

Genetic Variability and Heritability Studies in F₄ Progenies of Tef (*Eragrostis tef*)

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Abstract: The present investigation was conducted on F₂-derived F₄ bulk families of three crosses, viz, DZ-01-974 × DZ-01-2786, DZ-01-974 × DZ-Cr-37 and Alba × Kaye Murri. To estimate genetic variability, heritability, genetic advance; to assess cross performance, 63 F₄ families were taken randomly from each of the three crosses. The 189 F₄ families, five parents and two checks were space planted following in 14×14 simple lattice design at two locations, namely, Debre Zeit and Akaki. The F₄ families differed significantly for all the eleven agronomic characters studied except hundred kernel weight at both locations. At Debre Zeit, the families of the cross DZ-01-974 × DZ-Cr-37 were the highest yielders and at Akaki, the families of the cross DZ-01-974 × DZ-01-2786 were the highest yielders. Heritability and genetic advance were high for grain yield, harvest index and lodging index at Debre Zeit. At Akaki, heritability and genetic advance were high for lodging index, grain yield, plant height and days to heading.

Key words: Genetic advance, genetic variability, heritability, lodging index, tef (*Eragrostis tef*)

INTRODUCTION

Tef [*Eragrostis tef* (Zucc.) Trotter] is an indigenous cereal crop of Ethiopia. Tef has many prospects outside Ethiopia due to its gluten-freeness, tolerance to biotic and a biotic stress, animal feed and erosion control quality Hailu and Seyfu (2001). In Ethiopia, tef is cultivated on an area of about 1.8 million ha 15% of the total cereal crops production in the country is contributed by tef Central Statistical Authority (2003).

Despite the aforementioned importance and coverage of large area, its productivity is very low. The average national yield of tef is less than 1ton per hectare, i.e., 8 qt/ha Central Statistical Authority (2003). Some of the factors contributing to low yield of tef are; lack of high yielding cultivars, lodging, weed, water lodging, low moisture and low fertility conditions Fufa (1998). In order to ameliorate these problems, conventional research on tef has been going on for over 40 years in Ethiopia. Debre Zeit Agricultural Research Center has done a lot and currently the breeding program is focused on the development of varieties with high yield, good kernel quality and early maturity. The segregating generations are handled by modified bulk method, i.e., raising bulk families in F₃-F₄ generations that are derived from individual F₂ plants.

Keeping in view the need to generate more variability through hybridization and assessment of such crosses for

future breeding, the present study was proposed. The study was aimed at generating the information on those specific crosses made at Deber Zeit Agricultural Research Center (DZARC) to strengthen the selection program at the Center.

Thus, the objectives of the present studies were:

- To assess the variability and heritability of yield related traits
- Genetic advance for yield and yield related traits

MATERIALS AND METHODS

The experiment was conducted in 2004/05 cropping season at two locations, Debre Zeit and Akaki. The experimental materials comprised of F₂-derived F₄ bulk families developed from three tef crosses, DZ-01-974 × DZ-01-2786, DZ-01-974 × DZ-Cr-37 and Alba × Kaye Murri. They were obtained by bulking kernel from each F₃ family derived from each single F₂ plant for each F₂ population. DZ-01-974 and DZ-Cr-37 are released varieties. The former is a late maturing, high yielding variety and the latter is an early maturing white-kerneled variety. Alba and Kaye Murri are cultivars described by Tadesse (1975). From F₁ plants of the crosses indicated above, 1200 individual F₂ plants were grown on the field in 1.5 m long rows spaced 0.5 m at the Debre Zeit Agricultural Research Center with intra-row spacing of

0.1 m. About 200 plants were randomly selected from each F₂ population and advanced to F₃ by field planting of kernels of each individual F₂ panicle in 1m long rows spaced 0.5 m apart. About 63 plants were randomly taken from each F₃ population and advanced to F₄. A total of 189 F₄ (F₂-derived F₄ families) from three crosses were produced and field grown along with the five parents and two standard checks. DZ-01-1285 was used as a late maturing standard check and DZ-01-1681 was used as an early maturing standard check.

