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Cluster analysis of drought tolerant tef genotypes

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ABSTRACT

Aim: The study was aimed to investigate cluster analysis of drought tolerant tef genotypes**.**
Materials and Methods: Forty nine tef genotypes were studied for days to seedling emergence, days to heading, days to physiological maturity, plant height, panicle length, culm length, grain filling period, number of spikelet per panicle, lodging index, grain yield, number of primary panicle branches per main shoot, number of fertile tillers per plant, number of total tillers per plant, number of floret per spikelet, peduncle length, thousand seed weight, above-ground biomass and harvest index in simple lattice design at Alemtena and Melkassa Agricultural research sites with the objective to identify better yield and important traits drought tolerant genotypes after clustering them based on their response to yield and yield related traits at drought prone areas. All genotypes clustered based on 18 important traits used as variable and dendrogram prepared.
Results: UPGMA revealed that these genotypes formed twelve distinct clusters. Cluster II, was relatively low mean values of days toheading (30.21), days to physiological maturity (71.08), above-ground biomass (14812.00kg/ha) as compared to the other clusters. This indicated that genotypes in cluster II could be selected for early maturity performance of traits for future tef crop improvement. Cluster IV consisted of three genotypes (Dtt2 X Kaye Murri (RIL-117), DZ-Cr-387 X Dtt2 (RIL-118) and Dtt2 X Dtt13 (RIL-119)) and it were characterized by relatively high values for grain yield (3408 kg/ha).
Conclusion: The genotypes which had larger genetic distance indicate wide genetic divergence, therefore, if such lines are crossed, high variability and better transgressive sergeants may be developed.

Keywords: Tef, Cluster, Euclidean distance and Genetic distance.

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Introduction

Tef [Eragrostis tef (Zucc.) Trotter] is endemic to Ethiopia and its domestication is estimated to have occurred between 4000 and 1000 BC (Vavilov, 1951). Tef is also cultivated in very small quantities in Eritrea and recently in the USA, the Netherlands and Israel (Abraham, 2015). Ethiopia, where tef is the main cereal crop and food shortage is a recurring phenomenon, exerted an export ban on tef which increased interest in growing tef outside Ethiopia.

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 due to its high protein, high mineral content and good quality "*injera*", a pancake-like soft bread (Geremew*et al*., 2002), and the absence of gluten (Spaenij-Dekking*et al*., 2005), 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 for human being (Jeffrey, 2015; Provost and Jobson, 2014). It contains 11% protein, 80% complex carbohydrates and 3% fat (Piccinin, 2002).

Tef grows under a wide range of ecological conditions, from sea level up to 3000 meters above sea level (m.a.s.l). Tef has the genetic potential to yield up to 6 t ha^{-1} (Seyfu, 1993) Despite its numerous relative advantages and economic importance, the productivity of tef in Ethiopia is low, amounting to 1.75 t ha^{-1} (CSA, 2019). The major yield limiting factors to tef production arelack of cultivars tolerant to lodging and drought conditions (Kebebew*et al*., 2011), as well as small seed size. Yield losses are estimated to reach up to 40% during severe moisture stress (Mulu, 1993).

Although early studies showed considerable genotypic variations in drought tolerance in relation to depth of root growth and osmotic adjustment (Mulu*et al*., 2001), information on drought tolerance based on tef grain yield is scanty. Since abiotic stresses such

as drought, salinity and changing climate substantially affect the productivity of crops and food security, future research should focus on developing resistance or tolerance against these environmental calamities (Zerihun and Kebebew, 2012). Tef breeders need to continuously search for new sources of resistance or tolerance and introgress the candidate genes into susceptible cultivars. Screening of tef genotypes using both phenotypic and genotypic data is important to identify drought resilient breeding lines (Mizan*et al*., 2015). 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 tef genotypes in terms of high grain yield, tolerance or resistance to low moisture, lodging resistance, early maturity and desirable grain quality (Kebebew *et al*., 2013).

Cluster analysis refers to a group of multivariate techniques whose primary purpose is to group individuals or objects based on the characteristics they possess, so that individuals with similar descriptions are mathematically gathered into the same cluster (Hair *et al*., 1995). Individuals within a cluster shall be closer when plotted geometrically and different clusters shall be farther apart (Hair *et al*., 1995). Utilization of the genetic variability existing in conserved germplasm accessions, interspecific hybridization, intra-specific hybridization, mutant and landraces was chiefly employed for improvement in other crops. This was possible by employing breeding approaches that utilize multivariate statistical analysis (*i.e*., cluster, distance) as a tool to assess the genetic diversity. Classifying the existing tef germplasm and recombinant inbredlines into genetically distinct groups seems to be useful because the expression of the sub-traits (yield components) to yield and ease of selection depends on the genetic diversity and hence, it facilitates the effective and efficient utilization of gene pool in the population.

