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Research Article

Cluster and Principal Component Analysis of Drought Tolerant Tef [*Eragrostis Tef(Zucc.) Trotter*] Genotypes

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ABSTRACT

Breeding for high yield crop requires information on the nature and magnitude of variation in the available materials, relationship of yield with other agronomic characters and the degree of environmental influence on the expression of these components characters. Hierarchical cluster analysis and principal component analysis is useful guide to evaluation of different genotypes. This study was conducted with the aim of identifying better performing drought tolerant tef genotypes and related traits with the help of principal component analysis and cluster analysis of major quantitative traits of the crop. Cluster analysis based on Unweighted Pair Group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix estimated 12 clusters of 49 tef genotypes. The genetic distance of for all possible pair wise of tef genotypes ranged from 1.90 to 11.21. Principal components analysis revealed that five principal components with Eigen-values greater than unity accounted for 79% of tef genotypes.

Keywords: Tef, Cluster; Euclidean distance; Principal Components (PCs)

INTRODUCTION

Tef [*Eragrostis tef (Zucc.)*] Trotter is endemic to Ethiopia and its domestication is estimated to have occurred between 4000 and 1000 BC [1]. Tef is also cultivated in very small quantities in Eritrea and recently in the USA, the Netherlands and Israel. Ethiopia, where tef is the main cereal crop and food shortage is a recurring phenomenon, exerts an export ban on tef which increased interest in growing tef outside Ethiopia increased.

Currently, the crop is increasingly receiving global attention for its nutritional advantages because it is rich in nutrients and is gluten free. Consumers prefer tef not only because it makes good quality "injera", a pancake-like soft bread, but also it is nutritious due to its high protein and mineral content [2], and the absence of gluten [3] which makes it an alternative food for people suffering from celiac disease. Due to this "life-style" nature of the crop, it has been heralded as a super food or super grain [4,5]. It contains 11% protein, 80% complex carbohydrates and 3% fat [6]. Tef grows under a wide range of ecological conditions from sea level up to 3000 meters above sea level (m.a.s.l). It is annually cultivated on over three million hectares of land, and a such it accounting for about 30% of the total area and 20% of the gross grain production of cereals grown in the country [7]. Tef has the genetic potential to yield up to 6 tha-1 [8] and it is a staple food supporting over 70 million people in Ethiopia [7].

Despite its numerous relative advantages and economic importance, the productivity of tef in Ethiopia is low amounting to 1.66 tons ha-1 [7]. The major yield limiting factors in tef are lack of cultivars tolerant to lodging and drought [9], as well as small seed size. Yield losses are estimated to reach up to 40% during severe moisture stress [10]. Although early studies in tef showed considerable genotypic variations in drought tolerance in relation to depth of root growth and osmotic adjustment [10], information on drought tolerance based on grain yield is scanty. Since abiotic stresses such as drought, salinity and heat as well as the changing climate substantially affect the productivity of crops and food security, future research should focus on developing resistance or tolerance against these environmental calamities [11].

Tef breeders need to continuously search for new sources of resistance or tolerance and introgress these genes into susceptible cultivars. Screening of tef genotypes using both phenotypic and genotypic data are important to identify drought resilient breeding lines [12]. This requires knowledge on the extent and pattern of genetic variability present in a population. Similarly, information on the extent and nature of interrelationships among traits helps in planning, evaluating and formulating efficient scheme of multiple trait selection. Besides, knowledge of the naturally occurring diversity in a population helps identify diverse groups of

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tef genotypes in terms of high grain yield, tolerance or resistance to low moisture, lodging resistance, early maturity and desirable grain quality [13].

Dissimilarity will always exist among individuals in a population and assessing the origin and magnitude of variability is the key to success in a crop improvement program [14]. The genetic distance thus reflects the expected mean number of changes per site that have occurred, since two sequences diverged from their common ancestor. Euclidean distance developed by Sneath and Sokal (1973) [15], has been used to classify the divergent genotypes into different groups. According to Habte et al. tef genotypes were clustered in to seven. The genetic improvement through hybridization and selection depends on the extent of genetic diversity between parents. Crossing for desirable traits can be successful between clusters with the highest and the lowest divergent cluster [16,17].

