%) were the traits with high heritability values while low values were obtained for number of fertile tillers per plant (16.87 %), harvest index (20.00 %) and culm length (20.32 %). Unlike in the present study, Assefa *et al.* (2001) reported low heritability values (35%) for single plant phytomass, days to maturity, single plant grain yield and harvest index. Likewise, Assefa *et al.* (2000) also found low heritability values (<30%) for the first and second basal culm diameter, and shoot phytomass and grain yield per plant. On the other hand, the lowest heritability value observed for number of fertile tiller per plant in this study is different from the report of Tefera (1988). Grain yield per plant showed moderate to high percentage values for both heritability and genotypic coefficient of variability. This is in agreement with result of Tefera (1988). Different studies indicated heritability values ranging from less than 1% for first basal culm diameter to 71% for days to heading (Assefa *et al.,* 2000), 17% for single plant phytomass to 73% for days to

heading (Assefa *et al.,* 2001), 4% for panicle weight to 72% for number of tillers at Debre Zeit and 2% for plant height to 29% for days to grain filling period at Melkassa (Chanyalew, 2007).

5.3.4. Estimation of expected genetic advance

Estimates of genetic advance and genetic advance as percent of mean are shown in Table 8. GA values ranged from 0.029 for harvest index to as high as 48.04 for number of spiklet per panicle. The value of GA for number of spiklet per panicle is extremely high while lodging index (10.78 %) and disease severity index (8.44%) were the second and third traits with high GA values. Thus, lodging index, head smudge disease severity and incidence, plant height, days to maturity and to heading are traits with high GA in this study. On the other hand, extremely low values of GA (0.029 to 0.324) were estimated for harvest index, number of fertile tillers per plant, thousand seed weight, first basal culm diameter, grain yield per plant and second basal culm diameter in that order.

Likewise, the estimate of GA as percent of mean ranged from 3.09 % for days to grain filling to 54.35 % for lodging index. Thus, the estimate of GA as percent of mean is higher in this investigation as compared to the former two reports by Assefa *et al.* (2000, 2001a). On the other hand, the results of this investigation are in agreement with the results of Chanyalew (2007) who reported GA as percent of mean values ranging from 2.2% and 68%.

Table 5. The range, mean and standard error for 19 traits of 21 tef genotypes

Traits	Range of values for genotypes				Mean	S.E (±)
	Minimum		Maximum			
	Value	Genotypes	Value	Genotypes		
Days to heading	46 .00	DZ-Cr-37	55.75	DZ-Cr-387	51.262	0.396
Grain filling period (days)	40.50	Ho-Cr-136	46.50	DZ-01-1285	43.917	0.262
Days to maturity	86.75	Ho-Cr-136	101.00	DZ-Cr-44	95.214	0.465
Plant height (cm)	51.06	DZ-01-2053	76.50	DZ-01-974	62.782	0.944
Panicle length (cm)	24.25	DZ-01-2675	37.44	DZ-01-787	29.663	0.492
Culm length (cm)	27.91	DZ-01-2675	40.72	DZ-Cr-387	33.062	0.552
No. of fertile tillers per plant	1.09	DZ-01-1278	1.79	DZ-Cr-37	1.4619	0.036
No. of spkilets per main panicle	124.25	DZ-01-2053	287.60	DZ-01-787	208.63	6.21
No. panicle branch per main panicle	13.63	DZ-01-2053	22.22	DZ-01-787	18.917	0.285
First basal culm internode diameter (mm)	1.46	DZ-01-2053	2.34	DZ-01-974	1.927	0.038
Second basal culm diameter (mm)	1.44	DZ-01-2053	2.43	DZ-01-974	2.016	0.041
Harvest Index (%)	22.0	DZ-01-787	33.0	DZ-Cr-37	0.266	0.005
Single plant phytomass (g)	1.55	DZ-01-1681	4.08	DZ-01-974	2.479	0.070
Single plant grain yield (g)	0.38	DZ-01-196	1.05	DZ-01-974	0.650	0.019
Single plant straw yield (g)	1.13	DZ-01-1681	3.03	DZ-01-974	1.824	0.055
Thousand seed weight (mg)	0.40	DZ-01-1681	0.60	DZ-01-974	0.448	0.010
Head smudge disease incidence (%)	21.84	DZ-Cr-387	47.02	Ho-Cr-136	29.398	0.819
Head smudge disease severity (%)	12.83	DZ-01-99	36.10	Ho-Cr-136	20.040	0.674
Lodging index (%)	11.30	DZ-01-899	35.90	Ho-Cr-136	19.837	0.831

Table 6. Mean square and simple coefficient of variability for the 19 traits of 21 tef genotypes

Traits	Replications	genotypes	Error	CV (%)
Days to heading	1.19ns	47.60**	2.27	2.94
Grain filling period (days)	3.821 ns	310.61**	4.246	4.69
Days to maturity	5.10 ns	64.78**	3.254	18.95
Plant height (cm)	46.21 ns	174.1**	43.24	10.47
Panicle length (cm)	21.52 ns	51.55**	9.89	10.60
Culm length (cm)	16.32 ns	41.82*	20.70	13.76
No. of fertile tillers per plant	0.97 ns	0.154*	0.085	19.94
No. of spkilets per main panicle	3060 ns	7237**	1920	21.00
No. panicle branch per main panicle	15.82 ns	13.90**	4.03	10.61
First basal culm internode diameter (mm)	0.042 ns	0.245**	0.087	15.31
Second basal culm diameter (mm)	0.065 ns	0.316**	0.081	14.12
Harvest Index (%)	0.006ns	0.004**	0.002	16.83
Single plant phytomass (g)	0.027 ns	1.572**	0.039	7.97
Single plant grain yield (g)	0.016 ns	0.097**	0.008	13.76
Single plant straw yield (g)	0.0612 ns	0.984**	0.017	7.15
Thousand seed weight (mg)	0.002 ns	0.03**	0.001	7.06
Head smudge disease incidence (%)	26.20 ns	148.50**	27.14	17.72
Head smudge disease severity (%)	8.79 ns	116.72**	13.38	18.54
Lodging index (%)	28.79 ns	179.72**	18.85	21.89
Degrees of freedom	3	20	60	

*, ** significant at 5% and 1% probability level, respectively.

Table 7. Estimates phenotypic variance (Vp), genotypic variance (Vg) and error variance (Ve) for 19 traits of 21 tef genotypes

Traits	Vp	Vg	Ve
Days to heading	13.61	11.33	2.27
Grain filling period (days)	5.84	1.59	4.246
Days to maturity	18.64	15.38	3.254
Plant height (cm)	75.79	32.73	43.24
Panicle length (cm)	20.31	10.42	9.89
Culm length (cm)	25.98	5.28	20.70
No. of fertile tillers per plant	0.10	0.02	0.085
No. of spkilets per main panicle	3249.25	1329.25	1920
No. panicle branch per main panicle	6.5	2.47	4.03
First basal culm internode diameter (mm)	0.13	0.04	0.087
Second basal culm diameter (mm)	0.14	0.06	0.081
Harvest Index (%)	0.005	0.001	0.002
Single plant phytomass (g)	0.42	0.38	0.039
Single plant grain yield (g)	0.03	0.02	0.008
Single plant straw yield (g)	0.26	0.24	0.017
Thousand seed weight (mg)	0.01	0.01	0.001
Head smudge disease incidence (%)	57.48	30.34	27.14
Head smudge disease severity (%)	39.22	25.84	13.38
Lodging index (%)	59.07	40.22	18.85

Table 8. Estimates of phenotypic coefficient variability (PCV), genotypic coefficient of variability (GCV) and Heritability (%) for 19 traits of 21 tef genotypes

Traits	GCV (%)	PCV (%)	H (%)	GA	GA (% mean)
Days to heading	6.57	7.20	83.29	6.330	12.348
Grain filling period (days)	2.87	5.50	27.26	1.357	3.090
Days to maturity	4.12	4.53	82.54	7.341	7.710
Plant height (cm)	9.11	13.88	43.08	7.726	12.306
Panicle length (cm)	10.88	15.19	51.29	4.762	16.052
Culm length (cm)	6.95	15.42	20.32	2.134	6.453
No. of fertile tillers per plant	9.00	21.90	16.87	0.110	7.517
No. of spkilets per main panicle	17.48	27.32	40.91	48.038	23.026
No. panicle branch per main panicle	8.30	13.47	37.98	1.995	10.545
First basal culm internode diameter (mm)	10.3	18.43	31.23	0.232	12.037
Second basal culm diameter (mm)	12.00	18.51	42.04	0.324	16.073
Harvest Index (%)	8.41	18.80	20.00	0.029	10.952
Single plant phytomass (g)	24.97	26.21	90.76	1.212	48.878
Single plant grain yield (g)	22.95	26.76	73.55	0.262	40.374
Single plant straw yield (g)	26.96	27.89	93.43	0.981	53.804
Thousand seed weight (mg)	19.01	20.27	87.88	0.181	40.409
Head smudge disease incidence (%)	18.74	25.79	52.78	8.243	28.040
Head smudge disease severity (%)	25.36	31.25	65.88	8.499	42.411
Lodging index (%)	31.97	38.74	68.09	10.780	54.345

5.4. Quantitative character associations

Phenotypic and genotypic correlation coefficients among the 19 traits considered in this study were computed as per the procedure suggested by Singh and Chaudhury (1996) and presented in (Table 9 and 10)

5.4.1. Correlation between single plant grain yield and other traits

The presence of significant phenotypic correlation was detected between single plant grain yield and different quantitative traits except number of fertile tillers per plant and disease incidence (Table 9). Positive and significant ($p<0.01$) correlations were detected between single plant grain yield and all traits except days to grain filling period, harvest index, disease index (both incidence and severity) and lodging index. These four traits were highly significant ($P\leq0.01$) and negatively correlated with single plant grain yield. On the other hand, the relationships of days to maturity and number of fertile tiller per plant with single plant grain yield, respectively were significant and not significant ($p=0.05$). The presence of positive and significant correlations observed between grain yield and most of the quantitative traits is in agreement with the previous reports (Tefera, 1988; Adenew, 2002; Assefa *et al.,* 2003a).