Conservation of germplasm resources is fundamental to crop improvement programs. However, for practical exploitation of the apparent variability, classification of genetic stocks based on a suitable scale is quite imperative. Similarly, choice of genetically divergent parents for hybridization, under transgresive breeding program, is also dependent upon categorization of breeding materials based on appropriate criteria (Sharma, 1998). To develop a sound hybridization program, it is necessary that the varieties should be genetically divergent especially for quantitative characters that contribute towards yield (Singh, 1983). Thus, crosses between groups with maximum genetic divergence would be more responsive to improvement since they are likely to produce desirable recombination and segregation in their progenies after hybridization. In any breeding program, therefore, genetic diversity must be introduced periodically into the population to provide new recombination and selection potential (Welsh, 1981).

As suggested by Mizan *et al*. (2016) clustering of tef genotypes in drought stress area was fewer (four cluster) than the cluster pattern reported by Kebebew*et al*. (1999), who grouped 320 tef accessions into 14 clusters. Similarly, Kebebew*et al*. (2001) grouped 36 tef populations into six classes, each containing 2 to 15 populations. Habtamu *et al*. (2011) calculated five clusters for 37 tef lines collected from the Amhara Region. Habte *et al*. (2015) also found that 36 brown seeded tef genotypes in to seven clusters. Genetic gain in yield potential can be done by recombining elite genotypes followed by selection. The objective of the research was to identify better yield drought tolerant genotypes after clustering them based on their response to yield and yield related traits at drought prone areas.

Materials and Methods

Experimental sites, designs and experimental materials

A field study was conducted during the 2017 cropping season at two locations (Melkassa8^{o} 24' N, 39^{o} 21' E andAlemtena8^{o} 20' N, 38^{o} 57' E) in the Central Rift Valley of Ethiopia. Both Alemtena and Melkassa are drought prone areas, with Andosols of very light texture that show low water retention capacity (Alemayehu, 2015). The region experiences poor rainfall distribution (500 mm to 750 mm), coupled with relatively high

temperature (15°C to 30°C), which makes the area vulnerable to moisture stress.

Forty nine genotypes, including 42 drought tolerant advanced lines (*Dtt*), four parents of the advanced lines, two varieties and a local check were used for this study. Dtt_2(drought tolerant tef 2) and Dtt_{13}(drought tolerant tef 13) were obtained from ethylmethanesulfonate mutagenized populations of Tsedey using the targeted induced local lesions IN genomes (TILLING) method at the Institute of Plant Sciences of the University of Bern through the Tef Improvement Project supported by the Syngenta Foundation for Sustainable Agriculture. These lines aredepicted excellent performance under moisture scarcity. The unique morphological difference between the *Dtt* and the original parental tef line Tseday (DZ-Cr-37) is the size and number of stomata. The stomata at the adaxial or upper side of the two D*tt* lines are smaller both in size and number compared to the original parental tef line (Cannarozzi *et al*., 2018).

The seeds of all genotypes were obtained from DebreZeit Agricultural Research Center (DZARC). The experiment was laid out in a 7x7 simple lattice design. Each experimental plot was 1 m^2 (1m x 1m) 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. Seeds were sown at the recommended rate of 15 $kgha^{-1}$, amounting to1.5 g of seed per plot per row. The recommended full doses of blended fertilizer urea (21.74 kg) and NPS (158 kg) per hectare were applied at both locations.

Data collected

Data were recorded for days to 50% seedling emergence, days to 50% heading, days to 90% physiological maturity, grain filling period, plant height, panicle and , penduncle length, culm length, number of spikelets per panicle, number 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, total grain yield, harvest index (%), thousand grain weight.

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 9.2 version. 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 Mohammadi and Prasanna (2003) as follows:

$$ED_{jk} = \sqrt{\sum_{i=j}^{n} (Xji - Xki)^2} \quad \text{……..Equation 1}$$

Where: ED*jk*= distance between genotypes j and k; X*ij* and X*ik* = phenotype traits values of the i^{th} character for genotypes j and k, respectively; and n = number of phenotype traits used to calculate the distance. In addition, mean ED was 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) were closest or distant to others. The pre-standardized trait mean data of the test tef genotypes were used for cluster analysis in order to identify the major traits accounting for much of the gross observed variability among the genotypes.