The principal components is used to interpreted based on finding which variables are most strongly correlated with each component i.e, which of these numbers are larger in magnitude, the further from zero in either positive or negative direction. Having correlation value above 0.5 is deemed important [18]. According to Habtamu et al. Eigenvalues greater than one were only for the first three PCs, which together explained 75% of the observed variation [19]. Plaza-Wüthrich et al.(2013) observed four principal components (PCs), having eigenvalues between 5.16 and 1.12 [20]. According to Habte et al. report the first three principal components (PCs) with eigenvalue greater than one contributed for 78.3 % of the entire phenotypic variation observed among the 36 tef genotypes. Therefore, the current study was to assess better performing drought tolerant tef genotypes and related traits with the help of principal component analysis and cluster analysis.

MATERIALS AND METHODS

Experimental sites, designs and experimental materials

Field trials were conducted during the 2017 cropping season at two locations (Melkassa 8o 24' N, 39o 21' E and Alemtena 8o 20' N, 38o 57' E) in the Central Rift Valley of Ethiopia. Both Alemtena and Melkassa are drought prone areas with andosols of very light soils that show low capacity of water retention The poor rainfall distribution is coupled with relatively high temperature, which makes the area vulnerable to moisture stress.

The testing field at Melkassa is andosol with 20.4% sand, 39.6% silt, 40% clay, pH=7.4, 0.8% organic matter, 13.7 ppm available phosphorous (P), and Cation Exchange Capacity (CEC) of 20.4 Milli-Equivalents (MEQ)/100 g of soil. The soil at Alemtena is light soil with 22.4% sand, 37.6% silt, 40.0% clay, 7.7, pH (H2O 1:1), 0.8% organic matter, 0.08% total nitrogen (N), 7.79 ppm available phosphorous (P), and Cation Exchange Capacity (CEC) of 22.4 Milli-Equivalents (MEQ)/100 g of soil.

Forty nine genotypes, including 42 drought tolerant advanced lines, four parents of the advanced lines, two varieties, and a local check were used for this study. The seeds of all genotypes were obtained from Debre Zeit Agricultural Research Center (DZARC) (Table 1). The experiment was laid out in a 7x7 simple lattice design. Each experimental plot was 1 m2 (1 m x 1 m) and consisted of five rows spaced 20 cm apart. The distances between both incomplete blocks and plots within incomplete blocks were 1m, and that between replications was 1.5 m. As per the research recommendations of 15 kg/ha, 1.5 g/plot of seeds were hand broadcasted along the surface of each row. The full dose of blended fertilizer recommended for the study area were 21.74 kg Urea and 158 kg NPS per hectare at both locations. All other cultural and management practices were performed as per the recommendations for the test locations.

Table 1: Clustering of 42 drought tolerant tef advanced lines, 2 released varieties, 4 parental lines and a local check local check cultivar into 12 cluster estimated from 18 response traits.

Cluster	No. genotype	Genotype include in this cluster
C I	6	Dtt2 X Dtt13(RIL-22, RIL-125, RIL-72, RIL-119), Dtt2 and Simada
C II	8	Dtt2 X Dtt13 (RIL-30, RIL-69, RIL-106, RIL-92, RIL-56, RIL-70, RIL-11) and Dtt13
C III	6	Dtt2 X Dtt13 (RIL-37, RIL -78), Dtt2 X Kaye Murri (RIL-438, RIL-82, RIL-105, RIL-5)
C IV	3	DZ-Cr-387 X Dtt2 (RIL-15), Dtt2 X Kaye Murri (RIL-37) and Dtt2 X Kaye Murri (RIL-114)
C V	7	DZ-Cr-387 X Dtt2 (RIL-102, RIL-426), Dtt2 X Kaye Murri (RIL-168, RIL-103, RIL-117, RIL-135) and Tsedey
C VI	3	DZ-Cr-387 X Dtt2 (RIL-98, RIL-19) and Dtt2 X Kaye Murri (RIL-61)
C VII	4	DZ-Cr-387 X Dtt2 (RIL-85, RIL-207, RIL-179, RIL-160)
C VIII	6	DZ-Cr-387 X Dtt2 (RIL-106, RIL-136, RIL-118), Dtt2 X Kaye Murri (RIL-16, RIL-147) and local check
C IX	1	DZ-Cr-387 X Dtt2 (RIL- 287)
C X	1	Dtt2 X Kaye Murri (RIL-76)
C XI	3	Dtt2 X Dtt13 (RIL-45), DZ-Cr-387 X Dtt2 (RIL-115) and Quncho
C XII	1	Kaye Murri