The genotypes were sown at Debre Zeit and Akaki in 14×14 simple lattice designs. Each plot consisted of 2 rows of 2 m length spaced 0.2 m apart. A distance of 50 cm between plots was maintained and the distance between blocks and replications was 1 m. The recommended kerneling rate of 30 kg/ha and fertilizer rate of 60/60 kg/ha N/ P₂O₅ were used at both locations. Weeds were controlled manually and at early tillering all the stands were thinned to 10 cm-intra-row spacing. Thus plants row⁻¹ (40 plants plot) was maintained. In each row 5 plants (10 plants/plot) were tagged for data to be taken on individual plant basis.

Data on the following traits were taken on the basis of the two rows in each plot. Namely, Days to 50% heading, Days to 75% maturity, hundred kernel weight, biological yield, grain yield, harvest Index and Lodging index which was recorded using the method of Caldicott and Nuttall (1997). Ten randomly per-tagged plants were used for recording data on four characters, Panicle length, Panicle weight, Yield per panicle and Plant height.

Analysis of Variance (ANOVA) was carried out as per the procedure for simple lattice and RCBD described by Gomez and Gomez (1984). The analysis was done using the MSTATC Statistical package. Estimates of

phenotypic and genotypic coefficients of variation, heritability, genetic advance were done based on RCBD ANOVA using INDOSTAT computer program. Thus, RCBD ANOVA was used to derive variance components used in the following format Sharma (1998).

The Genotypic (GCV) and Phenotypic Coefficients (PCV) of variation were calculated as per the methods of Burton and Devane (1953). Broad sense heritability (h²) was estimated on genotype mean basis as described by Allard (1960). Expected Genetic Advance (GA) were estimated using the methods illustrated by Fehr (1987).

RESULTS

Analysis of variance: The results of analysis of variance of 11 characters for 196 genotypes tested at Debre Zeit and Akaki discussed individually as the homogeneity test significantly varies for the traits.

The results of analysis of variance of 11 characters for 196 genotypes tested at Debre Zeit suggested that genotypes exhibited highly significant variation (p<0.05) for days to heading, days to maturity, shoot biomass, harvest index, lodging index and grain yield. While, panicle length, panicle weight, plant height and panicle kernel weight exhibited significant variation (p<0.05). However, hundred kernel weights, showed non-significant variation (Table 1). At Akaki highly significant (p<0.01) genotypic differences were observed among the genotypes for all characters considered except hundred kernel weight and panicle weight, where the first showed no significant differences (p<0.05) and the second trait became significant (Table 2).

Homogeneity of error variance of each character was tested as per Hartley's procedure Hartley (1950). The F test result indicated that most traits except harvest

Table 1: Analysis of variance of 11 traits of tef genotypes at Debre Zeit

Source of variation	DF	DTH	DTM	HI	LI	SHB	GY	PH	PL	PW	PKW	HSW
Replication	1	0.1	55.88	15.1	3916.13	80036100.14	5243594.15	827.22	419.67	0.36	0.19	0.004
Treatment	195	18.9**	59.96**	24.7**	420**	10297651**	1036850**	54.46*	14.74*	0.1*	0.04*	0.043
Block with rep	26	7.2	8.13	9.2	183	9449902	648303.7	175.5	33.4	0.13	0.04	0.01
Intra block error	169	4.6	6.35	7.5	168	567626.9	323906.2	35.22	9.9	0.07	0.03	0.02
C.V (%)		5.6	2.65	17.2	23	17	25	6.24	8.29	18.1	24.3	17.17

** : Significant difference at 1% ; * : Significant difference and 5% ; DTH: Days to Heading; DTM: Days to Maturity; HI: Harvesting Index; SHB: Shoot Biomass; GY: Grain Yield; PH: Plant Height; PL: Panicle Length; PW: Panicle Weight; PKW: Panicle Kernel Weight; HSW: Hundred Seed Weight

Table 2: Analysis of variance of 11 traits of tef genotypes at Akaki

Source of variation	DF	DTH	DTM	HI	LI	SHB	GY	PH	PL	PW	PKW	HSW
Replication	1	39.22	89.21	153.13	0.21	25312.5	3407914.5	20.57	379.8	0.28	0.06	0.05
Treatment	195	28.68**	94.09**	21.57**	235.54**	13984736.9**	1289162.3**	68.29*	21.51**	0.09*	0.03**	0.03
Block with rep	26	4.33	35.49	17.04	150.84	34076116.93	2974547.8	70.35	14.99	0.25	0.09	0.02
Intra block error	169	2.87	17.94	14.19	103.27	7719257.71	780021.8	27.16	8.48	0.06	0.02	0.01
C.V (%)		3.16	3.39	16.24	16.51	17.42	23.58	6.16	8.41	16.61	18.07	18.61