Results and Discussion

Clustering of genotypes

The cluster analysis based on Unweighted Pair Group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix, 49 tef genotypes into 12 major clusters of 1 to 8 genotypes (Figure 1). Clustering method from Euclidean distances matrix estimated from 18 phenology, tef growth traits, grain yield and yield components.

Among 49 tested tef genotypes12% of tef genotypes, which compromise the commercial variety Simada, which was released for the low moisture stress areas and mutagenesis parent tef genotype (Dtt_2) included along with six recombinant inbred lines were grouped under the cluster (C I). The second cluster (C II) was the largest and included 16% of tef genotypes comprising a total of 8 genotypes, all genotypes resulting from parents crosses of (Dtt_2 X Dtt_{13}) and tef mutagenised parent (Dtt_{13}) itself. The third cluster (CIII) comprised of 6 tef genotypes resulting from crosses of Dtt_2 X Dtt_{13} and Dtt_2 X Kaye Murri. Clusters IV, V, VI, VII, VIII and XI consisted of 3, 7, 3, 4, 6 and 3 tef genotypes, correspondingly, resulting from two independent crosses DZ-Cr-387 X Dtt_2 and Dtt_2 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 (Quncho), respectively (Table 1). Clusters IX, X and XII were solitary, containing DZ-Cr-387 X Dtt_2 (RIL- 287), Dtt_2 X Kaye Murri (RIL-76) and Kaye Murri, respectively (Table 1). Similar findings were reported by Ayana *et al.* (1999) on sorghum, and Kebebew *et al.*(2003) and Habtamu *et al*. (2011) on *tef* accessions of different regions of collected germplams.

It was clear that in most cases the genotypes resulting from crosses of the same parents clustered together, perhaps 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. Demeke *et al*. (2013) also found variability in recombinant inbred lines of the cross of *Eragrostis tef* x *Eragrostis pilosa*. The study demonstrated availability of genetic variability for a number of heritable characters in the RILs for exploitation through selection and presence of promising inbred RILs for further breeding.

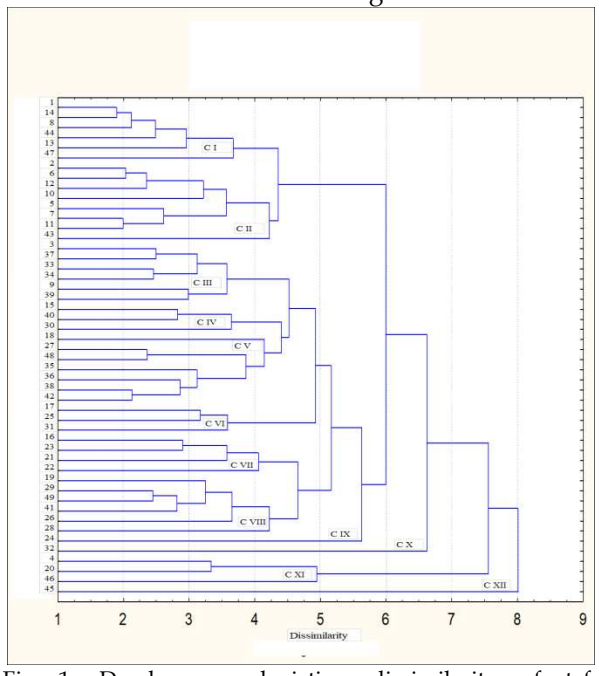

Fig 1. Dendrogram depicting dissimilarity of tef genotypes (1-49) genotypes code by Unweighted Pair Group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix estimated from 18 phenology, tef growth traits, grain yield and yield components in Ethiopia.

Clustering of mean analysis

The mean values of the 18 quantitative characters in each cluster are presented (Table 2). Cluster I is characterised 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). On the other hand, genotypes in this cluster exhibited high values for number of total tillers per plant (7.93), fertile tillers per plant (6.80), lodging index (91.58%) and harvest index (18.56%). Hence, the Dtt_2 X Dtt_{13} (RIL-22, RIL-125, RIL-72, and RIL-119), Dtt_2 and Simada were selected for tillering capacity and yield performance. Habtamu *et al*. (2011) also found that the highest number of productive tillers in the cluster, and conformed to biomass and grain yield on tef accessions.