RIL= Recombinant inbred line, DZ-Cr= Debre Zeit Cross

Data Collected

Data were recorded for days to seedling 50% emergence, days to 50% heading, days to 90% physiological maturity, grain filling period, plant height (cm), panicle length (cm), penduncle length (cm), culm length (cm), number of spikelets per panicle, numbers of primary panicle branches per main shoot, number of florets per spikelet, number of total tillers per plant, number of fertile tillers per plant, lodging index (%), total above-ground biomass (kg/ha), grain yield (kg/ha), harvest index (%), thousand-seed weight (g).

Statistical data analysis

The cluster analysis was performed based on Unweighted Pair Group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix following the average linkage method by Statistical Software. Genetic distance of 49 tef genotypes were estimated using Euclidean Distance (ED) calculated from quantitative traits after standardization (subtracting the mean value and dividing it by the standard deviation) as established by as follows; where; EDjk=distance between genotypes j and k; Xij and Xik = phenotype traits values of the ith character for genotypes j and k, respectively; and n=number of phenotype traits used to calculate the distance. In addition, mean ED will be calculated for each genotype by averaging of a particular genotype to the other 49 tef genotypes. The calculated average distance (ED) was used to estimate which genotype(s) are closest or distant to others.

The pre-standardized trait mean data of the test tef genotypes were used for principal components analysis in order to identify the major traits accounting for much of the gross observed variability among the genotypes. The principal component variables are

defined as linear combinations of the original variables Xl...,Xk... ,Xm. The Extracted eigenvectors table provides coefficients for equations below (Origin Lab. Corporation, 2016).

Where; Yk is the kth principal component k and C's are the coefficients in table.

According to Holland suggested standard criteria that permit to ignore components whose variance explained is less than 1 when a correlation matrix is used for determining number of PCs should be investigated was employed. The data were standardized to mean zero and variance of one before computing principal component analysis. The principal component based on correlation matrix was calculated using MINITAB software.

RESULT AND DISCUSSION

Clustering and Genetic Divergence Analyses

Clustering of genotypes: The cluster analysis based on Unweighted Pair Group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix estimated 49 tef genotypes into 12 major clusters of 1 to 8 genotypes (Figure 1 and Table 1). The first cluster (C I) comprised 12% of tef genotypes, and the commercial variety Simada, which was released for the low moisture stress areas and mutagenized parent tef genotype (Dtt2) included along with six recombinant inbred lines.

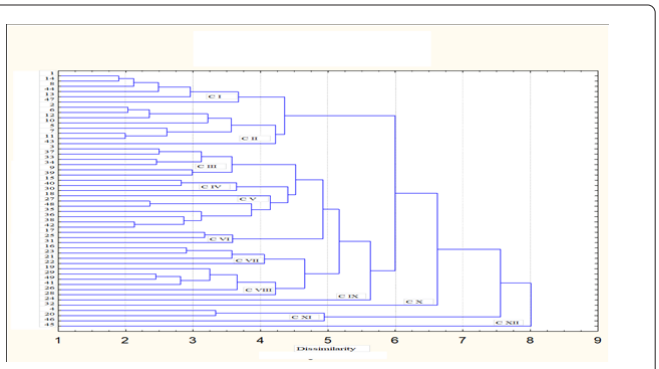

Figure 1: Dendrogram depicting dissimilarity of tef genotypes (1-49) genotypes code by Unweighted Pair Group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix estimated from 18 phenology, growth traits, grain yield and yield components.