Genotypic correlation coefficient revealed the presence of significant correlation between grain yield and different quantitative traits except for number of fertile tillers per plant, harvest index, disease incidence. Consequently, positive and significant ($P<0.01$) correlations were noted between single plant grain yield and all the other traits except days to grain filling period, number of fertile tiller per plant, harvest index, disease index (both incidence and severity) and lodging index (Table 10). Among the negatively correlated traits, days from heading to grain

filling, disease index (incidence) and lodging index showed highly significant (P<0.01) relationship with single plant grain yield; while the correlation of single plant grain yield with number of fertile tiller per plant, harvest index and disease severity index were non significant (P=0.05)

5.4.2. Correlation between phenological traits and other traits

5.4.2.1. Correlation between days to maturity and other traits

Days to maturity showed positive and highly significant phenotypic correlation (P≤0.01) with almost all of the traits studied while only culm length, number of fertile tiller per plant, harvest index, head smudge disease incidence and severity as well as lodging index showed negative and significant (P≤0.01) correlations. On the other hand, first culm basal diameter and single plant grain yield were significant (P≤0.05) while number of spikelet per panicle, second basal culm diameter and thousand weight were non significant (0.05) (Table 9).

On the other hand, days to maturity showed positive and highly significant (P≤0.01) genotypic correlation with almost all of the traits studied while only culm length, number of fertile tiller per plant , harvest index, head smudge disease incidence and severity as well as lodging index showed negative correlation. Among these negatively correlated traits, only head smudge disease incidence and number of spikelets per panicle, respectively was non significant and significant at 5% probability level while the remaining traits showed highly significant (P≤0.01) genotypic correlation with days to maturity (Table 10). This is in line with the previous reports on genotypic and phenotypic correlation (Tefera, 1988; Adenew, 2002).

5.4.2.2. Correlation between days to heading and other traits

Days to heading showed highly significant (P≤0.01) phenotypic correlations with all the quantitative traits considered in this study except days from heading to grain filling, culm length and number of spiklets per panicle which were non significant (p=0.05). Traits such as days from heading to grain filling, culm length, number of fertile tiller per plant, harvest index, head smudge disease incidence and severity as well as lodging index showed negative phenotypic correlation while all the rest traits were positively correlated with days to heading.

Likewise, days to heading showed a highly significant (P≤0.01) correlation with all the quantitative traits considered in this study except for culm length. Traits such as number of fertile tiller per plant, harvest index, head smudge disease incidence and severity as well as lodging index showed negative genotypic correlation while all the rest traits were positively correlated with days to heading

Significant and positive correlations between days to heading and traits such as plant height, panicle length, number of spikelets per panicle and panicle branch per main panicle were in line with (Adenew, 2002). Similarly, the negative phenotypic and genotypic correlation between days heading and number of fertile (r = -0.236, r = -0.484) is in agreement with the results of Tefera (1988) and Adenew (2002).

5.4.2.3. Correlation between days from heading to grain filling and other traits

Days to grain filling period significantly ($P \leq 0.01$) correlated with all of the traits except days to heading, panicle length, number of fertile tillers per plant and panicle branches per main panicle, single plant straw yield and thousand seed weight. Nevertheless, single plant phytomass showed significant ($P=0.05$) and negative correlation with days to grain filling period.

Similarly, days from heading to grain filling showed significant genotypic correlation with all of the traits other than panicle length and head smudge disease severity. Likewise, except for days to heading and maturity, all traits had negative correlation with days from heading to grain filling. In contrast to this finding, Adenew (2002) reported a positive and significant phenotypic correlation between days from heading to grain filling to plant height, number of fertile tillers per plant, spiklet per panicle and panicle branch per main panicle. With respect to level of significance, all were highly significant, except that of number of panicle branches per main panicle which was significant ($P \leq 0.05$), and panicle length and head smudge disease severity which were non-significant ($p=0.05$).

The results of simple correlation analysis by Teklu and Tefera (2005) indicated the presence of non significant association between grain yield and phenological traits. However, this is not in line with the present investigation which detected positive and highly significant genotypic and phenotypic correlation for grain yield with both days to heading and maturity.

5.4.3. Correlation between lodging index and other traits

Lodging is the most important traits that can play a very great role on the productivity of tef crop. It brings a direct and indirect effect resulting in both quantity and quality loss. The presence of significant ($p \leq 0.01$) phenotypic correlation was observed between lodging index and all traits of tef under consideration except for culm length and thousand seed weight which were non significant (0.05). Generally, lodging index showed a negative phenotypic correlation with all traits except for number of fertile tillers per plant, harvest index and disease index (both incidence and severity) while the rest had positive correlation with this character. Unlike this investigation, Assefa *et al.* (2003a) reported the presence of strong positive association between grain yield and lodging index.

Besides, the presence of significant genotypic correlation between lodging index and several traits of tef under consideration were observed and are shown in Table 10. A negative and significant genotypic correlation was observed with almost all of the traits except for number of fertile tillers per plant, harvest index and disease index (both incidence and severity) which showed highly significant ($P \leq 0.01$) and positive correlation. Thousand seed weight, on the other hand, showed non significant ($P=0.05$) and negative correlation with lodging index.

5.4.4. Correlation between head smudges disease index and other traits

Head smudge disease is another most important trait that is among the major production bottlenecks of tef. This investigation showed the presence of significant correlation between disease index and about 60 % of the quantitative traits of tef in the study (Table 9 &10). This

disease index includes both incidence and severity and each index is discussed separately as follows.

Disease incidence showed highly significant ($P \leq 0.01$) phenotypic correlation with all traits except that of culm length ($r = 0.046$), number of spiklet per panicle($r = -0.018$), first ($r = 0.005$) and second basal culm diameter($r = 0.058$), single plant grain yield($r = -0.040$) and thousand seed weight($r = -0.079$) which were non significant ($P=0.05$). Furthermore, this trait showed a positive correlation with number of fertile tillers per plant, culm length, harvest index, disease severity and lodging index while it showed negative correlation with the rest traits (Table 9).

Likewise, head smudge disease severity showed a negative phenotypic correlation with 13 of the 18 quantitative traits considered in this study while traits such as culm length, number of fertile tillers per pant, harvest index, disease incidence and lodging index had positive correlation. Besides, it showed a highly significant ($P \leq 0.01$) phenotypic correlation with all the traits except culm length($r = 0.033$) and the diameter of first ($r = -0.077$) and second basal culm($r = -0.020$) which were non significant ($P<0.05$).

On the other hand, disease incidence showed highly significant ($P \leq 0.01$) genotypic correlation with all traits except for number of spiklet per panicle ($r=0.013$), first ($r=0.016$) and second basal culm diameter ($r=0.065$) and single plant grain yield ($r = -0.075$) which were non significant ($P=0.05$). As to the sign, disease incidence had negative correlation with all traits other than culm length, number of fertile tillers, number of spiklet and panicle branch per panicle, first and second basal culm diameter, harvest index and disease incidence.

Head smudge disease severity, on the other hand, showed a negative genotypic correlation with 13 of the 18 quantitative traits considered in this study while a positive correlation was seen with culm length (r =0.083), number of fertile tillers per pant(r = 0.456), harvest index(r =0.769), disease incidence (r =0.932)and lodging index (r =0.638). On top of this, it showed a highly significant ($P \leq 0.01$) correlation with all the traits except for days from heading to grain filling (r =-0.059) and culm length which were non significant (r = -0.083) ($P<0.05$).