Cluster II, which consisted of 8 genotypes, had 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%); compared to the other clusters. This indicates that genotypes in this cluster could be selected for early maturity for future crop improvement. Habtamu *et al*. (2011) studied that low mean values of days to heading, days to physiological maturity the possibility of developing lines adapted to drought prone areas or where early cessation of rainfall is prevalent.

Cluster III that contained 6 genotypes was characterised by low values of peduncle length and thousand-seed weight. Cluster IV consisted of 3 genotypes (Dtt_2 X Kaye Murri (RIL-117), DZ-Cr-387 X Dtt_2 (RIL-118) and Dtt_2 X Dtt_{13} (RIL-119)) and it is characterised by relatively high values for grain yield (3408 $kgha^{-1}$) (Table 2). Hence, these genotypes could help improve tef varieties especially for yield improvement because this genotypes are still not used for yield potential and varieties from this cross was not released to date.

Cluster V, VI, VII, VIII, IX and X characterized as moderate mean values for all studied traits except low mean values of number of total tillers per plant (5.48) and number of fertile tillers per plant (4.43) and genotypes grouped under these cluster were not good for yield performance. Cluster XI comprised of 3 genotypes and characterised by high mean values of plant height, panicle length and number of spikeletes per panicle. This indicates that genotypes under this cluster can be selected

mainly for yield related traits of above mentioned characters. Cluster XII consisted only one genotype (Kaye Murri) characterized by low value of grain yield (1670.0 $kgha^{-1}$), 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. Thus, breeders dealing with high yield should use genotypes in cluster IV whereas those dealing with early maturity should focus on genotypes in cluster-II.The current cluster analysis indicated that the diversity presented in tef genotypes cannot be reduced into a few number of groups as was done in earlier studies (Melak-Hail *et al*., 1965; Kebebew *et al*., 2003 and Habte *et al*., 2020).

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	Dtt_2 X Dtt_{13}(RIL-22, RIL-125, RIL-72, RIL-119), Dtt2 and Simada
C II	8	Dtt_2 X Dtt_{13} (RIL-30, RIL-69, RIL-106, RIL-92, RIL-56, RIL-70, RIL-11) and Dtt_{13}
C III	6	Dtt_2 X Dtt_{13} (RIL-37, RIL -78), Dtt_2 X Kaye Murri (RIL-438, RIL-82, RIL-105, RIL-5)
C IV	3	DZ-Cr-387 X Dtt_2 (RIL-15), Dtt_2 X Kaye Murri (RIL-37) and Dtt_2 X Kaye Murri (RIL-114)
C V	7	DZ-Cr-387 X Dtt_2 (RIL-102, RIL-426), Dtt_2 X Kaye Murri (RIL-168, RIL-103, RIL-117, RIL-135) and Tsedey
C VI	3	DZ-Cr-387 X Dtt_2 (RIL-98, RIL-19) and Dtt_2 X Kaye Murri (RIL-61)
C VII	4	DZ-Cr-387 X Dtt_2 (RIL-85, RIL-207, RIL-179, RIL-160)
C VIII	6	DZ-Cr-387 X Dtt_2 (RIL-106, RIL-136, RIL-118), Dtt_2 X Kaye Murri (RIL-16, RIL-147) and local check
C IX	1	DZ-Cr-387 X Dtt_2 (RIL- 287)
C X	1	Dtt_2 X Kaye Murri (RIL-76)
C XI	3	Dtt_2 X Dtt_{13} (RIL-45), DZ-Cr-387 X Dtt_2 (RIL-115) and Quncho
C XII	1	Kaye Murri

RIL= Recombinant inbred line, DZ-Cr= DebreZeit Cross

Table 2. Cluster mean of 42 drought tolerant genotypes and four parents and, two standards and one local check for 18 phonological and morphological characters of combined data across two locations in the Central Rift Valley of Ethiopia