The second cluster (C II) was the largest cluster included 16% of tef genotypes comprising a total of 8 genotypes, all genotypes resulting from parents crosses of (Dtt2 X Dtt13) and tef mutagenized parent (Dtt13) itself. On the other hand, the third cluster (CIII) comprised 6 tef genotypes resulting from crosses of Dtt2 X Dtt13 and Dtt2 X Kaye Murri. Cluster IV, V, VI, VII, VIII and XI consisted 3, 7, 3, 4, 6 and 3 tef genotypes, correspondingly, resulting from two independent crosses DZ-Cr-387 X Dtt2 and Dtt2 X Kaye Murri except for cluster V, VIII and XI consisted of Tseday which was released for low moisture stress area, local check and popular variety, respectively (Figure 1). Finally, Cluster IX, X and XII were solitary containing DZ-Cr-387 X Dtt2 (RIL- 287), Dtt2 X Kaye Murri (RIL-76) and Kaye Murri, respectively (Figure 1 and Table 1).

The result showed that, in most cases the genotypes resulting from crosses of the same parents clustered together, this may be attributed to an exchange of genetic materials between the parents. The different genotypes grouped within a given cluster were assumed to be more closely related in terms of the studied traits than those genotypes grouped into different clusters. The current cluster analysis indicated the existence of variability even among the lines resulting from the crosses of the same parents. Similar to the present results, Demeke et al. found variability in recombinant inbred lines of the cross of Eragrostis tef x Eragrostis pilosa.

Clustering of mean analysis: The mean values of the 18 quantitative characters in each cluster are presented. Cluster I is characterized by low values of plant height (84.06 cm), panicle length (31.87 cm), culm length (52.19 cm) and number of florets per spikelet (5.94). While, the genotypes in this cluster exhibited high values for number of total tillers per plant (7.93), number of fertile tillers per plant (6.80), lodging index (91.58%) and harvest index (18.56%). These implies that the members of this cluster were generally short in plant height and culm length, and had large number of total and fertile tillers per plant. Hence, they can be selected for these traits but not for number of florets per spikelet, panicle length and lodging index.

Cluster II, which consisted of 8 genotypes, is relatively low mean values of days to heading (30.21), days to physiological maturity (71.08), above-ground biomass (14812.00 kg/ha) and high mean values of lodging index (92.25%) as compared to the other clusters. This indicates that genotypes in cluster II could be selected for early maturity performance of traits for future crop improvement. Cluster III that contained 6 genotypes is characterized by low values of peduncle length and thousand-seed weight. Cluster IV consisted of 3 genotypes (Dtt2 X Kaye Murri (RIL-117), DZ-Cr-387 X Dtt2 (RIL-118) and Dtt2 X Dtt13 (RIL-119)) and it is characterized by relatively high values for grain yield (3408 kg/ha) (Table 2). Hence these genotypes are better for yield and could help improve tef varieties especially for yield improvement.

Cluster V, VI, VII, VIII, IX and X characterized as medium mean values for all traits except low mean values of number of total tillers per plant (5.48) and number of fertile tillers per plant (4.43) for genotypes included in the cluster VI and low thousand-seed weight (0.25 g) for genotype in the cluster IX. Cluster XI comprised 3 genotypes and characterized by high mean values of plant height, panicle length and number of spikeletes per panicle. This indicates that genotypes in this cluster can be selected mainly for above mentioned characters. Cluster XII consisted only one genotype characterized by low value of grain yield (1670.0 kg/ha), harvest index (9.89%) and lodging index (70.50%) (Table 2). This indicates that this genotype can be selected mainly for lodging index for future breeding methods chiefly for hybridization.

Genetic distance analysis: The genetic distance for all possible pair wise of 1176 tef genotypes ranged from 1.90 to 11.21 with mean, standard deviation and coefficient of variation of 5.66, 1.44 and 25.58%, respectively (Table 2). The highest genetic distances (Euclidean distance) was computed between Quncho and Dtt13 (11.21) followed by between Quncho and Dtt2 X Dtt13 (RIL-92) (11.05) and Quncho and Dtt2 X Dtt13 (RIL-69) (11.0), Simada and Key Murri (10.7), Dtt2 X Dtt13 (RIL-92) and Dtt2 X Dtt13 (RIL-45) (10.7), Dtt2 X Dtt13 (RIL-69) and Dtt2 X Dtt13 (RIL-45) (10.5). Whereas, the lowest genetic distances (Euclidean distance) was estimated between Dtt2 X Dtt13 (RIL-125) and Dtt2 X Dtt13 (RIL-22) (1.90), Dtt2 X Dtt13 (RIL-125) and Dtt2 X Dtt13 (RIL-72) (1.99), Dtt2 X Dtt13 (RIL-69) and Dtt2 X Dtt13 (RIL-30) (2.0), Dtt2 X Dtt13 (RIL-106) and Dtt2 X Dtt13 (RIL-30) (2.1) and, Dtt2 X Dtt13 (RIL-72) and Dtt2 X Dtt13 (RIL-22) (2.3)