Table 9. Phenotypic coefficient of correlation for 19 quantitative traits of 21 tef genotypes

	DH	DGF	DM	PH	PL	CL	FT	SPK	PBM	FBCD	SBCD	SPP	SPSY	SPSty	HI	TSW	HIA	HSA	LA
DH	1.000																		
DGF	-0.010ns	1.000																	
DM	0.777**	0.538**	1.000																
PH	0.226**	-0.189**	0.148**	1.000															
PL	0.428**	-0.079ns	0.377**	0.846**	1.000														
CL	-0.017ns	-0.284**	-0.129**	0.795**	0.455**	1.000													
FT	-0.236**	-0.014ns	-0.191**	0.060ns	-0.065ns	0.150**	1.000												
SPK	0.079ns	-0.152**	0.062ns	0.691**	0.662**	0.459**	0.288**	1.000											
PBM	0.392**	-0.036ns	0.351**	0.510**	0.566**	0.292**	0.045ns	0.608**	1.000										
FBCD	0.197**	-0.143**	0.105*	0.526**	0.457**	0.363**	0.219**	0.640**	0.524**	1.000									
SBCD	0.180**	-0.165**	0.072ns	0.564**	0.478**	0.396**	0.153**	0.593**	0.468**	0.886**	1.000								
SPP	0.385**	-0.090*	0.296**	0.508**	0.588**	0.260**	0.093*	0.599**	0.426**	0.548**	0.523**	1.000							
SPSY	0.196**	-0.185**	0.096*	0.524**	0.490**	0.389**	0.090ns	0.587**	0.425**	0.516**	0.538**	0.787**	1.000						
SPStY	0.428**	-0.077ns	0.354**	0.454**	0.564**	0.212**	0.072ns	0.543**	0.429**	0.498**	0.470**	0.943**	0.740**	1.000					
HI	-0.271**	-0.187**	-0.312**	0.078ns	-0.109**	0.251**	0.034ns	0.068ns	0.031ns	-0.014ns	0.050ns	-0.258**	0.363**	-0.259**	1.000				
TSW	0.149**	-0.086ns	0.040ns	0.089*	0.134**	-0.036ns	-0.057ns	0.073ns	0.131**	0.178**	0.257**	0.270**	0.154**	0.323**	-0.193**	1.000			
HIA	-0.452**	-0.264**	-0.557**	-0.122**	-0.235**	0.046ns	0.220**	-0.018ns	-0.257**	0.005ns	0.058ns	-0.202**	-0.040ns	-0.275**	0.247**	-0.079ns	1.000		
HA	-0.555**	-0.165**	-0.550**	-0.177**	-0.334**	0.033ns	0.135**	-0.127**	-0.340**	-0.077ns	-0.020ns	-0.378**	-0.209**	-0.464**	0.258**	-0.140**	0.770**	1.000	
LA	-0.567**	-0.227**	-0.605**	-0.268**	-0.369**	-0.062ns	0.095**	-0.346**	-0.453**	-0.276**	-0.293**	-0.444**	-0.323**	-0.458**	0.142**	-0.032ns	0.424**	0.436**	1.000

*, ** =significant at 5 and 1 % probability level respectively.

DH=Days to heading, DM=Days to maturity, DGF=Days fro heading to grain filling, PH=plant height, PL=Panicle length, CL= culm length, FT= fertile tillers per plant, SPK=number of spkilets per main panicle, PBM=panicle branch per main panicle, FBCD=first culm basal diameter, SBCD=second culm basal diameter, HI= harvest Index, SPP=single plant phytomass, SPSY=single plant grain yield, SPStY=single plant straw yield, TSW= thousand seed weight, HIA=Head smudge disease incidence, HSA=Head smudge disease severity and LA=lodging index.

Table 10. Genotypic coefficient of correlation for 19 quantitative traits of 21 tef genotypes

	DH	DGF	DM	PH	PL	CL	FT	SPK	PBM	FBCD	SBCD	SPP	SPSY	SPSty	HI	TSW	HIA	HSA	LA
DH	1.000																		
DGF	0.347**	1.000																	
DM	0.958**	0.600**	1.000																
PH	0.443**	-0.526**	0.287**	1.000															
PL	0.622**	-0.003ns	0.597**	0.879**	1.000														
CL	0.041ns	-0.968**	-0.222**	0.815**	0.378**	1.000													
FT	-0.484**	-0.588**	-0.653**	-0.734**	-0.880**	-0.356**	1.000												
SPK	0.258**	-0.417**	0.110*	0.731**	0.725**	0.472**	-0.517**	1.000											
PBM	0.700**	-0.113*	0.559**	0.635**	0.724**	0.208**	-0.858**	0.854**	1.000										
FBCD	0.436**	-0.330**	0.278**	0.822**	0.851**	0.583**	-0.576**	0.948**	1.054**	1.000									
SBCD	0.367**	-0.300**	0.216**	0.818**	0.831**	0.573**	-0.547**	0.832**	0.833**	0.958**	1.000								
SPP	0.459**	-0.159**	0.357**	0.720**	0.778**	0.489**	0.048ns	0.861**	0.681**	0.905**	0.740**	1.000							
SPSY	0.208**	-0.190**	0.138**	0.753**	0.674**	0.649**	-0.030ns	0.965**	0.541**	0.856**	0.721**	0.942**	1.000						
SPStY	0.508**	-0.101**	0.406**	0.676**	0.773**	0.404**	0.071ns	0.790**	0.668**	0.900**	0.713**	*1.009***	0.877**	1.000					
HI	-0.815**	-0.231**	-0.766**	-0.010ns	-0.464**	0.447**	-0.118*	0.205**	-0.442**	-0.269**	-0.113*	-0.368**	-0.009ns	-0.591**	1.000				
TSW	0.206**	-0.200**	0.061ns	0.148**	0.188**	-0.045ns	0.025ns	0.128**	0.211**	0.504**	0.498**	0.312**	0.199**	0.337**	-0.452**	1.000			
HIA	-0.778**	-0.289**	-0.750**	-0.233**	-0.524**	0.208**	0.761**	0.013ns	-0.409**	0.016ns	0.065ns	-0.333**	-0.075ns	-0.388**	0.918**	-0.154**	1.000		
HA	-0.756**	-0.059ns	-0.647**	-0.357**	-0.598**	0.083ns	0.456**	-0.315**	-0.516**	-0.321**	-0.218**	-0.575**	-0.371**	-0.594**	0.769**	-0.231**	0.932**	1.000	
LA	-0.742**	-0.197**	-0.696**	-0.564**	-0.700**	-0.266**	0.364**	-0.591**	-0.855**	-0.616**	-0.484**	-0.555**	-0.432**	-0.560**	0.442**	-0.079ns	0.633**	0.638**	1.000

*, ** =significant at 5 and 1 % probability level respectively.

DH=Days to heading, DM=Days to maturity, DGF=Days fro heading to grain filling, PH=plant height, PL=Panicle length, CL= culm length, FT= fertile tillers per plant, SPK=number of spkilets per main panicle, PBM=panicle branch per main panicle, FBCD=first culm basal diameter, SBCD=second culm basal diameter, HI= harvest Index, SPP=single plant phytomass, SPSY=single plant grain yield, SPStY=single plant straw yield, TSW= thousand seed weight, HIA=Head smudge disease incidence, HSA=Head smudge disease severity and LA=lodging index.

5.5. Multivariate Analysis

Multivariate analysis is useful for the characterization and classification of varieties and landraces evaluated for multiple pheno-morphic and agronomic traits. In this study, cluster analysis (CA) and principal component analysis (PCA) were computed. The data were pre standardized to a mean zero and variance of unity before computing CA and PCA so as to avoid differences in scales used for recording data on different traits (Sneath and Sokal, 1973).

5.5.1. Cluster analysis

Cluster analysis was used to group the tef varieties and landraces into genetically distinct classes based on multiple traits following the average linkage Euclidean distance method. The means of each trait of the 21 varieties and landraces were used for cluster analysis. The 19 released varieties and 2 local landraces were clustered into four distinct classes at about 60 % similarity level using SAS (SAS Institute 2001). The number of varieties and landraces in each of the four clusters ranged from one to thirteen in the smallest and largest group, respectively (Fig. 1 & Table 11). Here, cluster number four remained solitary without grouping. Cluster number two was the largest one and it consisted of eleven varieties and two local landraces out of which five are varieties developed through hybridization and the rest six are cultivars. On the other hand, cluster number one and number three each consisted of five and two varieties, respectively. The varieties which remained solitary without grouping is DZ-01-974 and it became solitary due to its interesting traits such as longer plant height, culm and panicle length, thicker first and second culm diameter, higher yield of single plant phytomass, grain and straw yield and

relatively very low disease incidence and severity as well as lodging index. On the other hand, the varieties in cluster III are DZ-Cr-37 and Ho-Cr-136 which were characterized to have shortest days to heading, maturity and from heading to grain filling, low number of panicle branches per main panicle, low single plant straw yield and thousand seed weight but higher number of fertile tillers per plant, harvest index, disease incidence and severity as well as lodging index. Generally, all varieties developed through hybridization were grouped into the same cluster (Cluster-II) except for the two early maturing crosses namely DZ-Cr-37 and HO-Cr-136 which were grouped together in a separate cluster (Cluster III). Another surprising point in this cluster formation is that DZ-Cr-387, the hybrid between DZ-01-196 and DZ-01-974, was not grouped with any one of its parents.

The grouping of the 21 tef varieties and landraces into four clusters at about 60 % similarity in this investigation is more in line with Adenew (2002) formation of four and six clusters based on 14 traits from 144 heterogeneous germplasm populations using data obtained at Holetta and Ginchi, respectively and that of three clusters reported by Costanza *et al.* (1979) using 39 accessions. It is also in agreement with Ebba (1975) which formed six major clusters from 35 cultivars, Assefa *et al.* (2001) six main clusters at 75% similarity from 36 tef germplasm populations.