** : Significant difference at 1% ; * : Significant difference and 5% ; DTH: Days to Heading; DTM: Days to Maturity; HI: Harvesting Index; SHB: Shoot Biomass; GY: Grain Yield; PH: Plant Height; PL: Panicle Length; PW: Panicle Weight; PKW: Panicle Kernel Weight; HSW: Hundred Seed Weight

Table 3: Ranges, means, standard errors, genotypic variances, phenotypic variances, environmental variances, Genotypic Coefficient of Variation (GCV %), Phenotypic Coefficient of Variation (PCV %), Heritability in broad sense (H %), Genetic Advance (GA), and Genetic Advance as percent of Mean (GAM) at Debre Zeit

Characters	Range	Mean±SE	δ_p^2	δ_e^2	P.C.V	G.C.V	h^2 (%)	GA	GAM
Days to heading	30.0-47.0	39.48±0.17	7.38	12.37	8.91	6.88	59.7	4.33	10.97
Days to maturity	76.0-106.0	96.65±0.29	26.44	33.07	5.95	5.32	80.1	9.49	9.82
Plant height	78.4-122.1	100.03±0.41	10.76	64.68	8.04	3.28	16.6	2.75	2.75
Panicle length	28.3-54.8	39.79±0.19	1.50	14.53	9.58	3.08	10.3	0.81	2.04
Panicle weight	0.70-2.10	1.51±0.01	0.01	0.09	19.61	6.31	10.3	0.06	3.98
Panicle kernel weight (g)	0.30-1.30	0.71±0.01	0.00	0.03	25.66	7.52	8.6	0.03	4.24
Biomass yield/plot (kg)	6425.0-22675.5	14321.4±148.35	2265571.2	8443769.7	20.29	10.51	26.8	128.4	0.90
Grain yield/plot (kg)	775.0-5337.5	2343.02±44.2	387263.9	754390.2	37.07	26.56	51.3	918.3	39.20
Harvest index (%)	7.6-27.7	16.13±0.20	8.8	16.54	25.21	18.39	53.2	4.46	27.65
Lodging index (%)	20.0-81.0	57.93±0.88	126.7	296.43	29.72	19.43	42.7	15.16	26.17

Table 4: Ranges, means, standard errors, genotypic variances, phenotypic variances, environmental variances, Genotypic Coefficient of Variation (GCV %), Phenotypic Coefficient of Variation (PCV %), Heritability in broad sense (H %), Genetic Advance (GA), and Genetic Advance as percent of Mean (GAM) at Akaki

Characters	Range	Mean±SE	δ_p^2	δ_e^2	P.C.V	G.C.V	h^2 (%)	GA	GAM
Days to heading	44.0-66.0	54.75±0.48	16.24	13.18	7.36	6.63	81.2	6.74	12.31
Days to maturity	101.0-142.0	129.09±0.00	61	40.67	6.05	4.49	66.7	10.74	8.32
Plant height	66.8-115.0	87.98±0.45	54.23	21.25	8.37	5.24	39.2	5.95	6.76
Panicle length	20.3-58.7	35.64±0.00	16.13	6.79	11.27	7.31	42	3.48	9.76
Panicle weight	0.8-2.3	1.53±0.00	0.09	0	20.02	6.52	10.6	0.07	4.59
Panicle kernel weight (g)	0.3-1.5	0.80±0.31	0.03	0	22.28	7.94	12.7	0.05	6.23
Biomass yield/plot (kg)	6425.0-28962.5	16749.24±0.17	14621832	3388327	22.83	10.99	23.2	146.14	0.87
Grain yield/plot (kg)	1250.0-9750.0	3925.64±0.00	1303195	230501.3	29.08	12.23	17.7	416.12	10.6
Harvest index (%)	8.5-45.2	23.45±0.00	18	3.41	18.09	7.8	19	0.14	0.6
Lodging index (%)	22.0-88.0	62.77±0.08	184.19	74.61	21.62	13.76	40.5	11.33	18.05

index, panicle weight and panicle kernel weight showed significant differences. Thus, combined analysis was not performed and interpretation was given for each location separately.