Table 2: Molecular weight and amino acid frequency distribution of the

protein.

Genotype	Minimum	Maximum	Mean	SD	CV(%)
Dtt2 X Dtt13 (RIL-22)	1.9	9.61	5.51	1.84	33.4
Dtt2 X Dtt13 (RIL-30)	2.03	6.62	5.09	1.83	35.88
Dtt2 X Dtt13 (RIL-37)	2.5	7.15	4.75	1.07	22.59
Dtt2 X Dtt13 (RIL-45)	3.33	10.6	7.32	1.84	25.15
Dtt2 X Dtt13 (RIL-56)	2.22	10.33	5.83	1.66	28.37
Dtt2 X Dtt13 (RIL-69)	2.03	11.03	6.01	2.06	34.32
Dtt2 X Dtt13 (RIL-70)	1.99	9.74	5.46	1.69	31
Dtt2 X Dtt13 (RIL-72)	2.03	9.65	5.27	1.74	33.03
Dtt2 X Dtt13 (RIL -78)	2.81	7.06	5.04	1.13	22.52
Dtt2 X Dtt13 (RIL-92)	2.87	11.05	6.63	1.82	27.4
Dtt2 X Dtt13 (RIL-96)	1.99	9.73	5.2	1.89	36.34
Dtt2 X Dtt13 (RIL-106)	2.1	10.39	5.58	1.98	35.43
Dtt2 X Dtt13 (RIL-119)	2.57	9.66	5.85	1.78	30.5
Dtt2 X Dtt13 (RIL-125)	1.9	10.35	5.68	2.02	35.57
DZ-Cr-387 X Dtt2 (RIL-15)	2.83	7.88	5.37	1.18	21.98
DZ-Cr-387 X Dtt2 (RIL-85)	2.9	7.96	5.25	1.12	21.43
DZ-Cr-387 X Dtt2 (RIL-98)	3.17	7.67	5.15	1.13	22.01
DZ-Cr-387 X Dtt2 (RIL-102)	3.45	9.22	5.49	1.27	23.08
DZ-Cr-387 X Dtt2 (RIL-106)	2.89	7.14	4.86	1.13	23.25
DZ-Cr-387 X Dtt2 (RIL-115)	3.33	10.37	7.1	1.73	24.42
DZ-Cr-387 X Dtt2 (RIL-160)	3.18	8.52	5.67	1.12	19.72
DZ-Cr-387 X Dtt2 (RIL-179)	3.18	7.68	5.43	1.09	20.12
DZ-Cr-387 X Dtt2 (RIL-207)	2.9	7.37	5.27	1.05	20.01
DZ-Cr-387 X Dtt2 (RIL- 287)	4.1	9.36	6.38	1.39	21.7
DZ-Cr-387 X Dtt2 (RIL-19)	3.17	8.42	5.79	1.23	21.17
DZ-Cr-387 X Dtt2 (RIL-136)	3.49	8.55	5.89	1.37	23.33
DZ-Cr-387 X Dtt2 (RIL-426)	2.36	8.25	5.14	1.17	22.83
DZ-Cr-387 X Dtt2 (RIL-118)	3.33	9.15	6.48	1.46	22.55
Dtt2 X Kaye Murri (RIL-16)	2.45	7.91	5.43	1.34	24.73
Dtt2 X Kaye Murri (RIL-37)	3.46	8.23	5.44	1.1	20.28
Dtt2 X Kaye Murri (RIL-61)	3.58	9.04	6.02	1.27	21.16
Dtt2 X Kaye Murri (RIL-76)	4.75	9.98	6.77	1.1	16.23
Dtt2 X Kaye Murri (RIL-438)	2.46	8.3	5.4	1.25	23.24
Dtt2 X Kaye Murri (RIL-82)	2.46	7.54	5.05	1.25	24.66
Dtt2 X Kaye Murri (RIL-168)	2.33	8.34	5.52	1.3	23.5
Dtt2 X Kaye Murri (RIL-103)	2.68	8.07	4.54	1.24	27.35
Dtt2 X Kaye Murri (RIL-105)	2.5	7.28	4.88	0.98	20.15
Dtt2 X Kaye Murri (RIL-117)	2.13	8.17	5.04	1.29	25.71
Dtt2 X Kaye Murri (RIL-5)	2.99	8.39	5.08	1.14	22.53
Dtt2 X Kaye Murri (RIL-114)	2.83	7.67	4.86	1.11	22.92
Dtt2 X Kaye Murri (RIL-147)	2.68	7.3	5.11	1.27	24.82
Dtt2 X Kaye Murri (RIL-135)	2.13	8.82	4.8	1.43	29.68
Dtt13	3.38	11.21	6.19	1.94	31.36
Dtt2	2.19	10.16	5.46	1.91	34.91
Kay Murri	4.57	10.71	8.01	1.32	16.44
Quncho	4.13	11.21	7.91	1.87	23.69
Simada	2.88	10.71	6.49	1.74	26.85
Tsedey	2.36	9.45	5.06	1.43	28.3
Local check	2.45	8.08	5.67	1.46	25.76
Overall Mean	2.82	8.92	5.66	1.44	25.58
SD= Standard Deviation	Ala	Ala	Ala	Ala	Ala