Table 11. Lists of varieties and landraces grouped in different clusters

Cluster	No. of varieties and/landraces	Name of varieties and/landraces
1	5	DZ-01-1281, DZ-01-1681, DZ-01-196, DZ-01-2675, DZ-01-2053
2	13	DZ-01-354, DZ-01-99, DZ-01-787, DZ-Cr-44, DZ-Cr-82, DZ-Cr-255, DZ-Cr-358, DZ-01-899, DZ-01-1285, DZ-Cr-387, DZ-01-1278, Jimma local-1, Jimma local-2
3	2	DZ-Cr-37, HO-Cr-136
4	1	DZ-01-974

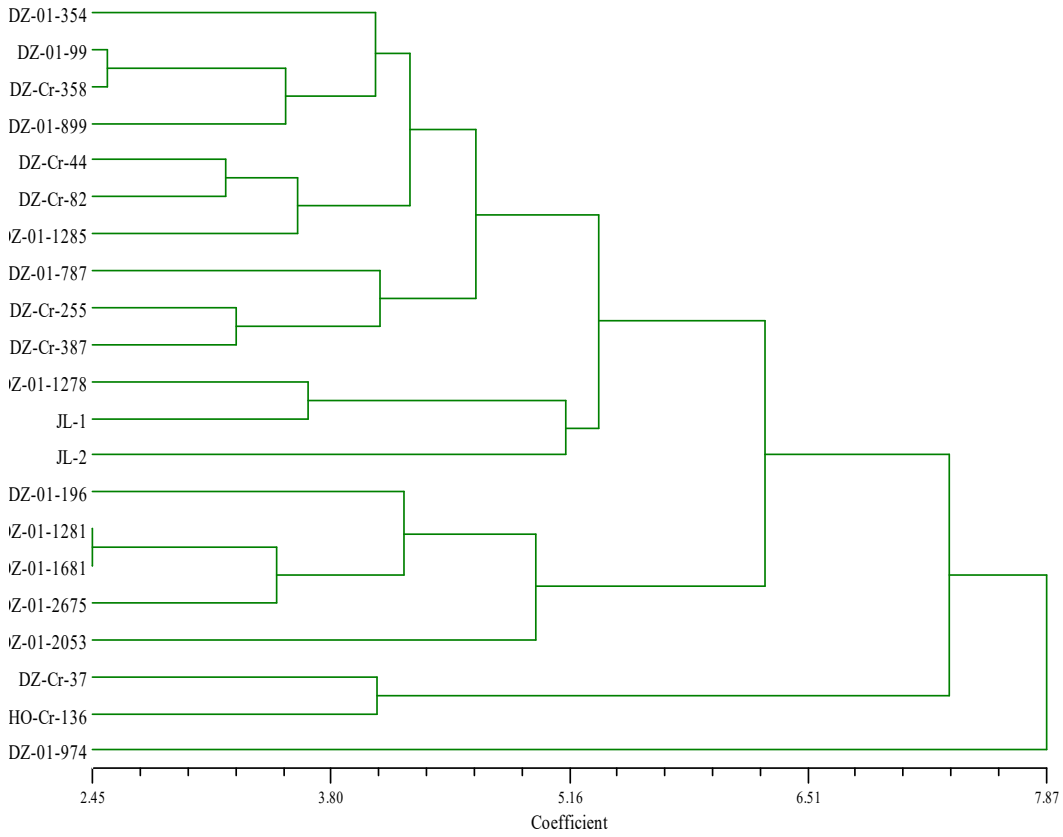


Figure 1. Dendrogram with UPGM and Euclidean distance showing similarity among 21 tef germplasm using 19 quantitative traits.

5.5.1.1. Intra and Inter cluster distances (D)

The pair wise generalized distances (D) among the four clusters are presented in figure 2. The distance analysis showed that all inter cluster distances were highly significant ($p<0.01$) while there was no significant ($P=0.05$) intra cluster distance. The highly significant ($P<0.01$) and maximum distance (9048.43) was detected between clusters 1& 4 while the minimum distance (937.06) was observed between cluster 2& 4. Similarly, the second and third most divergent clusters were C_1 and C_2 (8140.51) and C_3 and C_4 (5354.61), respectively. This high values of inter cluster distances may result due to the different genetic background of the materials, in which case some are hybrids the others are landraces and still others cultivars. On top of this, the released varieties were of different agro ecological releases (lowland moisture stress areas, medium altitude and highland water logged areas) and hence these all may contribute to it. Based on these variations, it can be suggested that crosses between materials selected from cluster 1& 4 are expected to give better genetic recombination and segregation in their progenies. This could be true since the so far developed and released hybrid variety DZ-Cr-387 (very white seed & high yielding), is a cross between DZ-01-196 from cluster number one and DZ-01-974 from cluster number four.

5.5.1.2. Cluster Mean Assessment

The cluster means of the 19 different traits were compared and are presented in Table 12. These mean cluster comparison showed that cluster number one was characterized to have longer days to grain filling, short plant height and panicle length, low number of spiklet per main panicle, thinner first and second basal culm diameter, low harvest index, single plant phytomass and grain yield while cluster two was characterized with a single unique character of longer maturity period. On the other hand, cluster three was known to have

shorter days to heading, grain filling & maturity, shorter plant height, higher number of fertile tillers, low number of panicle branch per main panicle, high harvest index, low thousand seed weight and higher scores for disease incidence, severity and lodging index. Contrary to this, cluster number four is said to have longer days to heading, plant height, panicle and culm length, higher number of spiklets per panicle and panicle branches per panicle, thicker first and second basal culm nodes, higher single plant phytomass, grain and straw yield and lower scores for disease incidence, severity and lodging index.

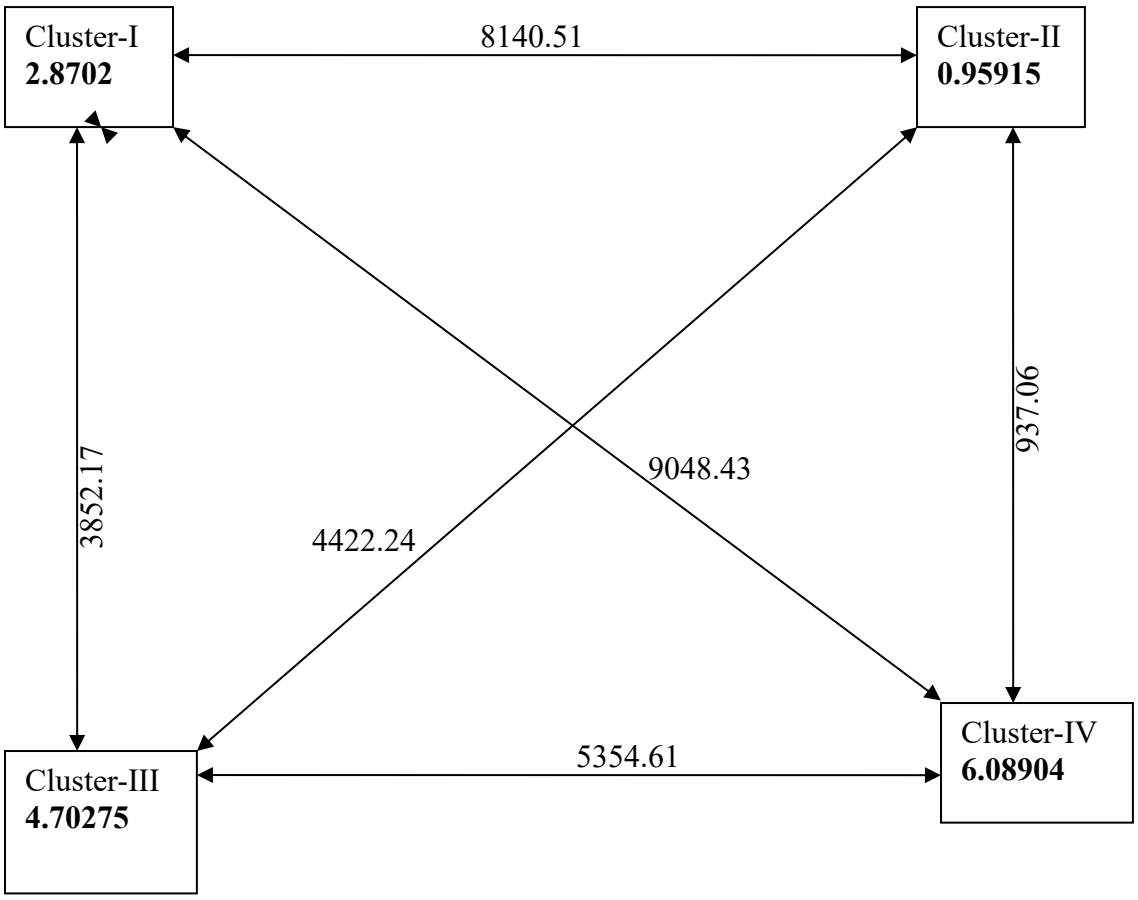


Figure 2. A diagram showing the intra and inter cluster distances using 19 Quantitative traits in 21 tef genotypes.

NB. The numbers in the above boxes are intra-cluster distances while the numbers written on each connecting lines represent inter-cluster distances (D).

Table-12 Cluster means for 19 quantitative traits of 21 genotypes

Traits	Cluster-I	Custer-II	Cluster- III	Cluster-IV
Days to heading	50.05	52.37	46.13b	53.25a
Grain filling period (days)	44.65a	44.23	41.13b	41.75
Days to maturity	94.95	96.48a	87.25b	96.00
Plant height (cm)	56.49b	64.17	62.47	76.50a
Panicle length (cm)	26.80	30.79	25.75b	36.84a
Culm length (cm)	30.32b	33.18	36.72	37.59a
No. of fertile tillers per plant	1.45	1.43	1.71a	1.40b
No. of spkilets per main panicle	149.68b	226.46	205.4	278.00a
No. panicle branch per main panicle	16.96	19.83	16.77b	20.56a
First basal culm internode diameter (mm)	1.60b	2.04	1.82	2.34a
Second basal culm diameter (mm)	1.67b	2.12	2.02	2.43a
Harvest Index (%)	0.25b	0.26	0.32a	0.26
Single plant phytomass (g)	1.79b	2.70	1.91	4.08a
Single plant grain yield (g)	0.45b	0.70	0.63	1.05a
Single plant straw yield (g)	1.34	2.01	1.29b	3.03a
Thousand seed weight (mg)	0.44	0.45	0.40b	0.60a
Head smudge disease incidence (%)	26.79	28.74	43.23a	23.84b
Head smudge disease severity (%)	20.73	18.45	31.30a	14.68b
Lodging index (%)	24.21	17.54	26.95a	13.64b

a= highest value, b= lowest value

5.5.2. Principal component analysis

In the principal component analysis (PCA), to estimate the relative contribution of traits towards the variation in the 21 tef genotypes, the first five principal components (PCs) with eigenvalue greater than one accounted for 85.2% of the entire diversity among the varieties and landraces for all the 19 traits. The percentage contribution of the first five principal

components to gross genetic variation obtained in the current study (85.2%) is not different from Assefa *et al.* (2003) 81%, Adenew *et al.* (2005) 80.6% in tef and Ayana (2001) 79% in sorghum while it is far greater than Assefa *et al.* (1999) 71%.