Trait	C I	C II	C III	C IV	C V-X	C XI	C XII	Overall mean
DTE	5.17	7.06	5.21	6.08	6.00	5.08	6.50	5.93
DTH	30.21	29.00	35.54	34.08	34.65	38.33	35.75	34.24
DTM	71.08	70.16	74.04	72.83	74.39	79.17	79.25	74.40
GFP	40.88	41.16	38.50	38.75	39.73	40.83	43.50	40.17
PH	84.06	85.45	96.07	99.57	98.73	111.87	103.65	97.75
PL	31.87	32.13	36.88	38.83	38.05	45.95	37.70	37.64
CL	52.19	53.32	59.19	60.73	60.67	65.92	65.95	60.11
PDL	17.06	17.41	17.00	18.58	17.04	15.72	22.00	17.50
NSPP	379.56	357.19	454.84	483.27	465.92	600.30	462.90	461.13
NPPBPS	19.27	19.01	23.07	24.25	22.90	25.65	20.85	22.46
NFPS	5.94	6.48	6.03	6.47	6.91	7.31	6.33	6.67
NTTPP	7.93	6.66	7.09	6.31	6.12	6.65	6.72	6.51
NFTPP	6.80	5.88	6.01	5.19	5.20	5.72	5.67	5.54
LI	91.58	92.25	87.79	87.33	88.78	83.75	70.50	87.16
BY	16500	14812	17291	20083	18134.67	22750	17000	18103
GY	3075	2520	2558	3408	2899.50	3253	1670.0	2823
HI	18.56	17.11	14.78	17.04	16.17	14.40	9.89	15.73
TSW	0.27	0.27	0.26	0.27	0.29	0.34	0.35	0.29

C= cluster, DTE= days to emergency, DTH =days to heading, DTM = days to physiological maturity, GFP = grain filling period, PH= Plant height, PL=panicle length, CL= culm length, PDL= peduncle length, NSPP=number of spikelets per panicle, PPBMS = number of primary panicle branches per main shoot, NFPS =number of florets per spikelet, NTTPP= number of total tillers per plant, NFTPP= number of fertile tillers per plant, LI= lodging index, BY=biomass yield, GY= grain yield, HI = harvest index and TSW= thousand-seed weight.

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 3). The highest genetic distances (Euclidean distance) was computed between Quncho and Dtt_{13} (11.21); followed by between Quncho and Dtt_2 X Dtt_{13} (RIL-92) (11.05) and Quncho and Dtt_2 X Dtt_{13} (RIL-69) (11.0).

Table 3. Range and Euclidean distance of tef genotypes estimated from 18 quantitative traits as evaluated in Central Rift Valley of Ethiopia

Genotype	Minimum	Maximum	Mean	SD	CV(%)
Dtt_2 X Dtt_{13} (RIL-22)	1.90	9.61	5.51	1.84	33.40
Dtt_2 X Dtt_{13} (RIL-30)	2.03	6.62	5.09	1.83	35.88
Dtt_2 X Dtt_{13} (RIL-37)	2.50	7.15	4.75	1.07	22.59
Dtt_2 X Dtt_{13} (RIL-45)	3.33	10.60	7.32	1.84	25.15
Dtt_2 X Dtt_{13}(RIL-56)	2.22	10.33	5.83	1.66	28.37
Dtt_2 X Dtt_{13}(RIL-69)	2.03	11.03	6.01	2.06	34.32
Dtt_2 X Dtt_{13}(RIL-70)	1.99	9.74	5.46	1.69	31.00
Dtt_2 X Dtt_{13}(RIL-72)	2.03	9.65	5.27	1.74	33.03
Dtt_2 X Dtt_{13}(RIL -78)	2.81	7.06	5.04	1.13	22.52
Dtt_2 X Dtt_{13}(RIL-92)	2.87	11.05	6.63	1.82	27.40
Dtt_2 X Dtt_{13}(RIL-96)	1.99	9.73	5.20	1.89	36.34
Dtt_2 X Dtt_{13}(RIL-106)	2.10	10.39	5.58	1.98	35.43
Dtt_2 X Dtt_{13}(RIL-119)	2.57	9.66	5.85	1.78	30.50
Dtt_2 X Dtt_{13}(RIL-125)	1.90	10.35	5.68	2.02	35.57
DZ-Cr-387 X Dtt_2 (RIL-15)	2.83	7.88	5.37	1.18	21.98
DZ-Cr-387 X Dtt_2 (RIL-85)	2.90	7.96	5.25	1.12	21.43
DZ-Cr-387 X Dtt_2 (RIL-98)	3.17	7.67	5.15	1.13	22.01
DZ-Cr-387 X Dtt_2(RIL-102)	3.45	9.22	5.49	1.27	23.08
DZ-Cr-387 X Dtt_2 (RIL-106)	2.89	7.14	4.86	1.13	23.25
DZ-Cr-387 X Dtt_2 (RIL-115)	3.33	10.37	7.10	1.73	24.42
DZ-Cr-387 X Dtt_2 (RIL-160)	3.18	8.52	5.67	1.12	19.72
DZ-Cr-387 X Dtt_2 (RIL-179)	3.18	7.68	5.43	1.09	20.12
DZ-Cr-387 X Dtt_2 (RIL-207)	2.90	7.37	5.27	1.05	20.01
DZ-Cr-387 X Dtt_2 (RIL- 287)	4.10	9.36	6.38	1.39	21.70
DZ-Cr-387 X Dtt_2 (RIL-19)	3.17	8.42	5.79	1.23	21.17
DZ-Cr-387 X Dtt_2 (RIL-136)	3.49	8.55	5.89	1.37	23.33
DZ-Cr-387 X Dtt_2 (RIL-426)	2.36	8.25	5.14	1.17	22.83
DZ-Cr-387 X Dtt_2 (RIL-118)	3.33	9.15	6.48	1.46	22.55
Dtt_2 X Kaye Murri (RIL-16)	2.45	7.91	5.43	1.34	24.73
Dtt_2 X Kaye Murri (RIL-37)	3.46	8.23	5.44	1.10	20.28
Dtt_2 X Kaye Murri (RIL-61)	3.58	9.04	6.02	1.27	21.16
Dtt_2 X Kaye Murri (RIL-76)	4.75	9.98	6.77	1.10	16.23
Dtt_2 X Kaye Murri (RIL-438)	2.46	8.30	5.40	1.25	23.24
Dtt_2 X Kaye Murri (RIL-82)	2.46	7.54	5.05	1.25	24.66
Dtt_2 X Kaye Murri (RIL-168)	2.33	8.34	5.52	1.30	23.50
Dtt_2 X Kaye Murri (RIL-103)	2.68	8.07	4.54	1.24	27.35
Dtt_2 X Kaye Murri (RIL-105)	2.50	7.28	4.88	0.98	20.15
Dtt_2 X Kaye Murri (RIL-117)	2.13	8.17	5.04	1.29	25.71
Dtt_2 X Kaye Murri (RIL-5)	2.99	8.39	5.08	1.14	22.53
Dtt_2 X Kaye Murri(RIL-114)	2.83	7.67	4.86	1.11	22.92
Dtt_2 X Kaye Murri(RIL-147)	2.68	7.30	5.11	1.27	24.82
Dtt_2 X Kaye Murri(RIL-135)	2.13	8.82	4.80	1.43	29.68
Dtt_{13}	3.38	11.21	6.19	1.94	31.36
Dtt_2	2.19	10.16	5.46	1.91	34.91
KayeMurri	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	28.30
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