The genetic distances among four independent parental crosses ranged between 11.21 (Quncho and Dtt13), 10.50 (Dtt2 and Kaye Murri) and 3.81 (Dtt2 and Dtt13). While, the two released varieties for moisture stress area which were used as check estimated genetic distances (Euclidean distance) of 4.64 (Simada and Tseday). The mean genetic distance, standard deviation and coefficient of variation among four independent parental crosses (Quncho, Dtt13, Dtt2, Kaye Murri and Quncho) were 6.89, 1.76 and 26.60%, respectively. The mean genetic distance, standard deviation and coefficient of variation among released varieties for moisture stress were 5.77, 1.58 and 27.57% respectively.

Generally, Euclidean distance among 49 tef genotypes estimated from 18 quantitative traits showed that 51% lower than minimum mean and 47% higher than maximum mean respectively. These suggested that the presence of large number of distant tef genotypes to others that could be used in crossing program to combine the desirable traits of the genotypes.

Principal Component Analysis (PCA)

Interpretation of the principal components is based on finding which of the studied variables are most strongly correlated with each component (i.e., which of these Eigenvectors are large in magnitude, the farthest from zero in either positive or negative direction).

As Holland suggested, standard criteria permit to ignore components whose Eigen values are less than 1 when a correlation matrix is used. In the present study, the principal components analysis revealed that five principal components with Eigen-values greater than unity accounted for 79% of the gross variability in 18 phenomorhic characters (Table 3 and Figure 2). Similarly, Kebebew et al. reported that about 71-79% of the variation in 320 tef germplasm lines was explained by five PCs. Likewise, Tsion reported that 76% of the total variation among 49 tef varieties evaluated for 23 traits

was explained by six PCs.

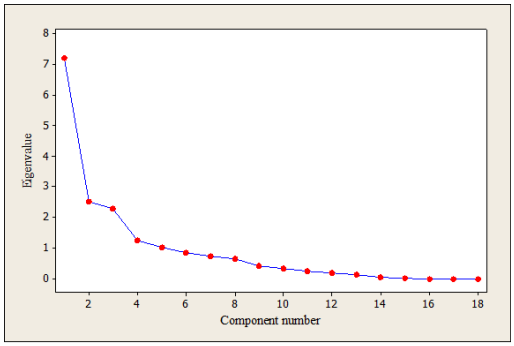

Figure 2: Screen plot of eigenvalue verses component number of 18 quantitative traits in 49 drought tolerant tef genotypes.