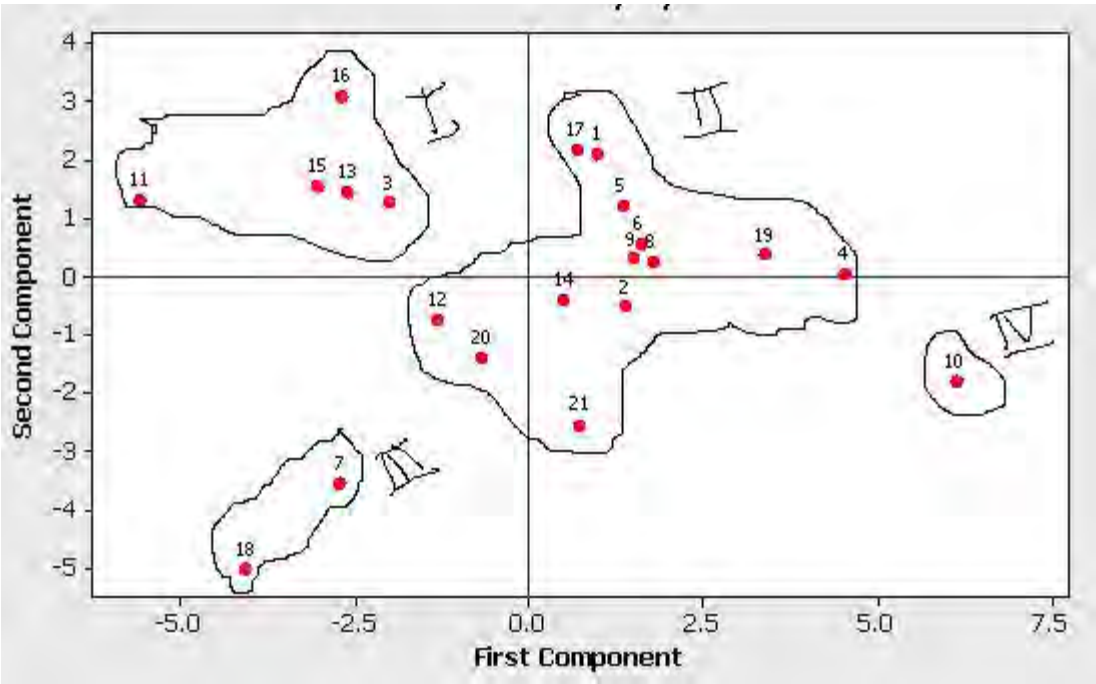
PC_1 accounted for 43.9 % of the variation among the genotypes under investigation. This variation in PC_1 was mainly due to the variation in panicle length, single plant phytomass and straw yield, number of panicle branch per main panicle, first culm basal diameter, plant height, number of spikelets per main panicle, second basal culm diameter, single plant grain yield and lodging index, in that order. All traits, except days to grain filling, fertile tillers per plant, harvest and lodging index as well as disease index (both incidence and severity), had shown a positive polarity (Table 13). Generally, the contribution of PC_1 obtained in this study is in line with Assefa *et al.* (2003) 40% while it is much higher than Assefa *et al.* (2000) 28% and slightly lower than Adenew *et al.* (2005) 55%.

PC_2, on the other hand, accounted for about 20.9 % of the total variation among the varieties and landraces. The variation in this component is mainly resulted from the variation in traits such as severity of head smudge disease, days to maturity, days from heading to grain filling, culm length, harvest index, days to heading and severity of disease index in that order. Except for the three phonological traits, panicle length and number of branch per main panicle all the rest traits showed negative polarity in this component (Table 13).

Furthermore, PC_3 contributed 8.4 % of the total variation in the varieties and landraces which was mainly resulted from number of fertile tillers per plant, harvest index, thousand seed weight and single plant straw yield. Similarly, PC_4 has also contributed for 6.2 % of the total variation in the varieties and landraces. The main source of variation in PC_4 was due to thousand seed weight, days from heading to grain filling and fertile tillers per plant (Table 13). On the other hand, PC_5 contributed for only 5.0 % of the total variation in varieties and landraces and this was mainly resulted from the variation in days from heading to grain filling, culm length, disease severity and incidence, and first and second basal culm diameter.

Table 13. Eigenvalues and eigenvectors of the first five principal components of the19 quantitative traits of 21 tef genotypes at Jimma.

Traits	PC_1	PC_2	PC_3	PC_4	PC_5
Eigenvalue	8.34	3.98	1.60	1.17	1.11
Percent of contribution	43.9	20.9	8.4	6.2	5.0
Cumulative percentage	43.9	64.8	73.2	79.4	85.2
Days to heading	0.233	0.290	0.050	0.063	0.046
Grain filling period (days)	-0.030	0.325	0.126	-0.389	-0.447
Days to maturity	0.195	0.364	0.133	-0.126	-0.112
Plant height (cm)	0.275	-0.180	0.239	0.089	0.229
Panicle length (cm)	0.306	-0.000	0.168	0.045	0.038
Culm length (cm)	0.145	-0.314	0.236	0.043	0.411
No. of fertile tillers per plant	-0.092	-0.155	-0.550	-0.347	0.123
No. of spkilets per main panicle	0.271	-0.228	0.026	-0.144	-0.124
No. panicle branch per main panicle	0.287	0.002	0.109	0.107	-0.257
First basal culm internode diameter (mm)	0.282	-0.184	-0.080	0.101	-0.308
Second basal culm diameter (mm)	0.264	-0.207	0.000	0.156	-0.318
Harvest Index (%)	-0.113	-0.330	0.434	-0.181	-0.063
Single plant phytomass (g)	0.302	-0.068	-0.254	-0.220	0.073
Single plant grain yield (g)	0.255	-0.202	-0.079	-0.290	0.041
Single plant straw yield (g)	0.297	-0.010	-0.311	-0.210	0.084
Thousand seed weight (mg)	0.095	-0.025	-0.348	0.609	-0.209
Head smudge disease incidence (%)	-0.162	-0.370	-0.063	-0.104	-0.327
Head smudge disease severity (%)	-0.215	-0.277	0.087	-0.068	-0.316
Lodging index (%)	-0.255	-0.160	-0.113	0.184	0.048



1=DZ-01-354, 2=DZ-01-99, 3=DZ-01-196, 4=DZ-01-787, 5=DZ-Cr44, 6=DZ-Cr-82, 7=DZ-Cr-37, 8=DZ=Cr-255, 9=DZ-Cr- 358, 10=DZ-01-974, 11=DZ-01-2053 12=DZ-01-1278, 13=DZ-01-1281, 14=DZ-01-1285, 15=DZ-01-1681, 16=DZ-01-2675, 17=DZ-01-899, 18=Ho-Cr-136, 19=DZ-Cr-387, 20=Jimma local-1, 21=Jimma local-2

Fig. 3. Relative position of the 19 released varieties and two landraces in the first and second principal axis.

As it is clearly seen (Fig.3), the varieties and landraces in this study were distributed in all the four quadrants of the principal component axis. DZ-01-974, which remained solitary in cluster IV (Figure 1), was plotted far apart from the group. Varieties number 10, 4 and 19 were highly and positively contributed to the first principal component while varieties number 11, 18, 7, 15 and 16 highly and negatively contributed to principal component one. On the other hand, the traits of varieties number 17, 16, 1, 11, 15, 13 and 3 contributed highly and positively to the second PC while that of number 18, 7, 21, 10 and 20 contributed highly but negatively to the same PC.