Estimates of phenotypic and genotypic coefficient of variability: At Debre Zeit, estimates of GCV ranged from 3% for panicle length to 26% for grain yield at Debre Zeit (Table 3). At Akaki it ranges from 5% for days to maturity to 14% for lodging index (Table 4). At both locations, the phenotypic coefficient of variation was the lowest for days to maturity (5.95, 6.06) and high for grain yield (37.07, 29.08), shoot biomass (20.29, 22.83) and harvest index (25.21, 18.09). In addition, panicle length (9.58, 11.27), panicle weight (19.61, 20.02), panicle kernel weight (25.66, 22.28) and lodging index (29.72, 21.62) also showed high phenotypic coefficient of variation values at Debre Zeit and Akaki respectively.

Heritability in broad sense: Heritability estimates were relatively high for days to maturity (80%), days to heading (60%), grain yield (51%) and harvest index (53%); intermediate for lodging index and low for panicle kernel weight (9%) plant height (17%), panicle length (10%) and panicle weight (10%) at Debre Zeit (Table 3). Heritability estimates (34%) relatively high for days to heading (81%), days to maturity (67%) and intermediate for panicle length (42%), plant height (39%), lodging index (41%) and very low for panicle weight and panicle kernel weight at Akaki (Table 4). Similarly, days to heading and days to maturity exhibited the highest broad sense heritability estimates at both Debre Zeit and Akaki. On the other hand, panicle weight and panicle kernel weight had the lowest broad sense heritability estimate at both locations.

Genetic advance: At Debre Zeit, the highest GA as percent of the mean was observed for yield (39.20%) followed by harvest index (26.17%) and lodging index (26.17). The genetic advance was low for yield related traits like plant height (2.75%), panicle length (2.04%), panicle weight (3.98%) and panicle kernel weight (4.24%) comparatively, the highest GA as percent of the mean was observed for lodging index (18.05%) followed by days to heading (12.31%), grain yield (10.6) and panicle length (9.76%).

DISCUSSION

In the present study, the wide range in days to maturity at Debre Zeit (76-106) and at Akaki (101-142) indicated that genotypes that can fit different length of growth period could be identified from families of the crosses under study (Table 3 and 4). The wide range of variability of genotypes in this study indicated that there is a high possibility for the genetic improvement of the traits under consideration. Traits like harvest index, grain yield and shoot biomass showed high genetic coefficients of variation (Table 3 and 4). In contrast, traits like day to heading, plant height and panicle length showed lower genetic coefficients of variation. Similar results of high genetic coefficients of variation and phenotypic coefficient of variation for grain yield shoot biomass, panicle kernel weight and were observed by Hailu *et al.* (2003) and Kebebew *et al.* (2001). Heritability studies indicated that estimates were relatively high for days to maturity (80%), days to heading (60%), grain yield (51%) and harvest index (53%). According to Allard (1960) if a trait has high heritability, it indicates that the influence of the environment on the trait is less. Moreover, as the value of broad sense heritability becomes high it is used

as an indicator of the ease of phenotype based selection particularly when it is accompanied by a relatively high variability and genetic advance value. In this particular study, yield per plot showed high heritability at Debre Zeit. As almost 90% of the genotypes achieved homozygosity, it might be possible to make direct selection for high yield. Though, days to maturity and days to heading recorded higher heritability but the genetic advance as percent of the mean was low. It is because, there was low variability for these traits as indicated by their respective GCV and PCV (Table 3). This showed the importance of genetic variability in crop improvement at Akaki (Table 4). In addition though, biomass yield (0.87%) and harvest index (0.59%) recorded higher heritability their genetic advance as percent of the mean was low. It is because; there was low variability for these traits as indicated by their respective GCV and genetic variance. According to Johnson *et al.* (1955) heritability along with genetic advances are usually more useful than heritability alone in predicting the resultant effect of selecting the best individuals. They also stated that high heritability along with high genetic advance as percentage of mean implies the role of additive genes for the expression of the characters and thus it could be very effective in improvement upon selection.

CONCLUSION

The results of the present study show that there exists variability among the progenies of the crosses for most important quantitative traits indicating high potential for the improvement of the traits. High genetic advance value as percentage of the mean and heritability for harvest index, grain yield and lodging index at Debre Zeit shows that these traits can be used as a selection criterion for this location was observed. At Akaki high genetic advance value as percentage of the mean also high to moderate GCV and PCV for lodging index, grain yield and panicle length. So these characters can be used as a selection criterion for this location. High genetic advance value and heritability for yield shows direct selection would be encourage for the improvement of the trait.

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