Table 3: Eigenvectors, eigenvalues and percentage of total variance explained by the first five principal components (PC) for 18 traits in 49 tef genotypes.

Traits	Eigenvectors				
	PC1	PC2	PC3	PC4	PC5
Days to seedling emergence	-0.11	-0.23	0.28	0.27	-0.5
Days to heading	0.33	0.17	-0.05	-0.17	0.15
Days to physiological maturity	0.32	-0.23	-0.05	0.00	0.1
Grain filling period (days)	0.05	-0.52	-0.01	0.2	-0.04
Plant height (cm)	0.36	-0.05	0.05	0.08	0.03
Panicle length (cm)	0.34	-0.05	-0.09	0.11	0.07
Culm length (cm)	0.32	-0.04	0.16	0.05	-0.01
Peduncle length (cm)	0.01	-0.36	0.21	0.09	-0.08
No. of spikelets/ panicle	0.29	-0.01	-0.13	-0.11	-0.31
No. of primary panicle branches per main shoot	0.28	0.17	-0.13	-0.23	-0.24
No. florets/spikelet	0.07	0.25	-0.08	-0.04	-0.72
No. total tillers/plant	-0.1	-0.4	-0.34	-0.38	-0.06
No. fertile tillers/ plant	-0.13	-0.39	-0.34	-0.36	-0.09
Lodging index (%)	-0.25	0.07	-0.22	0.27	0.05
Biomass yield (kg/ha)	0.28	-0.04	-0.32	0.2	0.07
Grain yield (kg/ha)	0.06	0.07	-0.56	0.39	0.01
Harvest index (%)	-0.25	0.13	-0.32	0.26	-0.09
Thousand-seed weight (g)	0.16	-0.19	0.04	0.4	-0.05
Eigen values	7.19	2.51	2.28	1.25	1.03
% of variance explained	40	14	13	7	6
Cumulative % of variance explained	40	54	67	74	79

The first principal component alone explained 40% of the total variation, while PC2, PC3, PC4 and PC5 in that order accounted for 14%, 13%, 7%, and 6% of the gross observed variation among the test tef genotypes. The first three PCs together accounted for a cumulative of 67% of the total variation indicting that much of the variability among the test genotypes originated from the traits included in these PCs.

Among the 18 traits studied, 10 of them had high contribution effect to the first PC, and these traits included days to heading, days to physiological maturity, plant height, panicle length, culm length, number of spikelets per panicle, number of primary panicle branches per main shoot, lodging index, above-ground biomass and harvest index. The second component predominantly illustrates variation in grain filling period, number of total tillers per plant, number of fertile tillers per plant, days to mature, peduncle length, number of florets per spikelet and thousand-seed weight.

DISCUSSION

The third principal component was chiefly accounted by variation in days to seedling emergence, culm length, peduncle length, lodging index, above-ground biomass yield, grain yield, harvest index, number of total and fertile tillers per plant. The fourth principal component indicated with high variation in grain filling period, fertile tiller per plant, total tiller per plant, days to seedling emergence, lodging index, grain yield, harvest index and thousand-seed weight. The fifth principal component that accounted for about 6% of the total variation was due mainly to high variation in days to seedling emergence, number of spikelets per panicle, number of primary panicle branches per main shoot and number of florets per spikelet (Table 4 and Figure 2).

CONCLUSION

The cluster analysis of the 49 tef test genotypes based on Unweighted Pair Group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix estimated from 18 quantitative traits gave 12 major clusters. Most of lines developed from Dtt2 X Dtt13 were grouped in the same clusters. The genetic distance for all possible pair-wise combinations of the tef test genotypes ranged from 1.90 to 11.21. The highest genetic distances (Euclidean distance) was computed between Quncho and Dtt13 (11.21). In most cases the lowest genetic distances was estimated for lines developed between Dtt2 X Dtt13. The principal components analysis revealed that five principal components with Eigen-values greater than unity accounted for 79% of the gross variability observed for 18 traits of 49 tef genotypes. The first principal component alone explained 40% of the total variation, while PC2, PC3, PC4 and PC5 in that order accounted for 14%, 13%, 7%, and 6% of the gross observed variation among the test tef genotypes.

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