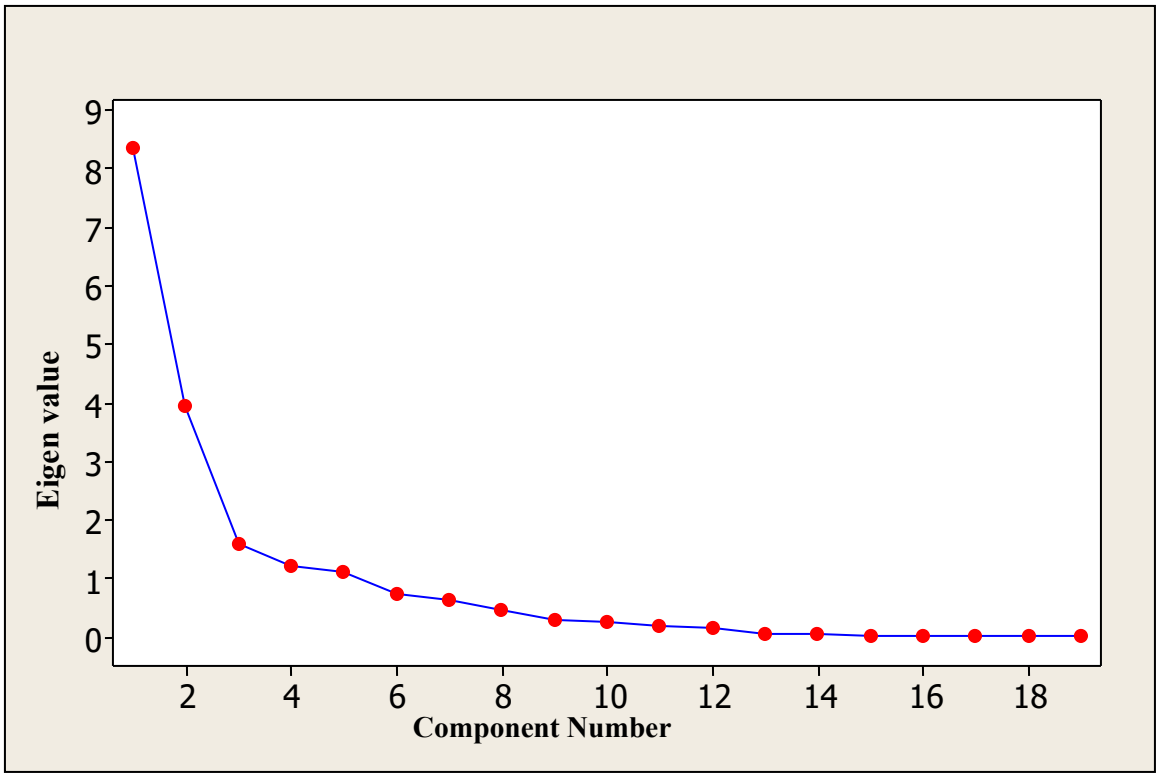


Fig.4 The relative magnitude of contribution of each component to the overall diversity in the 21 varieties and landraces.

The relative contribution of the different PCs were plotted and presented (Fig. 4). There was a sharp decline in contribution from PC1 to PC2 and then from PC2 to PC3 in that order while the rate of decrease in contribution became lower and lower for the remaining PCs. This shows that the first few principal components had the greatest contribution to the overall variation in the varieties and landraces for the 19 traits considered in this study.

5.6. Estimation of genotypes diversity using qualitative traits

The mean data of the three qualitative traits such as panicle form, color of lemma and seed coat showed that there is variation among released varieties and between the two local landraces as well as between landraces and released varieties (Table 14). For the released varieties, the variation was only between varieties and there was no variation within varieties. On the other hand, for the two landraces, the variation was both within and between the landraces.

5.6.1. Diversity among released varieties with respect to three qualitative traits

The 19 released tef varieties were grouped visually into three categories as very white (10.53%), white (73.68%) and brown (15.79%) based on seed coat color. Similarly, for lemma color, only two categories, yellowish white (73.68%) and variegated (26.32%) were obtained. With respect to panicle form, the 19 released varieties were grouped into three categories which include very loose (42.11%), loose (52.63%) and fairly loose (5.26%) while no other panicle forms were observed (Table 15). DZ-01-99, DZ-01-2053 and DZ-01-1681 were brown seeded varieties while DZ-01-196 and DZ-Cr-387 were very white seeded groups. The remaining varieties were found to be white seeded groups. Almost all of the high yielding varieties in this study are among those with very loose and loose panicle form. This is in agreement with what has been reported by Tefera (1988). DZ-Cr-37 and Ho-Cr-136 are varieties with very loose panicle form and they are of early maturing types. Theses two varieties have much more similarities in phenological traits as well as seed coat and lemma color.

5.6.2. Diversity among local landraces with respect to three qualitative traits

The two locals in this study are populations and the data showed that there were observable variations within and between groups (Table 14). These variations were attributed due to differences in panicle form and color of lemma and seed coat.

As to seed coat color, there were only two categories in both populations. Thus, 55 % white and 45 % brown seed coat color was observed for Jimma local-1 while it was 67% white and 33% brown for Jimma local -2. With respect to lemma color, Jimma local-1 had four categories such as yellowish white (51.55%), variegated (14.8%), red (30.25%) and purple (3.4 %) while Jimma local-2 had only three categories: yellowish white (61.6%), red (26.7%) and purple (11.7%). In both landraces, the yellowish white lemma color covered the major proportion as compared to the different lemma colors. Regarding panicle form, there were only two diversity groups in both populations which include 52.5% loose and 47.5 % fairly loose for Jimma local-1 and 40% loose and 60% fairly loose for Jimma local-2. This shows that the majority of the populations are loose panicle type which are said to be high yielder as compared to the compact and semi compact ones. The mean proportion of the seed coat color for the two populations was found to be 61% white and 39 % brown. Similarly, an average proportion of (56.58%) yellowish white, (7.4%) variegated, (28.48%) red and (7.55%) purple lemma color and 46.25% loose and 53.75% fairly loose panicle forms were observed for the two landraces.

Table 14. Mean values for three qualitative traits of 21 tef genotypes tested at Jimma

No.	Varieties/landraces	Seed color			Lemma color				Panicle form				
		1	2	4	1	2	3	4	1	2	3	4	5
1	DZ-01-354 (Enatit)	0	100	0	100	0	0	0	100	0	0	0	0
2	DZ-01-99	0	0	100	0	100	0	0	100	0	0	0	0
3	DZ-01-196 (Magna)	100	0	0	0	100	0	0	0	0	100	0	0
4	DZ-01-787	0	100	0	100	0	0	0	100	0	0	0	0
5	DZ-Cr-44	0	100	0	100	0	0	0	0	100	0	0	0
6	DZ-Cr-82	0	100	0	100	0	0	0	0	100	0	0	0
7	DZ-Cr-37 (Tseday)	0	100	0	100	0	0	0	100	0	0	0	0
8	DZ-Cr-255 (Gibe)	0	100	0	100	0	0	0	0	100	0	0	0
9	DZ-Cr-358 (Ziquala)	0	100	0	100	0	0	0	0	100	0	0	0
10	DZ-01-974 (Dukem)	0	100	0	100	0	0	0	100	0	0	0	0
11	DZ-01-2053(Holeta Key)	0	0	100	0	100	0	0	0	100	0	0	0
12	DZ-01-1278(Ambo-Toke)	0	100	0	100	0	0	0	0	100	0	0	0
13	DZ-01-1281(Gerado)	0	100	0	100	0	0	0	0	100	0	0	0
14	DZ-01-1285 (Koye)	0	100	0	100	0	0	0	0	100	0	0	0
15	DZ-01-1681(Key Tena)	0	0	100	0	100	0	0	100	0	0	0	0
16	DZ-01-2675 (Dega Tef)	0	100	0	100	0	0	0	0	100	0	0	0
17	DZ-01-899 (Gimbichu)	0	100	0	100	0	0	0	0	100	0	0	0
18	Dz-Cr-136 (Amarach)	0	100	0	100	0	0	0	100	0	0	0	0
19	Dz-Cr-387 (Quncho)	100	0	0	0	100	0	0	100	0	0	0	0
	Varieties Mean	**10.53**	**73.68**	**15.79**	**73.68**	**26.32**	**0**	**0**	**42.11**	**52.63**	**5.26**	**0**	**0**
20	Jimma local-1(*Dalasso*)	0	55	45	51.55	14.8	30.25	3.4	0	52.5	47.5	0	0
21	Jimma local-2(*Koche*)	0	67	33	61.6	0	26.7	11.7	0	40	60	0	0
	Population Mean	**0**	**61**	**39**	**56.58**	**7.4**	**28.48**	**7.55**	**0**	**46.25**	**53.75**	**0**	**0**