Whereas, the lowest genetic distances (Euclidean distance) was estimated between Dtt_2 X Dtt_{13} (RIL-125) and Dtt_2 X Dtt_{13} (RIL-22) (1.90) and, Dtt_2 X Dtt_{13} (RIL-125) and Dtt_2 X Dtt_{13} (RIL-72) (1.99).Chekole *et al*. (2016) studied that the maximum dissimilarity showed that there is a genetic distance between the pair tef genotypes. While, the minimum dissimilarity indicates the presence of few variation between the tef genotypes.

The genetic distances among four independent parental crosses ranged between 11.21 (Quncho and Dtt_{13}), 10.50 (Dtt_2 and Kaye Murri) and 3.81 (Dtt_2 and Dtt_{13}).On the other hand, the two released varieties for moisture stress area which were used as checks, 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, Dtt_{13}, Dtt_2, 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 (Simada and Tseday) were 5.77, 1.58 and 27.57% respectively. Unlike to this studies Chekole*et al*. (2016) found genetic distance ranged from 3.82 to 4.13 with mean and standard deviation of 0.77 and 1.12, respectively. Generally, Euclidean distance among 49 tef genotypes estimated from 18 quantitative traits showed that 51% lower than minimum mean and 47% higher than the 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.

Conclusion

Genetic characterization and evaluation of indigenous germplasm resources and/or genotypes are very essential towards development of new tef varieties with traits of interest. In the present study, 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 18quantitative traits gave 12 major clusters. Most of lines developed from Dtt_2 X Dtt_{13} were grouped in the same clusters which may be due attributed to an exchange of genetic materials between the parents. Breeders dealing with high yield should use genotypes in cluster IV and those dealing with early maturity should focus on genotypes in cluster-II since it is a possibility of developing lines adapted to drought prone areas. 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 Dtt_{13} (11.21). In most cases the lowest genetic distances was estimated for lines developed between Dtt_2 X Dtt_{13}. The genotypes which had larger genetic distance indicates wide genetic divergence, therefore, if such lines are crossed, high variability and better transgressive sergeants may be developed.

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