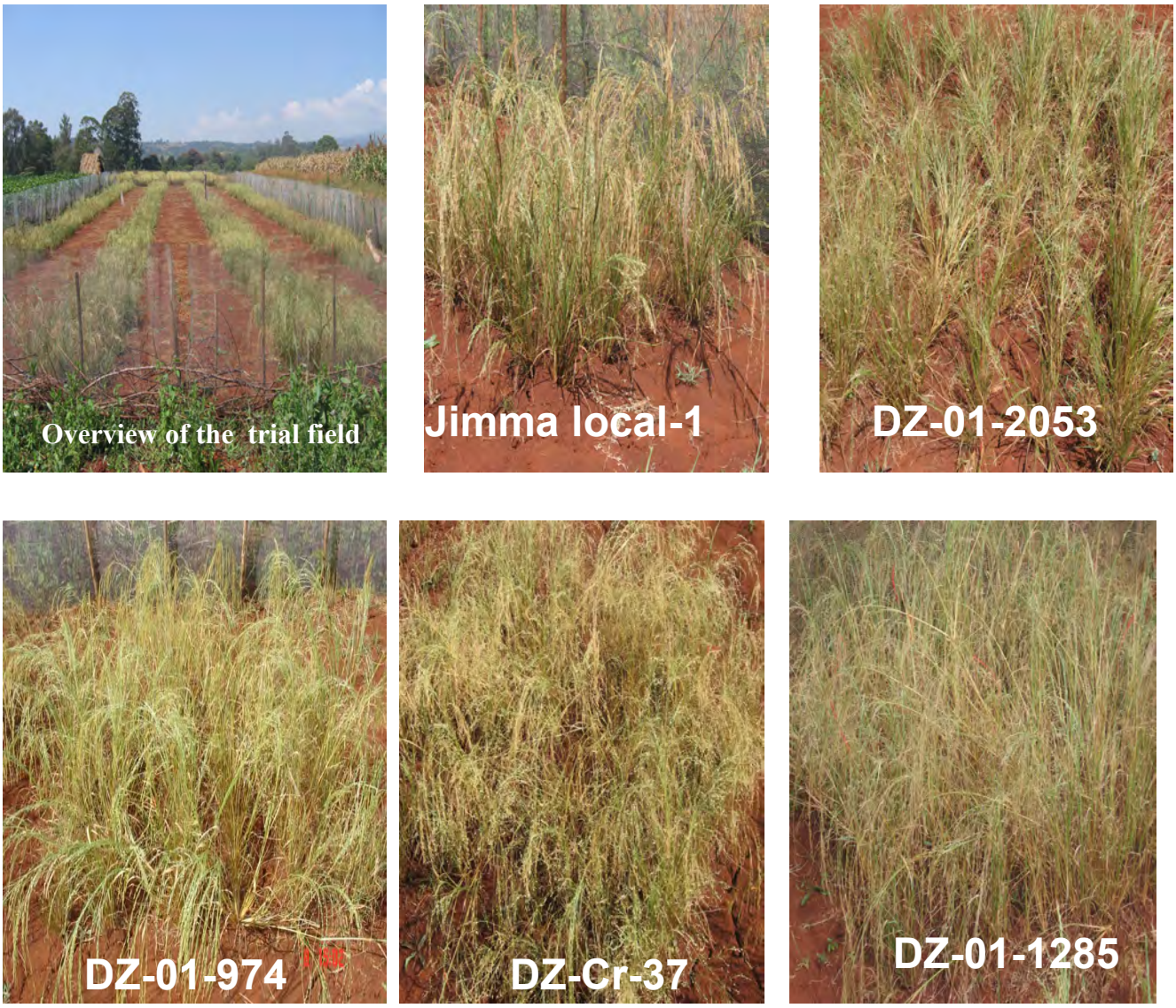


Fig. 5 some observable variation in tef genotypes evaluated at Jimma

6. CONCLUSIONS AND RECOMMENDATIONS

The analysis of variance showed the presence of highly significant differences for all traits except culm length and number of fertile tillers per plant which were significant ($p = 0.05$). Descriptive statistics also showed the presence of wide range of phenotypic variation in the varieties and landraces studied.

The three phonological traits had minimal estimate of GCV and PCV. Lodging index had the highest GCV (31.97%) and PCV (38.74%) values, moderate heritability (68%) and highest GA as percent of the mean values (54.34 %). Heritability in broad sense ranged from 16.87 for harvest index to 93.43% for single plant straw yield. Number of spiklets per panicle had the highest genetic advance (48.04) while harvest index had the lowest value of 0.029.

Single plant grain yield had significant genotypic correlation with all quantitative traits except number of fertile tillers per plant, harvest index and head smudge disease incidence. This trait also showed positive Phenotypic and genotypic correlation with all traits other than days to grain filling period, number of fertile tillers per plant, head smudge disease incidence and severity, and lodging index. The presence of significant genotypic and phenotypic correlation was also detected between phonological traits and most of the quantitative traits. Similarly, lodging index showed significant genotypic and phenotypic association with several traits of tef. It also showed negative phenotypic and genotypic correlation with all traits other than number of fertile tillers per plant, harvest index, head smudge disease incidence and head smudge disease severity. Likewise, head smudge

disease showed negative and significant correlation with most of the quantitative traits considered in this study.

Cluster analysis resulted in the formation of four distinct classes at about 60 % similarity level. The number of genotypes in each cluster ranged from one to thirteen in the smallest and largest cluster, respectively. The first five principal components (PC) with eigenvalue greater than one accounted for 85.2% of the entire diversity among the tef genotypes for the 19 traits. PC_1, PC_2, PC_3, PC_4 and PC_5 each contributed 43.9%, 20.9%, 8.4%, 6.2% and 5%, respectively to the gross genetic variation of the genotypes. Inter cluster distances were highly significant ($P<0.01$) while the intra cluster distance were not significant ($P=0.05$). The maximum (9048.3) and minimum (937.06) inter cluster distance was observed between cluster 1&4, and Cluster 2&4, respectively.

Variations among different released varieties, between, and within the two local landraces were detected on the basis of panicle form, caryopsis and lemma color. Thus, the released varieties were grouped into three caryopsis color (very white, white and brown), three panicle form (very loose, loose and fairly loose), and two lemma color (yellowish white and variegated). For the two landraces, variations were detected both between and within the landraces. Based on these qualitative traits, the landraces were grouped into two caryopsis color (white and brown), two panicle forms (loose and fairly loose), and three lemma colors yellowish white, varigated and red).

Due to some limitations, the present study utilized morphological data only. Future research in this area should, therefore, focus on data supported by DNA analysis. As the

two landraces used in the current study are mixed populations, they should be purified using proper breeding procedures based on their data on qualitative traits. DZ-01-974 was found to be the best performing one with respect to all important traits considered in this study. An adaptation trial should be conducted on this variety to recommend it for the area if its good performance is repeatable and reasonably sustainable.

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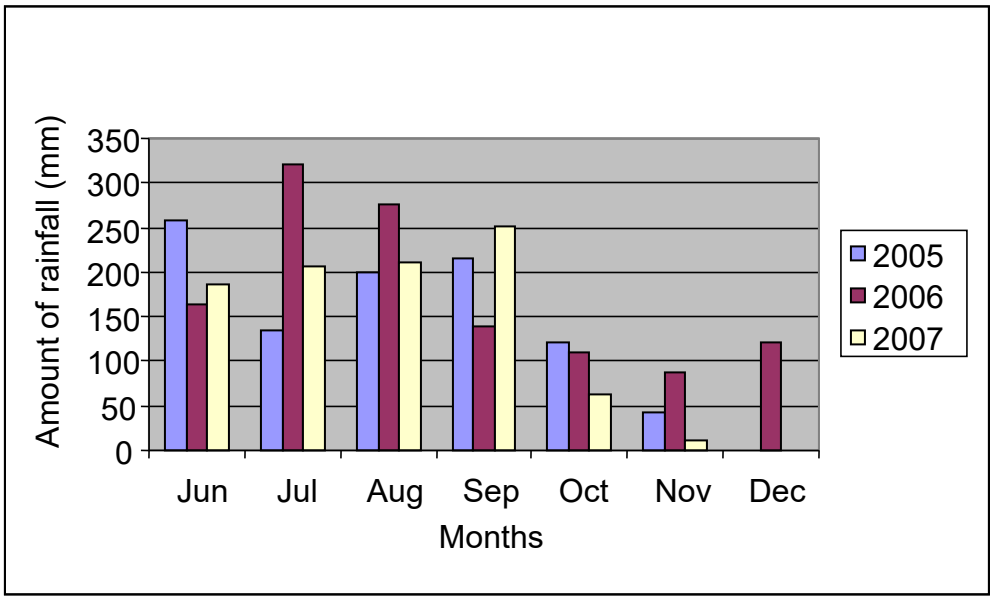
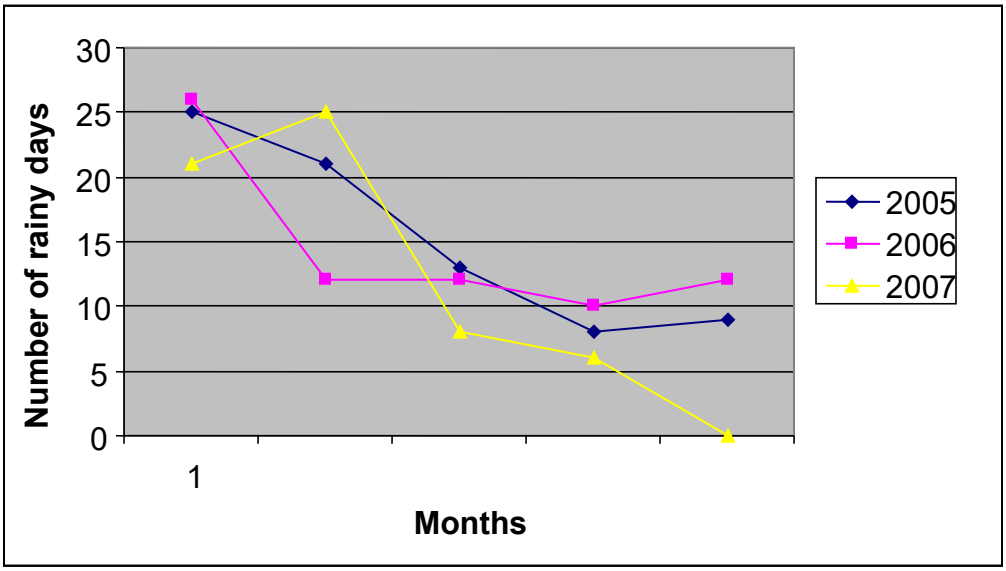
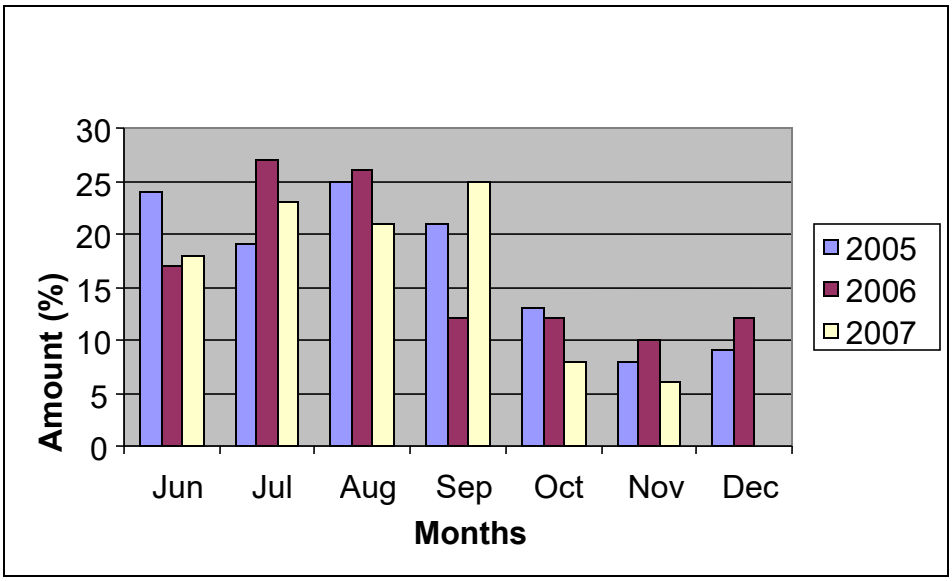
8. APPENDICES



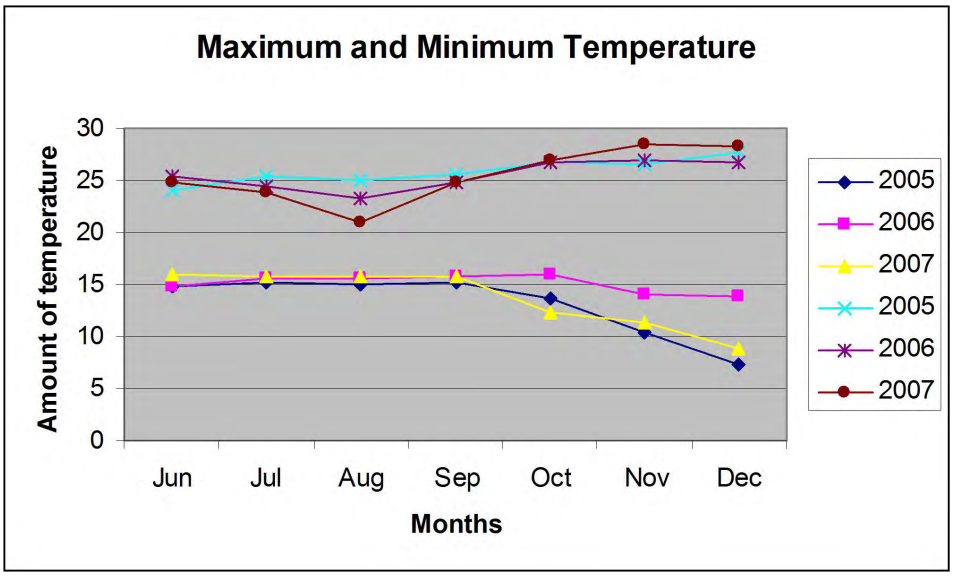
Appendix-1 Rainfall pattern of the study area



Appendix-2 Patterns of number of rain days of the study area



Appendix 3 Humidity of the study area



Appendix 4 Minimum and maximum temperature of the study area

Appendix 5. Mean performances, Standard error of mean, LSD (5%), and CV (%) of 21 tef genotypes

DH=Days to heading, DM=Days to maturity, DGF=Days fro heading to grain filling, PH=plant height, PL=Panicle length, CL= culm length, FT= fertile tillers

Entry	DH	DGF	DM	PH	PL	CL	FT	SPK	PBM	FBCD	SBCD	HI	SPP	SPSY	SPStY	TSW	HIA	HA	LA
1	55.25	44.00	96.75	54.69	27.88	28.72	1.47	192.45	20.06	2.02	2.18	0.23	2.70	0.60	2.10	0.60	24.65	14.47	13.84
2	50.50	43.00	93.50	65.56	30.66	34.41	1.72	213.00	18.44	2.00	2.18	0.25	3.13	0.78	2.35	0.40	26.13	12.83	20.37
3	50.75	42.75	93.50	61.44	28.69	31.97	1.23	147.50	17.41	1.77	1.97	0.23	1.63	0.38	1.25	0.60	26.01	19.21	23.75
4	55.25	42.25	98.50	73.47	37.44	34.50	1.35	287.60	22.22	2.20	2.40	0.22	3.08	0.68	2.33	0.40	25.30	16.26	14.93
5	55.75	45.25	101.00	63.59	30.63	33.19	1.28	198.90	20.47	2.11	2.29	0.28	2.25	0.63	1.63	0.40	29.75	18.42	12.44
6	55.00	45.50	100.50	66.75	33.16	31.19	1.39	220.70	19.25	2.06	2.28	0.28	2.58	0.70	1.88	0.60	31.10	19.10	21.75
7	46.00	41.75	87.75	62.38	26.31	36.06	1.79	230.55	16.41	1.73	1.96	0.33	2.00	0.68	1.33	0.40	39.45	26.50	18.01
8	52.00	45.00	97.00	69.25	33.91	34.25	1.28	236.05	19.22	1.85	1.99	0.29	2.85	0.80	2.05	0.40	26.65	16.83	15.27
9	52.50	45.00	97.50	61.97	30.06	31.91	1.72	236.50	19.56	2.08	2.06	0.25	3.08	0.78	2.30	0.40	29.73	17.79	15.88
10	53.25	41.75	96.00	76.50	36.84	37.59	1.40	278.00	20.56	2.34	2.43	0.26	4.08	1.05	3.03	0.60	23.84	14.68	13.64
11	47.25	45.00	92.25	51.06	25.63	28.50	1.64	124.25	13.63	1.46	1.44	0.23	1.93	0.45	1.48	0.40	33.32	22.64	35.48
12	47.00	45.25	92.25	58.84	28.13	31.81	1.09	228.10	18.47	1.83	1.97	0.32	2.35	0.75	1.60	0.40	29.89	21.58	25.98
13	48.00	45.50	94.75	56.63	28.13	29.34	1.41	175.25	18.41	1.78	1.76	0.26	1.75	0.45	1.30	0.40	27.24	23.05	18.82
14	49.75	46.50	96.25	61.97	31.00	30.97	1.39	225.85	19.56	2.18	2.33	0.26	2.60	0.68	1.93	0.40	35.47	27.64	16.40
15	50.25	45.50	95.75	61.19	27.31	33.88	1.46	146.95	17.66	1.52	1.67	0.28	1.55	0.43	1.13	0.40	24.58	22.32	20.60
16	54.00	44.50	98.50	52.16	24.25	27.91	1.53	154.45	17.69	1.50	1.53	0.26	2.10	0.55	1.55	0.40	22.81	16.44	22.40
17	55.50	44.50	100.00	60.50	28.97	32.34	1.54	205.45	19.72	1.84	1.67	0.23	2.63	0.60	2.28	0.40	26.81	18.96	11.30
18	46.25	40.50	86.75	62.56	25.19	37.38	1.63	180.25	17.13	1.92	2.08	0.32	1.83	0.58	1.25	0.40	47.02	36.10	35.90
19	55.75	43.50	99.25	73.75	33.03	40.72	1.20	214.30	19.84	2.14	2.16	0.26	2.88	0.75	2.13	0.40	21.84	14.66	14.03
20	48.75	41.75	90.50	62.25	28.50	32.66	1.36	241.10	20.91	2.03	1.89	0.30	1.98	0.60	1.38	0.50	31.15	18.11	23.32
21	47.75	43.50	91.25	61.63	26.94	34.69	1.79	244.00	20.03	2.26	2.25	0.26	2.98	0.78	2.25	0.60	35.15	23.25	22.48
Mean	51.26	43.92	95.21	62.78	29.66	33.06	1.46	208.63	18.92	1.93	2.02	0.27	2.48	0.65	1.82	0.45	29.40	20.04	19.84
S.E.±	0.396	0.262	0.465	0.944	0.492	0.552	0.036	6.210	0.285	0.038	0.041	0.005	0.070	0.019	0.055	0.010	0.819	0.674	0.831
LSD (5%)	2.133	2.915	2.551	9.300	4.45	6.44	0.41	61.97	2.833	0.42	0.40	0.063	0.28	0.127	0.184	0.045	7.37	5.17	6.142
CV(%)	2.94	4.69	18.95	10.47	10.60	13.76	19.94	21.00	10.61	15.31	14.12	16.83	7.97	13.76	7.15	7.06	17.72	18.54	21.89

per plant, SPK=number of spkilets per main panicle, PBM=panicle branch per main panicle, FBCD=first culm basal diameter, SBCD=second culm basal diameter, HI= harvest Index, SPP=single plant phytomass, SPSY=single plant grain yield, SPStY=single plant straw yield, TSW= thousand seed weight, HIA=Head smudge disease incidence, HSA=Head smudge disease severity and LA=lodging index.

DECLARATION

This thesis is my original work, has not been presented for a degree in any University and that all sources of materials used for the thesis have been duly acknowledged.

Name: Habte Jifar___

Signature: _____

Date: June 26, 2008____

This work has been presented with my approval as a supervisor.

1/ Name:

Signature: _____

Date: