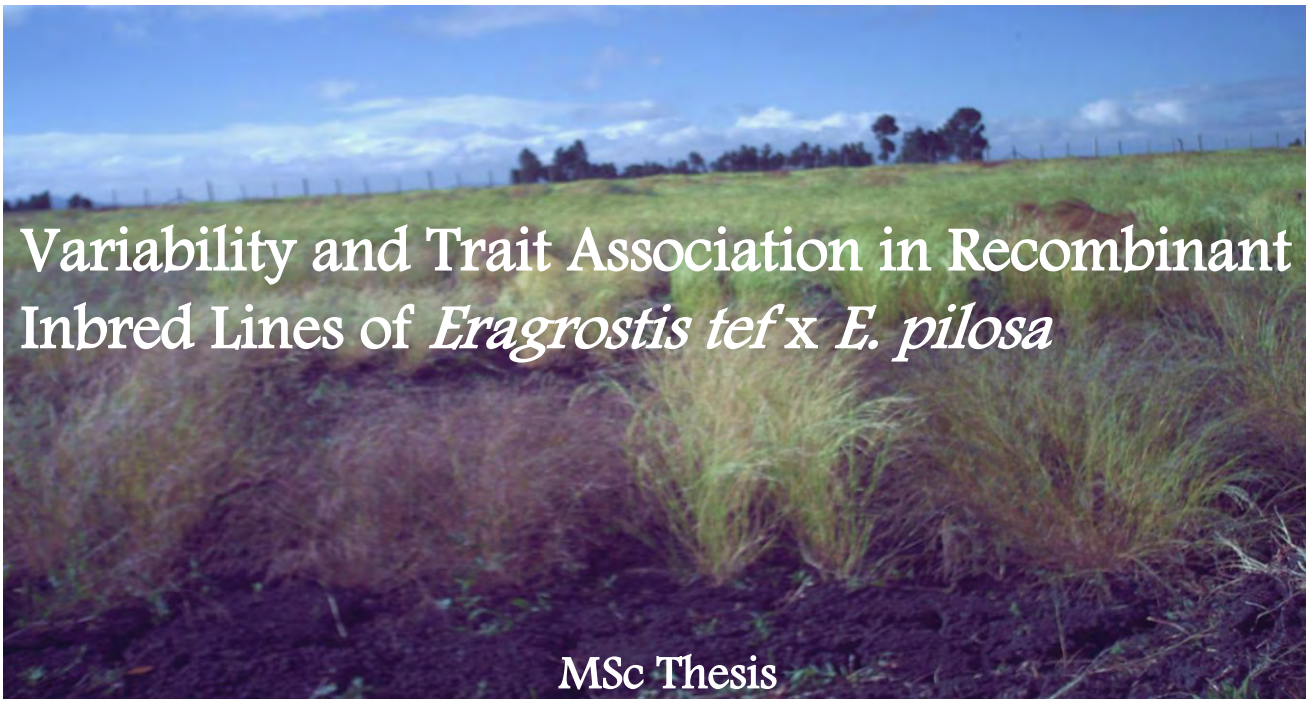
Addis Ababa University

School of Graduate Studies

Department of Biology



Variability and Trait Association in Recombinant Inbred Lines of *Eragrostis tef* x *E. pilosa*

MSc Thesis

BY

Demeke Mewa Bayable

June 2008

Addis Ababa University

School of Graduate Studies

Variability and Trait Association in Recombinant Inbred Lines of *Eragrostis tef* x *E. pilosa*

In Partial fulfillment of the requirement of degree of master of science in biology (Applied Genetics)

BY

Demeke Mewa Bayable

June 2008

Dedicated to Ethiopians

who have been victims of hunger and malnutrition ever

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DECLARATION

I, the undersigned, declared that 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: Demeke Mewa

Signature: _____

Date: June 26, 2008

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

Name: _____

Signature: _____

Date: _____

ADDIS ABABA UNIVERSITY

SCHOOL OF GRADUATE STUDIES

Variability and Trait Association in Recombinant Inbred Lines of *Eragrostis tef* x *E. pilosa*

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

By

Demeke Mewa

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_____ **(Chairman)** _____

June, 2008

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It was under the lovely care and prayer of my extended family and friends I reached here. My mother W/ro Alemnesh Tsehay and my brother (and father) Ato Enawgaw Abat put at risk their lives at the expense of my career, dignity and comfort. Little to mention, my grand-mother Emahoy Etinesh Yesigat, my sisters Wubayehu Mewa, Mastewal Mewa and Siraye Mewa, my brothers Kibret Aragaw, Belisti Aragaw, Simachew Yitayew and Belay Endalifer, and all in my extended family shall receive their gratitude. My brother Kasahun Biyalfew and my sisters Abaynesh Simachew, Bezuayehu Mewa, Mulubirhan Abebe and Mekdesework Damtie were disturbing my disturbance via telephone to extend my courageous journey throughout the study. I could not ever afford to overlook the brotherly love, concern and assistance in Tsehaynesh Gurumu, Mulugeta Atinaf, Welday Hailu, Neter Tessema, Dawit Mitiku, Demelash Alem, Challachew Abebe and Sileshi Andualem. Utmost I praise the almighty God for his timeless love and ultimate care.

Demeke Mewa

List of acronyms

RCBD = Randomized complete block design

CV = Coefficient of variation

PCV = Phenotypic coefficient of variation

GVC = Genotypic coefficient of variation

r_p = Phenotypic correlation coefficient

r_g = Genotypic correlation coefficient

ANOVA = Analysis of variance

RIL = Recombinant inbred line

QTL = Quantitative trait loci

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Abstract

A study was conducted to assess variability and trait association in recombinant inbred lines (RILs) of *Eragrostis tef* x *E. pilosa* crosses. A total of 81 lines were planted using RCB design with three replications at Debre Zeit and Akaki in 2007 main rainy season. The result indicated that there exists difference among the lines for most of the traits included in this study. High difference was also obtained for almost all the traits between the two environments such that more attention was given to single site analysis. Grain yield showed the maximum PCV (> 40%) and GCV (> 30%) followed by spikelet per panicle (PCV > 25%, GCV > 20%). High PCV (> 20%) and moderate GCV (> 15%) was recorded for lodging index. Moderate GCV (> 10%) was also recorded for plant height, panicle length, culm diameter and strength, and shoot biomass, but GCV was low for shoot biomass and 100-seed weight at Akaki. Most of the traits showed high heritability (not < 40%) except first culm strength and tiller. Genetic advance as % of mean was maximum for grain yield (> 50%) followed by spikelet per panicle (> 30%). For this parameter, panicle length, lodging index and plant height also revealed high values (> 20%), but large difference was recorded between the sites for shoot biomass and 100-seed weight; > 25% at Debre Zeit but < 10% at Akaki. Moderate genetic gain (> 10%) was recorded for length of growing period and culm characters. Genetic variability and potential of genetic gain for number of tillers was consistently very low. Most of the traits were found associated. Correlation study showed strong positive association of lodging index with most other traits except with culm diameter and spikelet per panicle at Debre Zeit. However, path analysis revealed that effect of some of the traits on lodging was weak mainly at Akaki and only culm strength at the second internode showed consistently strong positive effect. Plant height, days to maturity and spikelet per panicle showed strong negative effect and panicle length strong positive at Debre Zeit. Effect of most traits on grain yield was high-positive; only days to maturity showed consistently low effect. Principal component analysis showed that about 45% of the gross variance among lines laid in PC_1 and explained largely by traits like plant height, panicle length, days to maturity and days to heading. Generally, the study indicated that there exists considerably high genotypic variability, up to transgression beyond the better parent, for economically valuable traits including lodging index, which verified the importance of *E. pilosa* in diversifying the tef germplasm base. The complex associations implied the need to consider many traits in improving those traits as grain yield and its limiting factor, lodging. The high variability between the sites indicated the need to work with much more environments to represent most tef growing conditions.

Key Phrases: RIL, Variability, Association, E. tef, E. pilosa

Appendix

Table. Mean value of the 81 lines, grand mean and LSD for 14 traits at Akaki

Lines	FCD	SCD	FCS	SCS	LI	GY	DH	DM	PH	PL	SP	TR	SW	SB
DZ-01-974	0.17	0.17	1.34	0.63	1.45	32	66	113	60	26	312	3.6	0.029	567
PI-223259	0.09	0.09	0.64	0.37	1.05	18	42	87	32	13	146	5.67	0.018	433
PI-222988	0.1	0.09	0.74	0.58	1.98	22	41	91	39	14	157	6.87	0.017	433
RIL1-62	0.16	0.17	0.94	0.46	1.05	28	57	95	54	26	492	3.6	0.017	500
RIL1-13	0.11	0.1	0.57	0.37	1.05	15	43	88	42	17	191	5.53	0.021	400
RIL1-112	0.12	0.1	0.85	0.42	1.03	32	43	92	40	15	191	3.33	0.017	533
RIL1-197	0.15	0.14	0.96	0.46	1.07	22	45	96	47	19	228	4.27	0.017	467
RIL1-27	0.12	0.11	0.67	0.45	1.35	11	45	91	46	20	311	5	0.019	367
RIL1-24	0.13	0.11	0.73	0.54	1.73	22	44	90	41	17	211	4.67	0.019	467
RIL1-15	0.13	0.11	0.92	0.52	1.43	24	46	94	46	20	288	3.47	0.016	500
RIL1-105	0.11	0.12	0.87	0.54	1.62	26	43	95	47	21	249	4.2	0.018	500
RIL1-152	0.14	0.13	0.69	0.41	1.07	30	44	96	53	25	278	3.73	0.02	433
RIL1-75	0.13	0.14	0.95	0.51	1.35	36	51	96	51	24	243	5.13	0.012	533
RIL1-64	0.14	0.15	0.75	0.44	1.18	22	45	97	52	21	205	4.73	0.019	467
RIL1-77	0.17	0.14	0.74	0.58	1.95	13	51	95	45	22	368	3.07	0.02	433
RIL1-143	0.11	0.11	0.68	0.43	1.08	12	44	91	39	19	178	4.33	0.016	433
RIL1-135	0.11	0.11	0.81	0.55	1.7	16	60	96	57	25	202	3.07	0.018	433
RIL1-97	0.11	0.11	0.74	0.47	1.4	24	46	100	50	21	194	3.67	0.013	467
RIL1-17	0.14	0.13	0.74	0.42	1.1	14	46	91	46	20	292	4.53	0.02	367
RIL1-103	0.13	0.11	0.71	0.53	1.72	16	45	93	42	18	238	7.2	0.015	467
RIL1-149	0.14	0.13	0.78	0.48	1.35	22	56	95	46	21	297	4.4	0.019	433
RIL1-76	0.13	0.11	0.72	0.51	1.6	21	45	96	54	25	310	5.53	0.023	433
RIL1-49	0.1	0.09	0.7	0.46	1.42	16	45	92	42	18	236	5.53	0.02	433
RIL1-147	0.11	0.11	0.88	0.44	1.1	30	43	91	40	16	200	6.27	0.017	467
RIL1-52	0.1	0.1	0.73	0.4	1.1	22	44	92	40	17	184	5.27	0.018	433
RIL1-84	0.18	0.15	1.12	0.61	1.62	26	53	108	55	24	240	3.6	0.019	400
RIL1-32	0.15	0.14	0.82	0.5	1.38	25	43	95	44	20	287	4	0.017	467
Mean	**0.13**	**0.12**	**0.82**	**0.51**	**1.48**	**27**	**48**	**96**	**51**	**21**	**254**	**4.54**	**0.018**	**470**
LSD	**0.03**	**0.03**	**0.32**	**0.17**	**0.75**	**17**	**8**	**8**	**10**	**5**	**117**	**2.52**	**0.007**	**116**

FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, LI=lodging index, GY=grain yield, PH=plant height, PL=Panicle length, SP=spikelet per panicle, DH= days to heading, DM=days to maturity, TR=tiller number, SW=100-seed weight, SB=Shoot biomass

Table. Mean value of the 81 lines, grand mean and LSD for 14 traits at Akaki ...*continued*

Lines	FCD	SCD	FCS	SCS	LI	GY	DH	DM	PH	PL	SP	TR	SW	SB
RIL1-110	0.11	0.12	0.67	0.39	1.08	28	45	94	56	23	174	5.33	0.018	467
RIL1-70	0.12	0.1	0.68	0.38	1.02	18	47	94	53	21	178	4.8	0.021	533
RIL1-56	0.12	0.12	1.01	0.53	1.42	30	46	93	51	22	254	3.87	0.019	500
RIL1-80	0.11	0.11	0.72	0.53	1.63	35	44	92	47	18	232	4.33	0.018	500
RIL1-2	0.11	0.11	0.78	0.41	1.05	10	42	87	42	17	215	5	0.017	433
RIL1-154	0.14	0.15	0.78	0.54	1.63	23	45	96	53	21	229	4.73	0.019	433
RIL1-60	0.14	0.13	0.72	0.41	1.07	24	45	97	48	19	251	5	0.017	400
RIL1-79	0.12	0.12	0.82	0.49	1.37	40	45	94	43	18	233	6.07	0.016	533
RIL1-146	0.1	0.1	0.75	0.52	1.67	26	42	90	55	24	274	3.27	0.017	467
RIL1-5	0.1	0.1	0.7	0.51	1.65	22	50	94	42	20	353	3.8	0.019	400
RIL1-130	0.1	0.1	0.86	0.42	1.07	31	44	91	44	17	169	4.13	0.017	500
RIL1-119	0.11	0.11	0.74	0.46	1.35	37	44	93	59	23	285	4.87	0.017	500
RIL1-12	0.13	0.13	0.9	0.44	1.07	34	43	93	50	20	244	4	0.017	533
RIL1-126	0.11	0.11	0.61	0.45	1.43	20	48	93	46	19	251	3.87	0.017	433
RIL2-84	0.11	0.11	1.07	0.46	1	15	44	93	43	18	182	5.07	0.015	500
RIL2-131	0.13	0.11	0.71	0.46	1.38	26	48	95	54	23	262	4.2	0.015	533
RIL2-137	0.13	0.11	0.82	0.43	1.07	17	51	94	48	23	227	5.13	0.018	467
RIL2-36	0.19	0.17	1	0.67	2.02	33	54	101	67	28	375	4.27	0.019	433
RIL2-48	0.1	0.1	0.76	0.47	1.4	19	49	96	41	17	186	5.53	0.014	433
RIL2-51	0.15	0.13	1.02	0.54	1.42	34	48	94	62	26	283	3.53	0.018	500
RIL2-152	0.09	0.09	0.75	0.45	1.33	24	43	92	43	18	184	5.93	0.021	500
RIL2-166	0.12	0.11	0.95	0.53	1.45	35	43	92	52	21	192	2.8	0.019	567
RIL2-77	0.15	0.14	0.74	0.49	1.43	21	47	93	52	22	333	3.8	0.016	500
RIL2-14	0.1	0.1	0.9	0.63	2.07	18	48	100	44	18	177	4.87	0.019	467
RIL2-32	0.11	0.11	0.71	0.58	1.95	15	47	96	45	16	195	5.53	0.019	467
RIL2-178	0.11	0.11	0.71	0.46	1.38	29	45	101	54	21	263	3.67	0.017	467
RIL2-72	0.16	0.13	0.89	0.45	1.08	13	47	97	57	24	306	4.4	0.018	367
Mean	**0.13**	**0.12**	**0.82**	**0.51**	**1.48**	**27**	**48**	**96**	**51**	**21**	**254**	**4.54**	**0.018**	**470**
LSD	**0.03**	**0.03**	**0.32**	**0.17**	**0.75**	**17**	**8**	**8**	**10**	**5**	**117**	**2.52**	**0.007**	**116**

FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, LI=lodging index, GY=grain yield, PH=plant height, PL=Panicle length, SP=spikelet per panicle, DH= days to heading, DM=days to maturity, TR=tiller number, SW=100-seed weight, SB=Shoot biomass

Table. Mean value of the 81 lines, grand mean and LSD for 14 traits at Akaki ...*continued*

Lines	FCD	SCD	FCS	SCS	LI	GY	DH	DM	PH	PL	SP	TR	SW	SB
RIL2-148	0.18	0.18	1.07	0.67	1.93	56	65	122	68	32	353	4.27	0.021	533
RIL2-180	0.18	0.18	1.05	0.62	1.68	22	46	103	69	29	420	3.8	0.018	467
RIL2-20	0.12	0.11	1.09	0.48	1.08	15	59	96	46	20	193	3.67	0.016	500
RIL2-147	0.13	0.1	0.89	0.44	1.07	23	43	97	55	23	237	3.93	0.016	500
RIL2-143	0.11	0.11	0.87	0.55	1.67	13	47	96	49	19	158	5.4	0.017	433
RIL2-113	0.11	0.11	0.84	0.54	1.63	30	44	95	55	23	257	4.67	0.019	467
RIL2-87	0.11	0.1	0.79	0.54	1.68	32	47	101	54	20	273	4.53	0.017	500
RIL2-126	0.18	0.17	1.17	0.71	2.05	66	58	112	70	32	399	5.87	0.021	633
RIL2-118	0.12	0.11	0.68	0.4	1.07	26	48	103	47	20	344	3	0.021	433
RIL2-130	0.15	0.15	1.04	0.48	1.08	21	45	96	57	25	322	4.67	0.021	500
RIL2-13	0.15	0.15	0.82	0.62	1.97	18	48	96	60	22	264	4.93	0.02	467
RIL2-69	0.13	0.13	0.65	0.51	1.62	37	42	95	53	22	281	4.73	0.019	500
RIL2-56	0.13	0.13	0.87	0.5	1.37	38	53	104	53	22	309	4.73	0.017	433
RIL2-57	0.14	0.12	0.92	0.62	1.92	47	55	103	62	24	251	3.4	0.022	533
RIL2-133	0.11	0.11	0.76	0.59	1.98	53	50	94	57	22	222	3.73	0.021	567
RIL2-168	0.12	0.13	0.7	0.66	2.33	31	49	92	53	23	262	3.87	0.02	533
RIL2-177	0.1	0.1	0.74	0.52	1.67	40	44	92	47	17	170	5.6	0.015	533
RIL2-62	0.11	0.11	0.66	0.5	1.63	27	44	94	50	19	230	4.27	0.015	467
RIL2-160	0.11	0.1	0.78	0.52	1.62	24	48	99	57	22	193	3.87	0.017	433
RIL2-67	0.12	0.11	0.7	0.46	1.38	36	46	98	53	22	234	5.2	0.015	500
RIL2-185	0.11	0.1	0.58	0.49	1.67	35	42	96	42	18	173	3.53	0.02	433
RIL2-33	0.12	0.12	0.75	0.66	2.32	19	48	98	54	23	210	4.73	0.025	433
RIL2-172	0.15	0.15	1.03	0.7	2.17	25	55	110	57	27	379	5	0.017	433
RIL2-111	0.12	0.12	0.66	0.46	1.4	24	45	104	49	21	197	5.6	0.016	400
RIL2-47	0.11	0.11	0.76	0.57	1.88	16	48	103	48	23	262	5.4	0.015	367
DZ-Cr-37	0.13	0.12	0.78	0.62	2.07	51	52	102	60	25	238	3.6	0.028	467
Quncho	0.18	0.18	1.26	0.67	1.73	53	68	104	77	36	492	5.93	0.017	500
Mean	**0.13**	**0.12**	**0.82**	**0.51**	**1.48**	**27**	**48**	**96**	**51**	**21**	**254**	**4.54**	**0.018**	**470**
LSD	**0.03**	**0.03**	**0.32**	**0.17**	**0.75**	**17**	**8**	**8**	**10**	**5**	**117**	**2.52**	**0.007**	**116**

FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, LI=lodging index, GY=grain yield, PH=plant height, PL=Panicle length, SP=spikelet per panicle, DH= days to heading, DM=days to maturity, TR=tiller number, SW=100-seed weight, SB=Shoot biomass

Table. Mean value of the 81 lines, grand mean and LSD for 14 traits at Debre Zeit

Lines	FCD	SCD	FCS	SCS	LI	GY	DH	DM	PH	PL	SP	TR	SW	SB
DZ-01-974	0.26	0.27	1.88	1.26	1.80	151	52	112	108	45	753	9.33	0.026	858
PI-223259	0.16	0.15	1.43	1.03	1.37	64	31	86	67	22	337	9.73	0.020	400
PI-222988	0.21	0.23	1.65	1.11	1.63	23	33	94	83	33	442	8.07	0.016	475
RIL1-62	0.23	0.25	1.76	0.93	1.18	61	40	97	82	33	721	7.40	0.022	517
RIL1-13	0.16	0.17	1.20	1.22	1.93	35	34	84	68	22	330	7.27	0.013	342
RIL1-112	0.21	0.21	1.17	0.77	1.10	68	33	92	76	24	398	7.60	0.018	692
RIL1-197	0.23	0.21	0.84	0.70	1.10	56	33	94	76	25	423	6.87	0.024	675
RIL1-27	0.20	0.19	1.48	1.30	1.67	29	37	92	73	26	399	6.53	0.023	458
RIL1-24	0.17	0.16	1.11	1.18	1.65	50	33	86	66	21	287	9.20	0.015	400
RIL1-15	0.18	0.19	1.27	0.99	1.85	54	34	89	71	27	497	9.87	0.018	483
RIL1-105	0.24	0.23	1.18	0.88	1.08	49	36	90	79	27	516	8.87	0.015	467
RIL1-152	0.21	0.21	1.16	1.14	1.87	91	34	91	83	28	469	6.93	0.024	642
RIL1-75	0.21	0.21	1.64	1.00	1.13	88	34	90	77	32	433	9.60	0.020	575
RIL1-64	0.19	0.20	1.68	1.23	1.88	71	34	87	81	28	517	6.80	0.022	550
RIL1-77	0.25	0.25	1.42	1.01	1.65	37	37	88	72	29	510	9.40	0.020	458
RIL1-143	0.15	0.16	1.45	0.92	1.52	7	36	89	58	24	214	7.80	0.014	300
RIL1-135	0.19	0.19	1.49	0.99	1.63	71	35	93	84	34	325	11.3	0.021	650
RIL1-97	0.22	0.21	1.41	1.08	1.55	58	34	92	83	27	350	9.80	0.021	708
RIL1-17	0.21	0.21	1.25	0.94	1.18	55	36	92	79	28	436	7.87	0.021	517
RIL1-103	0.19	0.17	1.29	1.02	1.50	66	32	88	70	22	309	8.40	0.027	467
RIL1-149	0.21	0.21	1.34	1.17	1.75	72	33	93	79	29	405	8.40	0.021	600
RIL1-76	0.22	0.21	1.69	1.20	1.83	72	34	92	82	29	430	8.73	0.022	567
RIL1-49	0.19	0.18	1.28	1.00	1.20	48	36	93	76	27	459	8.13	0.014	492
RIL1-147	0.17	0.17	1.24	0.88	1.05	48	32	87	60	21	297	11.3	0.014	442
RIL1-52	0.23	0.22	1.64	0.88	1.05	106	32	88	75	29	418	8.20	0.020	550
RIL1-84	0.23	0.24	1.77	1.20	1.68	82	38	101	91	31	322	8.27	0.023	767
RIL1-32	0.22	0.21	1.59	1.10	1.35	63	32	92	76	29	354	7.07	0.019	592
Mean	**0.21**	**0.21**	**1.51**	**1.12**	**1.59**	**69**	**36**	**94**	**81**	**29**	**422**	**8.55**	**0.021**	**583**
LSD	**0.05**	**0.05**	**0.62**	**0.28**	**0.58**	**38**	**4**	**5**	**10**	**6**	**193**	**2.94**	**0.008**	**204**

FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, LI=lodging index, GY=grain yield, PH=plant height, PL=Panicle length, SP=spikelet per panicle, DH= days to heading, DM=days to maturity, TR=tiller number, SW=100-seed weight, SB=Shoot biomass

Table. Mean value of the 81 lines, grand mean and LSD for 14 traits at Debre Zeit *...continued*

Lines	FCD	SCD	FCS	SCS	LI	GY	DH	DM	PH	PL	SP	TR	SW	SB
RIL1-110	0.21	0.20	1.72	1.11	1.32	63	37	94	82	30	392	6.67	0.023	583
RIL1-70	0.23	0.23	1.52	0.95	1.15	33	36	88	82	30	328	7.33	0.018	550
RIL1-56	0.19	0.18	1.79	1.08	1.08	76	34	88	73	27	404	8.73	0.021	575
RIL1-80	0.17	0.15	1.29	1.18	1.52	74	33	90	71	24	336	8.13	0.022	492
RIL1-2	0.18	0.16	1.21	1.01	1.47	29	32	84	70	27	320	8.53	0.017	433
RIL1-154	0.22	0.23	1.59	1.24	1.78	33	36	99	78	27	315	7.60	0.025	467
RIL1-60	0.21	0.21	1.24	1.06	1.58	67	33	92	84	27	411	9.07	0.020	575
RIL1-79	0.20	0.19	1.26	1.27	1.38	128	34	89	85	30	408	10.7	0.023	675
RIL1-146	0.20	0.21	1.73	1.33	1.83	57	34	93	82	32	571	8.53	0.023	517
RIL1-5	0.25	0.25	1.72	1.32	1.67	45	33	91	80	32	451	10.5	0.015	458
RIL1-130	0.16	0.15	1.44	1.01	1.07	74	34	88	68	23	247	8.27	0.017	517
RIL1-119	0.21	0.20	1.59	1.23	1.83	95	33	95	89	29	354	7.53	0.021	708
RIL1-12	0.27	0.26	1.42	0.97	1.17	47	34	95	90	31	457	5.93	0.015	575
RIL1-126	0.23	0.25	1.54	0.93	1.10	69	36	94	82	29	402	7.33	0.017	467
RIL2-84	0.18	0.19	1.65	0.84	1.07	51	35	91	72	27	368	9.87	0.019	525
RIL2-131	0.19	0.17	1.30	0.99	1.83	69	36	95	84	32	441	8.87	0.020	583
RIL2-137	0.21	0.20	1.61	0.99	1.42	30	38	91	80	30	440	9.20	0.016	492
RIL2-36	0.25	0.24	1.49	1.29	1.78	72	40	100	95	36	323	8.40	0.018	658
RIL2-48	0.23	0.25	1.78	1.42	1.75	53	38	99	79	30	454	8.13	0.020	483
RIL2-51	0.21	0.21	1.48	1.32	2.00	62	35	97	87	34	498	8.60	0.024	617
RIL2-152	0.22	0.20	1.65	1.14	1.60	69	34	92	85	29	334	9.07	0.020	717
RIL2-166	0.19	0.20	1.08	1.30	2.13	94	33	91	79	28	349	11.4	0.020	633
RIL2-77	0.23	0.24	1.17	1.19	1.63	43	36	90	81	27	542	8.33	0.022	408
RIL2-14	0.21	0.22	1.51	0.95	1.10	78	36	93	79	26	310	9.27	0.020	692
RIL2-32	0.19	0.20	1.78	1.36	1.37	64	35	93	78	23	383	7.67	0.022	517
RIL2-178	0.19	0.19	1.60	1.39	2.07	59	33	95	85	27	306	9.13	0.022	642
RIL2-72	0.19	0.21	1.75	1.11	1.73	12	38	86	84	28	379	7.60	0.016	333
Mean	**0.21**	**0.21**	**1.51**	**1.12**	**1.59**	**69**	**36**	**94**	**81**	**29**	**422**	**8.55**	**0.021**	**583**
LSD	**0.05**	**0.05**	**0.62**	**0.28**	**0.58**	**38**	**4**	**5**	**10**	**6**	**193**	**2.94**	**0.008**	**204**

FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, LI=lodging index, GY=grain yield, PH=plant height, PL=Panicle length, SP=spikelet per panicle, DH= days to heading, DM=days to maturity, TR=tiller number, SW=100-seed weight, SB=Shoot biomass

Table 8b. Mean value of the 81 lines, grand mean and LSD for 14 traits at Debre Zeit ... *Continued*

Lines	FCD	SCD	FCS	SCS	LI	GY	DH	DM	PH	PL	SP	TR	SW	SB
RIL2-148	0.18	0.19	1.32	0.84	1.10	25	36	93	78	42	438	8.67	0.016	525
RIL2-180	0.17	0.19	1.56	1.07	1.43	43	33	95	80	28	490	7.87	0.020	583
RIL2-20	0.20	0.21	1.55	0.89	1.05	52	36	91	76	26	345	8.73	0.017	525
RIL2-147	0.22	0.23	1.66	1.36	1.90	62	34	97	85	30	346	7.20	0.027	608
RIL2-143	0.19	0.19	1.48	1.05	1.93	37	36	88	77	25	403	9.27	0.016	425
RIL2-113	0.21	0.21	1.24	1.14	1.88	66	33	94	88	30	396	7.80	0.020	667
RIL2-87	0.20	0.21	1.54	1.32	1.98	62	35	98	84	29	392	8.40	0.016	608
RIL2-126	0.26	0.27	2.37	1.24	1.57	166	45	113	111	46	772	8.07	0.018	933
RIL2-118	0.25	0.25	2.00	1.36	1.85	206	43	111	106	42	640	8.47	0.034	917
RIL2-130	0.19	0.17	1.54	1.06	1.95	49	35	91	74	27	358	10.3	0.015	458
RIL2-13	0.19	0.17	1.78	0.97	1.22	11	34	90	70	24	292	7.40	0.016	375
RIL2-69	0.21	0.23	1.87	1.26	1.87	84	35	94	83	30	338	9.00	0.017	717
RIL2-56	0.24	0.23	1.59	1.19	1.75	58	35	93	82	29	419	8.80	0.023	617
RIL2-57	0.19	0.20	1.72	1.31	2.05	192	43	105	88	31	672	8.47	0.034	900
RIL2-133	0.19	0.19	1.33	1.21	1.87	109	37	108	82	30	417	8.87	0.028	683
RIL2-168	0.20	0.19	1.89	1.33	1.97	135	42	97	85	33	586	9.40	0.034	733
RIL2-177	0.18	0.18	1.29	1.21	1.83	77	34	91	76	27	263	12.1	0.020	625
RIL2-62	0.16	0.17	1.41	1.33	2.12	55	32	94	82	27	449	9.00	0.021	617
RIL2-160	0.23	0.21	1.39	1.03	1.73	38	36	95	82	30	447	8.80	0.016	583
RIL2-67	0.23	0.22	1.78	1.42	2.42	62	34	99	83	30	374	8.73	0.020	642
RIL2-185	0.17	0.16	1.45	1.15	1.77	40	33	94	78	25	322	7.40	0.017	550
RIL2-33	0.18	0.19	1.46	1.05	1.48	63	35	94	84	29	427	8.20	0.020	650
RIL2-172	0.19	0.20	1.11	1.13	1.80	53	36	92	72	26	392	8.07	0.018	558
RIL2-111	0.21	0.21	1.54	1.12	1.62	41	37	95	72	27	265	8.27	0.016	533
RIL2-47	0.29	0.28	1.69	1.24	1.83	159	44	110	109	49	712	9.27	0.026	858
DZ-cr-37	0.20	0.21	1.55	1.27	1.62	174	42	108	88	34	532	7.73	0.030	850
Quncho	0.30	0.29	2.25	1.29	1.50	158	51	113	126	50	854	8.73	0.036	917
Mean	**0.21**	**0.21**	**1.51**	**1.12**	**1.59**	**69**	**36**	**94**	**81**	**29**	**422**	**8.55**	**0.021**	**583**
LSD	**0.05**	**0.05**	**0.62**	**0.28**	**0.58**	**38**	**4**	**5**	**10**	**6**	**193**	**2.94**	**0.008**	**204**

FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, LI=lodging index, GY=grain yield, PH=plant height, DH= days to heading, DM=days to maturity, PL=Panicle length, SP=spikelet per panicle, TR=tiller, SW=100-seed weight, SB=Shoot biomass

Contents

1. Introduction

Tef belongs to the family of grasses (Poaceae) and the genus *Eragrostis* with specific nomenclature of *Eragrostis tef* (zucc.) Trottor. Tef originated and diversified in Ethiopia (Vavilov, 1951), and grown only in its center of origin as food crop. It is not uncommon to see enjera (bread prepared from tef) as a staple food in most Ethiopian‟s dish mainly in the central highlands. The crop also has numerous desirable agronomic- and storage- features, and high cultural and socio-economic values (Tefera and Ketema, 2000).

The wide range of agro-climatic conditions in the country favors the existence of large amount of genetic diversity for characters that impart adaptation to specific environments. Effect of natural selection on total variance of characters in one region is obviously different from the other regions due to differences in the type and intensity of selection factors involved (Bekele, 1996). Polymorphism were studied at various levels including seed quality; there are potentials to exploit polymorphism in albumins and globulins in order to identify genotypes with enhanced nutritional quality (Bekele *et al.,* 1995*)* and to select for high protein content without affecting its composition (Bekele, 1995).

However, the diversity does not impart substantial variation to develop cultivars that are stiff or dwarf enough to resist lodging through intra-specific crossing. Studies so far indicated that none of the existing germplasm accessions resist lodging satisfactorily under good growth (Tefera, *et al.,* 2000); lodging persisted as the major bottleneck constraining tef husbandry (Assefa *et al.,* 2000). Grain yield of tef is not competitive with that of the world‟s more popular cereals. This is partly due to the low basic productivity of currently available cultivars, together with susceptibility to lodging (Tefera and Peat, 1997). The total annual production of tef is surpassed by maize because the national average grain yield of tef is low (0.9ton/ha). Tef has a potential of yielding four to five tons of grain per hectare if the lodging problem is resolved. Presently, there is a compelling interest in using the wild relatives to create genetic variability and improve some production limitations of tef (Tefera *et al*., 2003a).

Generally, the stature of tef plant is characterized by bearing of heavy panicles consisting of numerous kernels on relatively thin culms. Owing to such peculiar physio-morphological features, the crop lends itself very much to lodging particularly under growth and yield promoting environmental and management conditions. This feature of the crop forces breeders to search for alternate traits in related species. Tef has many closely related species, which might be useful in improvement of some traits through conventional breeding (Bekele and Lester, 1981; Tavassoli, 1986). *E. pilosa* is the only wild relative found to interbreed with tef. Phylogenetic analysis of sequence data from the nuclear gene *waxy* and the plastid locus *rps16* strongly supports the widely held hypothesis of a close relationship between *E. tef* and *E. pilosa*, a wild allotetraploid (Ingram and Doyel, 2002).

For crop improvement and development of superior genotypes, such high level of polymorphism aid in detecting loci that potentially control desirable traits. This is especially important in interspecific hybridization. *Eragrostis pilosa* (L.) P. Beauv. crosses relatively easily with *E. tef* varieties and as a wild-relative it may bring a source of new genes (Tefera *et al.,* 2003a). The close relationship of *E. pilosa* to *E. tef*, and the highly variable plant morphology and lodging characteristics between the two parents provide a unique opportunity for discovering and introducing much needed morphological improvements to this crop (Virginia, 2003). Polymorphism between species can result from different events and is an important aspect of plant breeding (Bornet and Branchard, 2004).

E. pilosa may deliver gene(s) responsible for lodging resistance to *E. tef* mainly because it has short stature. In a study conducted to characterize four cultivars of *E. tef* and fourteen accessions of *E. Pilosa*, significant difference was found among accessions for many traits including plant height. Earliness is another useful trait, which could be transferred from *E. pilosa* to *E. tef*. (Ayele *et al.,* 1999; Tefera *et al.,* 2003a). A wide range of variation in flavonoids and in proteins was also found both amongst the wild species of *Eragrostis* and amongst the cultivars of *E. tef* (Bekele and Lester, 1981). *E. pilosa* was collected as food in many parts of Africa including Ethiopia during the famine periods (Ketema, 1997).

Inter-specific hybridization, especially through conventional techniques, could not usually serve to produce stable crosses. The meiotic process rarely function with complete normality; even when pairing appears to be fairly regular, segregation often does not fit classical patterns (Allard,

1960); but in crosses of interest to this study, both parental materials (*E. tef* and *E. pilosa*) have chromosome numbers: 2n = 4x = 40, allopolyploids. Hence, no sizable irregularity during meiosis is expected during crossing (Gugsa *et al.,* 2001) and over the generations of gene introgression, which is partly evident by high survival rate of the inter-specific cross progenies themselves. The species is easily crossable conventionally with tef and may serve as a donor species for some desirable traits in tef crop improvement (Gugsa and Mengistu 1999). The species boundary between *E. tef* and *E. pilosa* is blurred due to such crosses.

The fact that *E. pilosa* has the same chromosome number with that of *E. tef* might have led to the success in direct hybridization and for the first time in the history of tef breeding, to generating and evaluating their RILs; RILs of *E. tef cv. Kaye-murri x E. pilosa (30-5)* shaped transgressive segregants for a number of traits. The hybrid status of the F_1 plants was ascertained using morphological markers such as lemma color; seed color and panicle form (Tefera *et al*., 2003a). This is also true for RILs of interest to this study. Characteristic physical features of each of the parental lines such as plant height, stalk thickness, panicle form, lemma color, seed color and maturity duration segregated among RILs in different combination.

It is evident that self-pollination excluding special genetic circumstances rapidly reduces any population to the homozygous condition regardless of the number of heterozygous gene pairs present in the beginning. These simple expectations can never be complete because the attainment of equilibrium is disrupted by a combination of mutation, differential fitness, linkage, drift and variations in mating system. However, inbreeders are adapted to a predominant homozygous (Simmonds, 1979). The materials of interest to this study are assumed to be predominantly homozygous; RILs of the seventh filial generation (F_7). The heterogeneity /diversity/ will be tremendous especially when many varying traits are considered at a time (Allard, 1960); more for inter-specific crosses where many distinct features are available among the parental lines.

The combination of characters represented by each parental species is likely to be adaptive ones but the chances that any new combination will be equally adaptive is small. Hence, the nearer a segregant is to one or the other parental species is characters of adaptive value, the better its chance of perpetuation, whether in nature or in plant breeders nursery (Allard, 1960). There was no any sort of deliberate selection from among the RILs of concern to this study and never

backcrossed to one of the parents to equally favor accumulation of characters of both parental species. The RILs are reflections of the nature of gene introgression in the recombinants over generation of the interspecific crosses, and associated adaptive values and selective advantages of trait combinations.

A study on the earlier similar set of crosses has demonstrated the importance of *E. pilosa* in diversifying the germplasm pool for tef breeding; main aim of this crossing was to identify loci attributing to lodging resistance. Highly significant quantitative trait loci were identified for several agronomic traits including plant height, culm length and culm diameter. It is the first evaluation of tef germplasm derived from interspecific crosses for breeding purposes (Tefera, *et al*., 2003a). More polymorphism is expected from crosses pertinent to this study (Tefera, Pers. Comn.).

2. Literature Review

2.1. Eragrostis tef

2.1.1. Brief description

Tef *(Eragrostis tef* (Zucc.) Trotter) belongs to the family Poaceae, subfamily *Eragrostoideae*, tribe *Eragrosteae* and genus *Eragrostis* (Espelund *et al.,* 2000). The common vernacular name of the crop in Ethiopia is *tef*. It is also known by the vernacular names *tafi* in Oromifa and *taf* in Tigrigna. Tef is a C_4, self-pollinated, chasmogamous annual cereal (Espelund *et al.,* 2000). It has a fibrous root system with mostly erect stems, although some cultivars are bending or elbowing types. The flowers of tef are hermaphroditic with both the stamens and pistils being found in the same floret. A very good production results can be obtained at an altitude range of 1700-2200 m and season rainfall of 300-550 mm and a temperature range of 10-27°C (Ketema, 1997).

2.1.2. Importance of tef

Tef *(Eragrostis tef* (Zucc.) Trotter) is a traditional crop that grows very well under various stress conditions and is extensively used in Ethiopia. The area under tef cultivation is over two million hectares of land each year (Ketema, 1997). Tef is widely grown in both high-potential and marginal production areas. The area include most parts of the vertisols that suffer from waterlogging and other non vertisol parts of Ethiopia that suffer from low moisture stress (Ketema, 1997).

Tef is considered to be well adapted to drought and waterlogged conditions (Ayele *et al.,* 2001); adapted to a wide range of climatic and soil conditions and shows an exceptional level of resistance to biotic stresses (Yu *et al.,* 2007). Tef performs better than wheat, maize and barley on waterlogged vertisol soils but also outperforms other cereals in moisture stressed semiarid areas (Tefera and Peat, 1997). Identifying, maintaining and using crop types that can grow under various stress and limiting conditions is essential (Ketema, 1997). Tef is a diverse species grown in different climatic and edaphic zones in Ethiopia, at elevations of 1000 to 2500 meter (Ayele *et al.,* 2001).

Outside Ethiopia, there is a growing interest in using tef. For example, small-scale commercial production of tef has begun in a few areas of the wheat belts of the USA, Canada and Australia (Bekele, Pers. Comn.). Tef has been introduced to South Africa and cultivated as a forage crop, and in recent years cultivated as a cereal crop in northern Kenya (Ketema, 1997). Tef contains an excellent balance among the essential amino acids and is also rich in mineral content (Bekele, 1978; Lester and Bekele, 1981). Above all, its grain, which fetches a higher price, can be stored for many years without insect damage. Cattle prefer to feed on tef straw to any other cereal straw.

2.1.3. Inheritance of some traits

Basic genetic information is needed for a rapid and planned crop improvement program. This information helps from designing appropriate breeding procedure all the way to marking desirable crosses by segregation pattern of marker genes to setting ultimate cultivar selection criteria. These all are influenced by gene actions and interactions, number of genes involved, presence or absence of maternal effects, presence or absence of linkage and the ploidy level in

general and the kind of tetraploidy in tef (Ketema, 1997). Little attempt has so far been made to study the genetics of these traits although concern is now growing due to the crop‟s importance in the national diet of Ethiopia (Tefera and Peat, 1997). The genetics of observable traits is mainly in use as marker to identify crosses during tef crossing programs.

2.1.3.1. Qualitative traits

In a study to identify inheritance of three traits in tef, six crosses were made among four cultivars that have contrasting phenotypic characteristics (Berhe, 1981). Results of the inheritance of lemma color showed that four pairs of genes were involved. Dominance, complementary and epistatic gene action and interactions were found. Duplicate pairs of genes were identified for the inheritance of seed color. Panicle form was found to be conditioned by duplicate pairs of genes for degree of looseness and another pair of genes for branching pattern. No maternal effects or linkages were detected. All the results showed a disomic inheritance pattern for all three traits which indicates that tef is an allotetraploid. This, in turn, indicates that quantitative genetic theory developed for diploids is applicable to tef (Berhe, 1981). These easily observable qualitative traits are being used as marker in tef crop improvement programs.

2.1.3.2. Quantitative traits

In a study conducted to estimate gene effects controlling grain yield and related agronomic characters in tef, significant additive and dominance x dominance interaction effects were detected for grain yield. The variations of yield per panicle and panicle weight were explained in terms of additive, dominance, and additive x additive interactions (Tefera and Peat, 1997).

The simple additive-dominance model explained the variation for panicle length, culm diameter and plant weight, allowing unbiased estimates of additive and dominance variance components. Large dominance variances were estimated for grain yield, yield per panicle, and panicle weight. The additive variances for plant height, panicle length, days to heading and days to maturity were higher than their respective dominance variances. Non-allelic gene interactions were also detected for kernel weight, harvest index, tiller number, plant height, days to heading and days to maturity (Tefera and Peat, 1997). Future quantitative genetic analysis in the tef plant must consider procedures that may allow the detection of epistasis to avoid biased estimates of additive and dominance components (Ketema, 1997).

High narrow-sense heritability values (> 0.50) were estimated for plant height, panicle length, days to heading and days to maturity. Lowest heritability (0.09) was obtained for kernel weight for which there was little variability. Since grain yield and several important agronomic characters of tef are influenced by non-allelic gene interaction, it is advisable to delay selection for yield to later generations with increased homozygosity (Tefera and Peat, 1997).

2.1.4. Wild relatives

2.1.4.1. Brief description

The genus *Eragrostis* contains about 300 species (Bekele, 1986); about 350 species (Yu *et al.,* 2006). The genus *Eragrostis* has a world-wide distribution; in this large genus the variation is continuous and hence delimitation of groups is difficult (Bekele, 1986). Numerical taxonomic analysis of leaf phenolic and electrophoresis studies of tef cultivars and wild species revealed similarities of tef to different wild species of *Eragrostis* suggesting the possibility of many species involvement in the formation of the gene pool of tef (Bekele, 1986).

Many species of *Eragrostis,* then, are obviously attractive food plants: they produce abundant seeds; they are free threshing; and, above all, they are weeds, inhabiting land disturbed by human activity. "Transition from gathering seeds of selections of readily available weeds to encouraging and cultivating them seems an easy and logical process (Ketema, 1997)."

Wild relatives of cultivated crops play an important role as sources of useful and transferable genes. They enrich and broaden the available genetic base in crop improvement programs and assist in developing superior genotypes. Accordingly, the wild relatives of tef should be considered for improvement work, identified, collected, conserved, characterized and utilized.

2.1.4.2. Relationships with tef

Several studies were made to identify the wild *Eragrostis* species that are related to tef (Ketema, 1997). Relationships of cultivated and wild *Eragrostis* species have been studied using different characters. A widely accepted view is that *E. pilosa* is one of the main progenitors of *E. tef.* Nowadays many scientists are with an opinion that tef should have come from *E. pilosa* via selection. *E. pilosa* is a cosmopolitan species and is sympatric with the cultivated type and even it might have introgressed with some of the occasionally out-breeding *E. tef* (Bekele, 1986).

Overall resemblance of several cultivars of tef to various wild species and the variation that exists within tef calls for a fair number of evidence to work out the relationships of cultivated ones to the wild and in the genus as a whole. Since variation within species is the pool from which evolutionary changes proceed, some associations between intraspecies variability and evolutionary rate must exist. However, the extent to which such associations should hold over long periods of evolutionary time, during which changes in both intraspecies variability and character values are possible is not clear (Bekele, 1986).

2.1.5. Crop improvement

2.1.5.1. Potentials

Genetic variation can be assembled and utilized through hybridization to create new favorable gene combinations and crosses between genetically divergent parents which are expected to result with large genetic variance among progenies in subsequent selfing generations that can be exploited as line cultivar than crosses from closely related parents (Allard, 1988; Tekle-wold, 2005). In a study on regional distribution patterns of morphological characters of tef, accessions were found to be variable for some characters and constant for others (Bekele, 1996). Landraces and cultivars used are not lodging resistant and the development of genetically lodging-resistant cultivars is essential (Ketema, 1997).

Genetic diversity analysis of 47 accessions of tef, three accessions of *E. pilosa*, and six accessions of *E. curvula* using random amplified polymorphic DNA (RAPD) showed that the level of polymorphism among the wild species was high, while low polymorphism was detected among tef accessions (Bai *et al.,* 2000). Cultivated tef and *E. pilosa* differ greatly for most agronomic traits and the close relationship between these two species facilitate hybridization providing a unique opportunity to develop a new pool of genetic variation. In a study to see sequence variation of in some regions of chloroplast DNA some *E. tef* and *E. pilosa* accessions were grouped together while other tef accessions alone (Feyissa, 1999). Utilization of *E. pilosa* as a donor in an interspecific cross is a useful strategy for broadening the genetic diversity of the existing gene pool in cultivated tef (Yu *et al.,* 2007).

There are only few studies conducted to concretely reveal variabilities between the cultivated and wild species of *Eragrostis*. Protein content of 11 cultivars of tef and 14 wild *Eragrostis* species were studied whereby the accessions of tef were found to be lower in total protein content than that of wild species (Bekele, 1978). The wild species has smaller seeds and higher proportion of protein, but the cultivated tef has more lysine. *E. barrelieri* and *E. pilosa* were relatively similar to *E. tef,* especially in having more lysine than the rest of the wild species (Bekele and Lester, 1981).

In a study to evaluate relationships of wild and cultivated species of *Eragrostis* using flavonoid patterns, caryopsis and pollen morphology as a marker, some tef cultivars showed resemblance to different *Eragrostis* species suggesting that many species of *Eragrostis*, in particular *E. pilosa, E. aethiopica* and possibly *E. curvula* and *E. cilianensis* are involved in the origin of tef. The size of both pollen and seed showed little consistent variation but the detailed structure of caryopsis and pollen are found to be helpful taxonomic marker to assess relationships. Numerical value of flavonoid spots studied on 32 wild and 115 cultivated individuals resulted in non-distinctive groups in tef and in distinct groups in wild species that differ from morphological groupings (Bekele, 1986).

2.1.5.2. Interspecific breeding effort

Several attempts were made to investigate the possibility of crossing tef with other wild *Eragrostis* species. However, attempt to make a cross between *E. tef* and *E. curvula* was not successful (Ketema, 1997). Ketema also quoted the work of Tavassoli (1986) that interspecific hybridization attempts using three tetraploids, i.e. *E. tef* x *E. cilianensis (4x); E .tef* x *E. pilosa (4x);* and *E. tef* x *E. minor (4x)* were not successful until the year specified by this publications.

Later on, crossing between *E. tef* and *E. pilosa* was made possible. Genetic linkage map was created for the first interspecific crosses. In an attempt to assess the potential merits of using wild relatives for tef improvement, interspecific cross was made between *E. tef* and *E. pilosa* (Tefera *et al.,* 2003a). The result showed that 156 loci were grouped into 121 markers and 21 linkages. Sixteen percent of the loci deviated from normal segregation with a predominance of *E. tef*, and majority of the distorted loci were clustered into three linkage groups (Yu *et al.*, 2006). For 29.3% of the QTLs, the alleles from *E. pilosa* (30-5) had a beneficial effect (Yu *et al.,* 2007).

Such crossing activities are common in related more popular crops like rice (Khush and Brar, 2003). Wild species are an important reservoir of useful genes for resistance to major diseases and pests, tolerance to abiotic stresses and cytoplasmic male sterility. Genetic variability for agronomic traits is the key component of breeding programs for broadening the gene pool of both rice and other crops (Khush and Brar, 2003).

2.2. Segregation in interspecific hybrids

Allopolyploids combine in more or less blending fashion the characteristics of species from which they are derived. Three general features should be thought of in relation to interspecific crosses. First, tremendous diversity of types appear in the F_2 and later generations as a result of the extreme heterozygosity of interspecific F_1 hybrids. Each individual in an F_2 progeny is likely to be different from each other individual in a large number of characters. Moreover, many segregants are likely to have entirely new characteristics, different from those of either parent that could not have been predicted from a study of the morphology or physiology of the parental species (Allard, 1960).

Secondly, although segregation in the F_2 or later generations produces extremely heterogeneous recombination types, the recombination that actually appears are by no means a random sample of the total possible recombination of parental characteristics. Powerful restriction to recombination is operating in interspecific hybrids; may be due to gametic or zygotic elimination, pleiotropy and linkage. Thirdly, male gametogenesis is more easily upset by chromosomal or genic disharmonies than female gametogenesis. Male gametes with gene contributed by both parents tend to be inviable. Any tendency towards inviability of intermediate types of gametes leads to an excess of the parental zygotes. In addition, variety of recombination zygotes is drastically checked by adaptation requirements (Allard, 1960).

Many field crops are originally derived from hybrids between highly differentiated species. The value of hybridization in the improvement of established allopolyploids has been through the transfer of individual characters from one species to another without limiting to only the different types in segregating generations. The value of hybridization is less when a particular attribute of quality are more important than total quantity of yield. The breeder therefore, usually can not destroy existing genic systems by large number of genes from different species (Allard, 1960).

3. Objective

3.1. General objective

To investigate the extent of variability and trait relationships in the RILs for some morphological traits

3.2. Specific Objectives

To identify traits accounting to gross variability in lodging and grain yield of the RILs

To identify RILs with desired combination of traits for further study/improvement of tef

4. Materials and Methods

4.1. Experimental Materials

The plants materials were made kindly available from the National Tef Research Project which is found in Debre Zeit Agricultural Research Center. They were consisting of 76 RILs derived from two separate crosses of *E. tef x E. Pilosa*; the three parents and two other cultivars. The crosses were *E. tef* (DZ-01-974) x *E. pilosa* (PI-2232259) and *E. tef* (DZ-01-974) x *E. pilosa* (PI-222988). In both crosses, *E. pilosa* was used as a pollen parent. The 76 RILS were randomly taken from the two crosses progenies (38 lines from each) at F_7 generation. The two improved tef cultivars (DZ-cr-37 and Quncho) were included as standard check. (Table 1)

Figure 1. Phenotypic appearances of the parents at field level:
E. pilosa (PI-222988), *E. tef* (DZ-01-974) and *E. pilosa* (PI-223259) [from left to right]

The RILs are descendants of the interspecific cross through continuous maintenance of progenies up to the seventh filial generation (F_7) in the natural reproductive system /predominantly self/ by single-seed-decent-method. The tef cultivar DZ-01-974 is late maturing, thick culmed, tall, has loose panicle and pale white seed color. *E. pilosa* has quite different features: early maturing, thin culmed and shorter in stature; PI-223259 has red seed color while PI-222988 has deep brown.

Table 1. List of the 76 *E. tef* x *E. pilosa* RILs, parental lines and standard check tef cultivars used in the study

Serial number	Lines designation	Serial number	Lines designation	Serial number	Lines designation	Serial number	Lines designation
1	DZ-01-974*	21	RIL1-149	41	RIL1-126	61	RIL2-87
2	PI-223259**	22	RIL1-76	42	RIL2-84	62	RIL2-126
3	PI-222988**	23	RIL1-49	43	RIL2-131	63	RIL2-118
4	RIL1-62	24	RIL1-147	44	RIL2-137	64	RIL2-130
5	RIL1-13	25	RIL1-52	45	RIL2-36	65	RIL2-13
6	RIL1-112	26	RIL1-84	46	RIL2-48	66	RIL2-69
7	RIL1-197	27	RIL1-32	47	RIL2-51	67	RIL2-56
8	RIL1-27	28	RIL1-110	48	RIL2-152	68	RIL2-57
9	RIL1-24	29	RIL1-70	49	RIL2-166	69	RIL2-133
10	RIL1-15	30	RIL1-56	50	RIL2-77	70	RIL2-168
11	RIL1-105	31	RIL1-80	51	RIL2-14	71	RIL2-177
12	RIL1-152	32	RIL1-2	52	RIL2-32	72	RIL2-62
13	RIL1-75	33	RIL1-154	53	RIL2-178	73	RIL2-160
14	RIL1-64	34	RIL1-60	54	RIL2-72	74	RIL2-67
15	RIL1-77	35	RIL1-79	55	RIL2-148	75	RIL2-185
16	RIL1-143	36	RIL1-146	56	RIL2-180	76	RIL2-33
17	RIL1-135	37	RIL1-5	57	RIL2-20	77	RIL2-172
18	RIL1-97	38	RIL1-130	58	RIL2-147	78	RIL2-111
19	RIL1-17	39	RIL1-119	59	RIL2-143	79	RIL2-47
20	RIL1-103	40	RIL1-12	60	RIL2-113	80	DZ-Cr-37***
						81	Quncho***

The suffixes 1 or 2 after „RIL" in designating each RIL represents the type of cross: 1 for Dz-01-974 x PI-223259 (cross 1) and 2 for Dz-01-974 x PI-222988 (cross 2): RIL1-22 implies RIL number 22 of the first cross for example; * = tef parent; ** = pilosa parents; *** = check cultivars

4.2. Experimental site

The experiment was conducted at Debre Zeit Agricultural Research Center and at Akaki site in the 2007 main rainy season to account for variations in response to some agro ecological differences. The planting was done on typical black soil / vertisol / at both sites.

Debre Zeit is located at about 45 km East of Addis Ababa and its geographical extent ranges from $08^0 45' 15''$ to $08^0 46' 45''$ north latitude and from $38^0 46' 45''$ to $39^0 01' 00''$ east longitude. The soil textural class is loam and having haplic andosol, vitric andosol and vertisol soil types. The mean annual rainfall is 801.3 mm. The mean maximum and minimum temperature is 25.5^0C and 10.5^0C, respectively. Monthly temperatures: 23.7^0C in July, 27.7^0C in May. Minimum temperature ranges between 7.4^0C in December to 12.1^0C in July and August. It has hot to warm sub-humid climate in an altitude of about 1850 m above sea level (Debre Zeit Agricultural Research Center).

Akaki is located at about 30 km North of Debre Zeit and its geographic location is at $08^0 53'' 39$" north latitude and $38^0 49'' 13$" east longitude. It has a soil type dominated by heavy clay and Eutric Vertisol. Its altitude is 2120 m above sea level and hot to warm sub-humid climate; cooler than the Debre Zeit site. Akaki is cool highland relatively to Debre Zeit (Tefera *et al.,* 2003a).

4.3. Design, layout and crop management

The experiment was laid out in RCB design in three replications. Each line was planted in two-row basis. Row length was 1.5 meter. Hence, each replication/block had a total of 162 rows. Therefore, total land allotted in each location was about 48.2m x 7.5m including spaces between blocks. Very similar set of experiments were done on rice to investigate associations among yield components of 80 breeding lines derived from crosses in the F_6 and their parents were tested in RCBD with two replications (Surek and Beser, 2003)

Sowing was done on August 04, 2007 at Debre Zeit and on August 11, 2007 at Akaki. The standard spacing between rows was 0.2 m. Double row spacing (0.4 m) was used to separate each double-row (plot) representing every single entry in a block. Seed was drilled in rows and thinned to about 0.1 m spacing when grown to retain 15 plants per row at Debre Zeit but left as such at Akaki in response to weak emergence of plant stands.

Growing packages and other management practices were done as recommended for tef in the area. DAP was applied at a rate of 3.98 gm/row (132.5 kg per hectare basis) all at planting. Application of urea was done once at a rate of 2.32 gm/row (77.5 kg per hectare basis) at about three to four leaf stage/ after two weeks from planting. Weeding practice was uniform especially in a block but not so scheduled to maintain the blocks as clean as possible in response to erratic pattern of appearance of weed flora.

4.4. Data collected

Data was collected for the following traits based on standard procedure.

Days to heading: - Number of days from sowing up to emergence of panicle from the flag leaf sheath in 50% of the population.

Days to maturity: - Number of days from sowing to the time that 50% of the plants in a population (in a plot) reaches maturity stage.

Plant height *(cm)*: - Height of the plant from the base (ground level) up to the tip of the main panicle; *taken from five sample plants at maturity.*

First and second culm diameters *(mm):* - Diameters at the middle of first and second basal culm internodes; *measured in laboratory by an automated machine from five sample plants.*

First and second culm strength *(pound):* - Strength of the stack at the middle of the first and second basal internodes*; taken by Rind Penetrometer from five sample plants.*

Figure 2. During data collection at Akaki

Lodging index: - Degree of leaning of the plants from the vertical axis; *estimated by relative observation of percent of plant stands per some average categories of degrees of leaning in a plot. Not all plants in a plot can have uniformly similar intensity of lodging.*

Panicle Length *(cm):* - Measured starting from the node where the first panicle branch emerges up to the tip of the main panicle*; taken from five sample plants.*

Tiller number: - Number of tillers that have produced panicle; *taken from five sample plants.*

Spikelet per panicle: - Number of spikelets on the main panicle; *taken from five sample plants.*

Shoot biomass *(gm)*: - Weight of whole parts of plants above the ground harvested from a plot.

Grain yield *(gm)*: - Weight of grains from whole plants in a plot at 12.5% moisture content; weighted after the grain was sun dried.

100-seed weight *(gm)*: - Weight of hundred seeds at 12.5% moisture content; *manually counted from single sample from the grain in each plot from well dried seeds.*

4.5. Statistical Procedures

Homogeneity and normality of error variance was done mainly using relationships of predicted means and residuals for all traits. Though all Fmax test, Bartlet‟s test and the graphical illustrations were made, emphasis was made on the third method as the former two methods (significance tests) may not sufficiently reveal the nature of raw-data when number of repeats (replications) become very small; only three in this case. The predicted mean - residual relationship was also used to select appropriate transformation method to homogenize error variances and normality of data of traits that showed some heterogeneity.

The data for all the parameters was subjected to analysis using SAS statistical computer package for ANOVA. Range, coefficients of phenotypic and genotypic variances, heritability and genetic advance were done from mean square value and grand mean for each trait. Estimation of phenotypic correlation coefficient was done by SPSS statistical software while genotypic correlation coefficient and path coefficient analysis were done using SPAR software.

Average data taken from five sample plants in each double-row (plot) was used in the analyses for traits that required sampling. Sites were considered as random effects and genotypes as fixed effects. ANOVA was done for single site and sites data combined. All other analyses including the test for homogeneity of error variance were done with emphasis on individual sites.

The two check cultivars included in the study were taken out in all analyses to reveal variability and correlation parameters within the families of the interspecific crosses. The ANOVA was repeated as such (including the check cultivars) to compare performance of the RILs in relation to the improved cultivars of tef. This was actually the primary objective of including the cultivars in the study thereby assist breeder in selection of promising lines for further study.

4.5.1. Analysis of variance

Total variability present among the lines for each of the traits was partitioned into known and unknown effects following the standard procedures of ANOVA using the following model (Gomez and Gomez, 1984).

Table 2. Source of variation, degree of freedom and mean squares for RCB design

Source of variation	Degree of freedom	Mean square	Expected mean square
Replications per location	(r -1)	MS_r	$\sigma^2_e + g\sigma^2_r$
Location	(L-1)	MS_L	$\sigma^2_e + g\sigma^2_L$
Genotypes	g-1	MS_g	$\sigma^2_e + r\sigma^2_{gI} + rL(\sigma^2_g)$
Genotype x Location	(g-1) (L-1)	MS_I	$\sigma^2_e + r\sigma^2_{gI}$
Error	(r-1)(g-1)L	MS_e	σ^2_e

r=number of replication, g=number of genotypes, L=number of location, I=interaction, MSe = mean square of error, MSr=mean square of replication, MSg=mean square of genotypes, MS_I = Mean square of interaction

Genotypic, environmental and phenotypic variances were estimated according to Falconer (1981) as:

Genotypic variance (σ^2_g) for single location = (MS_g - MS_e) / r

Over locations genotypic variance (σ^2_g) = (MS_g – MS_I) / rl

Interaction variance (σ^2_I) = (MS_I – Ms_e) / r

Environmental variance (σ^2_e) = MS_e /r

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

Model of the experiment used

For single location: $Y_{ij} = \mu + r_j + g_i + e_{ij}$

Yij = observation of the i^{th} genotype in the j^{th} replication, μ=grand mean of trait Y, g_i= effect of the i^{th} genotype, e_{ij} =effect of experimental error, $r_{j=}$ the effect of $_j^{th}$ replication

For combined data over locations: $Y_{ijk} = \mu + g_i + L_j + r_k + (I)_{ij} + e_{ijk}$

Y_{ijk} = observation of the i^{th} genotype in the j^{th} location and K^{th} replication, μ = grand mean of trait Y, g_i = effect of the i^{th} genotype, Lj = effect of j^{th} location, r_k = effect of k^{th} replication, e_{ij} = effect of experimental error

4.5.2. Estimation of components of variance

Phenotypic and genotypic coefficients of variation were calculated according to the method suggested by Burton (1953) as:

4.5.2.1. Phenotypic coefficient of variation

$PCV = [(\delta^2_P)^{1/2}/\mu] \times 100$

PCV= phenotypic coefficient of variation; μ= Population mean

4.5.2.2. Genotypic coefficient of variation

$GCV = [(\delta^2_g)^{1/2}/\mu] \times 100$

GCV= phenotypic coefficient of variation; μ= Population mean

PCV and GCV values > 20% is regarded as high, 10 - 20% is considered as medium and < 10% is considered as low (Kherdade et al. 1985).

4.5.2.3. Heritability

Heritability in broad sense (H) was calculated according to Allard (1960) as:

$$H = (\sigma^2_g / \sigma^2_p) \times 100$$

σ^2_g and σ^2_p are defined as above

Dabholkar, (1992) mentioned that according to Robinson et al. (1954), broad sense heritability in cultivated plants can be placed in the following category. Heritability estimates from 5 - 10% is as low, values from 10 - 30% medium and values 30% and above estimated to be high.

4.5.2.4. Genetic Advance

Genetic Advance (GA) was estimated using the formula of Johnson *et al*. (1955) as:

$$GA = (\sigma^2_g / \sigma^2_p) \times k^* \sigma_p$$

σ^2_g and σ^2_p are defined as above, k (= 2.056) is the selection differential expressed in phenotypic standard deviation depending on the selection intensity chose (= 5%), σ_p is the phenotypic standard deviation.

Genetic advance as percent of mean = (GA / mean) x 100%

4.5.3. Estimation of correlation

Phenotypic and genotypic Pearson‟s correlation coefficients between two variables were estimated as follows (Miller *et al*., 1958).

$$r_{pxy} = \sigma^2_{pxy} / [(\sigma^2_{px})(\sigma^2_{py})]^{1/2}$$

$$r_{gxy} = \sigma^2_{gxy} / [(\sigma^2_{gx})(\sigma^2_{gy})]^{1/2}$$

r_{pxy}=phenotypic and r_{gxy}=genotypic correlation coefficients between characters x and y;
σ^2_{pxy}= phenotypic covariance and σ^2_{gxy}= genotypic covariance between x and y

Tests for significance of coefficients of correlation at phenotypic level used g-2 degree of freedom as suggested by Gomez and Gomez (1984).

$$t = r_{pxy} * (g-2)^{1/2} / (1-r_{pxy}^2)^{1/2}$$

4.5.4. Path-coefficient analysis

Path analysis followed the correlation analysis using the formula suggested by Dewey and Lu (1959) to assess direct and indirect effects of different variables on lodging index and grain yield.

$$r_{ij} = p_{ij} + \sum r_{ik}p_{kj}$$

r_{ij} is the mutual association between independent trait (i) and dependent variable (j), p_{ij} is component of direct effect of the independent (i) on the dependent (j) and $\sum r_{ik}p_{kj}$ is sum of components of indirect effect of a given independent trait (i) on the dependent variable (j) via all other independent traits (k)

The residual effect (U) was calculated using the formula suggested by Dewey and Lu, (1959).

$$U = \sqrt{1 - R^2}$$

$R^2 = \sum r_{ik}p_{kj}$, U= the residual; unexplained variation of the dependent variable; (not accounted for by path coefficient)

4.5.5. Principal Component Analysis

Principal component analysis was done using MINITAB statistical software. The software was ordered such that data of every variable was pre-standardized into a mean of zero and variance of one. Eigenvalue of one was used as minimum threshold to explain the entire variability (Assefa *et al*., 2001).

5. Results and Discussion

5.1. Variability

5.1.1. Analysis of variance

Mean squares due to various sources of variation are presented in Table 3. An F-test showed that variation among lines was significant ($p < 5\%$) for all the traits studied except for number of tiller and 100-seed weight at Akaki (Table 3a). At Debre Zeit, significant ($p < 1\%$) variation was obtained for all traits under study except for strength of the first culm strength and number of tillers (Table 3b).

When combined over locations, a trait that showed no significant ($p > 5\%$) variation was only number of tiller. Variation in first culm strength was significant at $p < 1\%$ and all other traits showed very highly significant ($p < 0.1\%$) variation. Similar result was obtained among the earlier interspecific RILs at F_9 generation. Highly significant differences were obtained for all traits studied; grain yield, shoot biomass, lodging index, days to heading and maturity, plant height, panicle length, panicle weight and yield per panicle (Tefera *et al.,* 2003a).

NB: Throughout the discussion comparable results for similar traits are inclusively stated (for example: first and second culm diameters are stated together without prefix as culm diameter).

Figure 3. A segment of segregants /RILs/ in a block at Akaki experimental field

Table 3a. ANOVA mean square values, CV and R^2 of 14 traits for 79 lines of the *E. tef* x *E. pilosa* crosses at Akaki

Source of variation	Degree of freedom	Mean square								
		Days to heading	Days to maturity	Plant height	First culm diameter	Second culm diameter	First culm strength	Second culm strength	Lodging index	Log (x+1) Lodging index
Replication	2	0.266 ns	203.60***	88.43 ns	0.00012 ns	0.0002 ns	0.054 ns	0.016 ns	0.21 ns	0.007 ns
Genotype	78	78.26***	101.16***	170.01***	0.0017***	0.0014***	0.065**	0.0193**	0.36**	0.0100**
Error	156	22.39	25.48	34.78	0.00044	0.00039	0.041	0.0117	0.21	0.0059
CV (%)		9.99	5.25	11.75	16.66	16.37	24.68	21.33	31.41	19.95
R^2		64	68	71	66	65	45	46	46	47

*Significant at 5%, **Significant at 1%, ***Significant at 0.1%, ns = none significant, Log (x+1) = transformed,

R^2 = the degree (in %) by which a trait explains variability in the study materials

Table 3a. *Continued*

Source of variation	Degree of freedom	Mean square						
		Panicle length	Spikelet per panicle	Grain yield	Arcsine grain yield	Biomass	Tiller number	100-seed weight
Replication	2	28.99*	20623.00*	64.11 ns	0.144 ns	10000 ns	46.51***	0.000055*
Genotype	78	40.40***	13670.43***	315.91***	0.453***	7964.95**	2.47 ns	0.00002 ns
Error	156	8.50	5226.64	107.78	0.190	5128.21	2.44	0.000016
CV (%)		13.80	28.8	40.12	11.42	15.25	34.45	22.35
R^2		71	58	60	55	45	43	38

*Significant at 5%, **Significant at 1%, ***Significant at 0.1%, ns = none significant, Arcsine = Arcsine transformed data

Table 3b. ANOVA mean square values, CV and R^2 of 14 traits for 79 lines of the *E. tef* x *E. pilosa* crosses at Debre Zeit

Source of variation	Degree of freedom	Mean square								
		Days to heading	Days to maturity	Plant height	First culm diameter	Second culm diameter	First culm strength	Second culm strength	Lodging index	Log (x+1) lodging index
Replication	2	59.56***	15.65	247.16**	0.00018	0.00022	0.54*	0.54	0.84**	0.021**
Genotype	78	33.94***	105.76***	257.9***	0.0024***	0.0027***	0.19	0.081***	0.33***	0.0094***
Error	156	5.23	11.44	35.71	0.0011	0.0010	0.15	0.030	0.13	0.0033
CV (%)		6.45	3.62	7.44	15.73	15.02	25.41	15.47	22.52	0.60
R^2		77	82	79	53	58	41	58	58	14.40

*Significant at 5%, **Significant at 1%, ***Significant at 0.1%, ns = none significant, Log (x+1) = transformed

Table 3b. *Continued*

Source of variation	Degree of freedom	Mean square						
		Panicle length	Spikelet per panicle	Grain yield	Arcsine grain yield	Biomass	Tiller number	100-seed weight
Replication	2	19.6 ns	63744.5**	7548.5***	2.9***	899106***	7.29 ns	0.000023
Genotype	78	81.25***	38394.68***	4088.87***	1.02***	50699.79***	4.06 ns	0.000056***
Error	156	15.65	14277.98	553.24	0.1234	16055.80	3.33	0.000023
CV (%)		13.57	28.75	35.26	7.47	22.04	21.34	23.80
R^2		72	58	79	82	70	39	55

*Significant at 5%, **Significant at 1%, ***Significant at 0.1%, ns = none significant, Arcsine = Arcsine transformed data

Table 3c. ANOVA mean square values, CV, and R^2 of 14 traits for 79 lines of *E. tef* x *E. pilosa* crosses sites data combined

Source of variation	Degree of freedom	Mean square								
		Days to heading	Days to maturity	Plant height	First culm diameter	Second culm diameter	First culm strength	Second culm strength	Lodging index	Log (x+1) lodging index
Replication	2	33.50 ns	53.22 ns	280***	0.00008	0.0003 ns	0.412*	0.011 ns	0.553*	0.013 ns
Genotype	78	88.11***	161.31***	323.26***	0.0025***	0.0026***	0.14**	0.057***	0.434***	0.0124***
Location	1	16729***	907***	107916***	0.765***	0.865***	56***	44.38***	1.65**	0.060***
Genotype x location	78	24.10***	45.61***	104.68***	0.0015***	0.0014***	0.11 ns	0.043***	0.259**	0.0070**
Error	312	13.89	19.40	35.38	0.0007	0.00067	0.09	0.021	0.173	0.0047
CV (%)		9.00	4.64	9.11	16.41	15.85	26.41	17.78	27.17	17.28
R^2		85	74	93	82	85	72	89	51	52

*Significant at 5%, **Significant at 1%, ***Significant at 0.1%, ns = none significant, Log (x+1) = transformed

Table 3c. *Continued*

Source of variation	Degree of freedom	Mean square						
		Panicle length	Spikelet per panicle	Grain yield	Arcsine grain yield	Biomass	Tiller number	100-seed weight
Replication	2	46.38*	67668.266**	4370***	1.92***	478889***	11.62*	0.00002 ns
Genotype	78	95.77***	38177.52***	2747***	1.10***	36800***	3.33 ns	0.00004***
Location	1	7615***	3208992***	197440***	92.63***	1315929***	1911***	0.0005***
Genotype X location	78	25.88***	13887.59*	1658***	0.37***	21864**	3.20 ns	0.00003**
Error	312	12.01	9796.56	349.06	0.16	13264.78	3.14	0.00003
CV (%)		13.79	29.70	40.36	9.47	22.05	27.06	23.33
R^2		82	71	83	81	62	71	51

*Significant at 5%, **Significant at 1%, ***Significant at 0.1%, ns = none significant, Arcsine = Arcsine transformed data

5.1.2. Estimates of variability parameters

Data on observed variations were examined in terms of range of mean values, PCV, GCV, heritability and genetic advance to get clue about the extent to which the variation among the study materials was genetically determined (Table 4a,b,c).

5.1.2.1. Akaki

PCV ranged between 6.03% and 39.65%, while GCV between 5.01% and 32.01%. The highest PCV and GCV values were obtained for grain yield while the lowest values were obtained for days to maturity in PCV and 100-seed weight followed by day to maturity (5.22 %) in GCV. Three traits (lodging index, panicle length and tiller) showed PCV in the range of 20 - 30%, but only panicle length fall in this range in GCV value. Culm diameter, lodging index, panicle length, plant height and first culm strength showed medium GCV (10 - 20 %) and the remaining six traits below 10%. General pattern of similarity was observed in other studies that did not consider the culm characters: grain yield showed a relatively high GCV (12-16%); GCV was doubled by the crossing (> 30%) (Tefera *et al.,* 2003b). 100-seed weight was not improved in the past breeding efforts (Teklu and Tefera, 2005) which may partly imply absence of variability.

Table 4a. Range, grand mean, phenotypic and genotypic coefficients of variation, heritability and genetic advance for 14 traits in 79 lines of *E. tef* x *E. pilosa* crosses at Akaki

Trait	Min	Max	Mean	PCV (%)	GCV (%)	H (%)	GA % mean
DH	41.33	66.00	47.34	10.79	9.12	71.40	15.84
DM	86.67	121.67	96.22	6.03	5.22	74.81	9.28
PH	31.87	70.07	50.20	15.00	13.37	79.54	24.52
LI	1.00	2.33	1.47	23.64	15.16	41.13	19.99
FCD	0.09	0.19	0.126	18.79	16.14	73.78	28.50
SCD	0.087	0.18	0.120	17.99	15.31	72.40	26.78
FCS	0.57	1.34	0.815	18.03	11.04	37.52	13.91
SCS	0.37	0.71	0.507	15.84	9.96	39.54	12.87
PL	12.80	32.00	21.13	17.37	15.43	78.96	28.20
SP	146.33	492.07	251.00	26.89	21.14	61.77	34.15
TLR	2.80	7.20	4.54	20.01	2.19	1.19	0.49
SBM	366.67	633.33	469.62	10.97	6.55	35.62	8.03
Yield	10.10	66.41	25.88	39.65	32.18	65.88	53.71
SWT	0.012	0.029	0.018	13.84	5.01	13.10	3.73

DH=days to heading, DM=days to maturity, PH=plant height, LI=lodging index, FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, PL=Panicle length, SP=spikelet per panicle, TR=tiller number, SBM=Shoot biomass, Yield=grain yield, SWT=100-seed weight

Variation in heritability was wide among the 14 traits. Eight of the 14 traits were heritable to over 60% but all were below 80%. Unlike the GCV values, heritability of days to heading and maturity was among the highest. This also resembles the earlier study; a comparatively high heritability was obtained from days to heading (31%) followed by panicle length (25%) (Tefera *et al.,* 2003b). From the remaining six, four traits showed relatively low heritability (<40%); and the other two (number tiller and 100-seed weight) were least heritable (< 15%). The potential of genetic gain as % of mean was low for most of the traits; only two traits showed >30% and only four out of the 12 remaining showed values > 20%.

5.1.2.2. Debre Zeit

Similar pattern of the variability measures were obtained in this location. PCV ranged between 6.35% and 55.35% while GCV ranged between 5.76% and 51.47%. Like in the Akaki site, the highest PCV and GCV were recorded for grain yield and the lowest values were recorded for different traits; the lowest PCV for tiller followed by days to maturity (6.00%) and days to heading (8.72%).

Table 4b. Range, grand mean, phenotypic and genotypic coefficients of variation, heritability and genetic advance for 14 traits in 79 lines of *E. tef* x *E. pilosa* crosses at Debre Zeit

Trait	Min	Max	Mean	PCV (%)	GCV (%)	H (%)	GA % mean
DH	31.33	52.00	35.46	9.49	8.72	84.59	16.50
DM	84.00	112.67	93.46	6.35	6.00	89.19	11.65
PH	58.20	110.53	80.37	11.54	10.71	86.15	20.43
LI	1.05	2.42	1.59	20.86	16.31	61.14	26.22
FCD	0.15	0.29	0.21	13.59	10.11	55.32	15.46
SCD	0.15	0.28	0.21	14.45	11.56	63.98	19.01
FCS	0.84	2.37	1.50	16.54	7.64	21.32	7.25
SCS	0.70	1.42	1.119	14.66	11.63	62.90	18.96
PL	20.67	48.93	29.15	17.85	16.04	80.74	29.64
SP	214.20	771.60	415.56	27.22	21.58	62.81	35.16
TLR	5.93	12.13	8.55	13.60	5.76	17.91	5.01
SBM	300.00	933.33	575.00	22.61	18.69	68.33	31.76
Yield	7.09	206.34	66.70	55.35	51.47	86.47	98.40
SWT	0.013	0.034	0.020	21.42	16.43	58.84	25.90

DH=days to heading, DM=days to maturity, PH=plant height, LI=lodging index, FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, PL=Panicle length, SP=spikelet per panicle, TR=tiller number, SBM=Shoot biomass, Yield=grain yield, SWT=100-seed weight

All except grain yield showed PCV < 30% and yet only five out of the 13 traits showed PCV value > 20%. The genotypic variability parameter (GCV) was narrower at this location; only two traits: grain yield (51.47%) and spikelet per panicle (21.58%) showed high variability.

Though the amount of heritable variation showed similarity between the two environments, heritability values were generally higher at this site; 12 out of the 14 characters showed heritability value > 50% and five of them were between 80 to 90%. Accordingly, potential of genetic grain from improvement program based on these materials was compromised to a higher value for some traits. Highest value in genetic advance as % of mean (98.80%) was recorded for grain yield, which is actually the only trait attributing by far high GCV (51.47%) in addition to its strong inheritance (86.47%). Greater than 25% genetic advance as % of mean was obtained for five other traits.

5.1.2.3. Sites data combined

When combined over the sites, both PCV and GCV showed slightly lower than the single site values for all the 13 traits may be due to interaction effect of genotypes to the different environments. Like in the single site analysis, grain yield showed the highest PCV (46.22%) and GCV (29.10%) followed by spikelet per panicle (PCV=23.93%, GCV=19.09%). All other traits showed GCV values less than 15%; yet for panicle length and lodging index GCVs were above 10%. Grain yield goes to be highest in variability may be due to the fact that it is a highly quantitative trait and is a function of many other traits including spikelet per panicle, which showed consistently higher variability next to grain yield.

Consistent to the single site results, tiller (PCV=11.38%, GCV=2.19%) followed by days to maturity (PCV=5.45%, GCV=4.63%) and days to heading (PCV=9.26%, GCV=7.89%) followed showed the lowest variability. The apparent lion share of the phenotypic variability and its insignificance in tiller would also be an implication of the significant variability in stand-count as plant stands (rows) that are sparsely populated may tend to produce more tillers.

Table 4c. Range, mean, phenotypic and genotypic coefficients of variability, heritability and genetic advance for 14 traits in 79 lines of *E. tef x E. pilosa* crosses combined over sites

Trait	Min	Max	Mean	PCV (%)	GCV (%)	H (%)	GA % mean
DH	34.16	59.00	41.40	9.26	7.89	72.65	13.83
DM	85.33	112.50	94.84	5.47	4.63	71.72	8.06
PH	48.73	90.30	65.29	11.24	9.25	67.62	15.63
LI	1.03	2.15	1.53	17.56	11.14	40.22	14.52
FCD	0.13	0.22	0.17	12.33	7.76	39.57	10.03
SCD	0.12	0.22	0.16	12.81	8.59	44.97	11.84
FCS	0.88	1.77	1.16	13.25	6.40	23.31	6.35
SCS	0.58	1.00	0.81	12.01	6.02	25.10	6.20
PL	17.27	39.20	25.14	15.89	13.58	72.98	23.85
SP	196.20	606.30	333.28	23.93	19.09	63.62	31.31
TLR	4.97	8.87	6.55	11.38	2.19	3.70	0.87
SBM	350.00	783.33	522.31	14.99	9.55	40.59	12.51
Yield	9.44	119.42	46.29	46.22	29.10	39.63	37.66
SWT	0.015	0.028	0.019	13.89	6.72	23.42	6.69

DH = days to heading, DM = days to maturity, PH = plant height, LI = lodging index, FCD = first culm diameter, SCD = second culm diameter, FCS = First culm strength, SCS = second culm strength, PL = Panicle length, SP=spikelet per panicle, TR = tiller, SBM=Shoot biomass, Yield=grain yield, SWT=100-seed weight

Heritability estimates in the combined analysis revealed that only five out of the 13 traits had values greater than 60% but < 75%. These are panicle length (72.98%), days to heading (72.05%), days to maturity (71.72%), plant height (67.62%) and spikelet per panicle (63.62%). Other five traits namely: culm diameter, biomass, lodging index and grain yield showed heritability in the range of 39 - 45%. The rest three were medium heritable (20-25%) and tiller number was the least (15%).

General possibility of genetic advancement is low. Only two traits (grain yield and spikelet per panicle) showed genetic advance as % of mean between 30-40% followed by panicle length (23.85%). Perhaps the contribution of spikelet per panicle and panicle length to grain yield relatively increased its potential genetic gain to remain the highest. All other traits showed no far wide possibilities of advancement (genetic advance as % of mean < 16%). High genetic advance as % of means was obtained for grain yield (16%) in the earlier study (Tefera *et al*., 2003b); which is low relative to the higher variability obtained in this study. High heritability coupled with high genetic advance was observed for plant height, panicle length, spikelet per panicle and grain yield indicating the operation of additive gene action.

In all, except first culm strength and tiller number lines significantly ($p < 1\%$) interacted with the environments. For spikelet per panicle, the significance was uniquely valuable only at $P < 5\%$. The two sites were significantly ($P < 1\%$) different with respect to all the traits included in the study, which was actually apparent even from morphological observation. Hence emphasis was given to location wise effects to exploit heterogeneity of the environments in the two sites rather than the result obtained when the sites data was combined.

Variance for the interaction between lines and sites were significant for grain yield, shoot biomass, lodging index, days to maturity, panicle length and panicle weight (Tefera *et al*., 2003b). But genotypic variance was greater than genotype x location interaction variance for all the 13 traits, which contrasts with higher genotype x environment interaction variance than genotypic variance for shoot biomass, lodging index, days to maturity, panicle length and plant height (Tefera *et al*., 2003b). In addition to yearly variations the referred study was conducted in one more site that may contribute to such contrasts.

5.1.3. Trait-wise estimates of variability

5.1.3.1. Duration of growing period

The range observed for day to heading was 43 to 66 at Akaki and 31 to 52 at Debre Zeit. Both PCV and GCV were low (not > 10%) though the trait was highly heritable (> 70%) to result in moderate genetic advance as % of mean (about 16%). Genetic gain is a function of both the GCV and heritability; if one of them goes low no recovery in genetic advancement could be attained.

The number of days added to the heading to maturity did not alter the pattern of changes in variability parameters though their amount shrinks during seed-setting. The lines took days to mature in the range of 87 to 122 at Akaki, 84 to 113 at Debre Zeit. Though the trait showed significant difference ($P < 0.1\%$) and was highly heritable (71.40% in Akaki and 89.19% in Debre Zeit), GCV was too low (not > 6%) to minimize the genetic gain as % of mean below 10%. The result was sufficient to reveal the widely held view that *E. pilosa* is early and the crossing may provide huge variability into the duration of growing periods among the RILs though it was relatively variable than the earlier study on similar lines; GCV = 4.12% (Tefera *et al.,* 2003a), GCV = 1.58% (Tefera *et al.,* 2003b).

5.1.3.2. Plant height

Variation in height of plants of the lines ranged from 31.87 cm to 70.07 cm, which implies a range of difference > 76% of the grand mean at Akaki. The difference was relatively low at Debre Zeit (58.20 cm to 110.53 cm), which is about 60% of the grand mean in the area. PCV and GCV were moderate (10 - 20%) but closer to the lower range (10%) at Debre Zeit. Maximum heritability was recorded for plant height over all other traits. Together with the moderate variability, the strong inheritance of the trait maintained a high genetic advance as percent of means (> 20%) but less than 25%. The values moderately reconcile with the level of significance (P < 1%) obtained in F-test.

5.1.3.4. Culm diameter

At Akaki, range of values for culm diameter was 0.09 to 0.19 with mean of 0.126 at the basal internode and 0.087 to 0.1 with mean of 0.12 at the next basal internode. Moderate variability (PCV and GCV > 15% and < 20%) were recorded at both internodes‟ diameters. Heritability of the trait was very high in general (70 - 75%) to boost the moderate GCVs into considerably high potential genetic advance as percents of the means (25 - 30%).

At Debre Zeit the range of values in culm diameter was 0.15 mm to 0.29 mm at the first basal internode and 0.15 mm to 0.28 mm at the second basal internode with approximately similar (0.21 mm) mean; 65% greater than mean values at Akaki. But PCV and GCV of culm diameter were generally lower than the value at Akaki (10 - 15%) at both internodes. Heritability of the trait was also slightly lower than at Akaki but still considerably high (55 - 65%). Ultimate effects turned out only moderate potential of genetic gain as opposed to the relatively higher value recorded at Akaki. Interaction effects added to the relatively lower general variability attributes at Debre Zeit to hold on the trait to moderate variability when combined over the locations. Even the heritability was drastically reduced (to about 40%) relative to the analogues in individual location.

5.1.3.5. Culm Strength

The variability in culm strength between the two internodes followed the same general pattern to the diameter. To elaborate, first basal culm internode exhibited more rigidity compared to the internode above it. The same pattern of difference was recorded location wise also. That is, the corresponding internodes were stronger ($p < 0.01\%$) at Debre Zeit than at Akaki.

The F-test showed that variability of the trait was significant ($p = 1\%$) at Akaki; but only at the second basal internode was the trait significant ($p < 0.01\%$) at Debre Zeit. Combined analysis turned out significant ($p = 1\%$) for culm strength at both internodes coping up only no interaction recorded for the first culm strength. That is, no interaction was seen for the first culm strength to deduct the power of significance. At Akaki, culm strength ranged between 0.57 and 1.34 for the basal and 0.37 to 0.71 for the second basal internodes. GCV was almost low (around 10) for the trait at both internodes with moderately high heritability (35 - 40%) to retain genetic advance as % of mean in the range of 10 - 15%; which could be considered moderate.

The case followed some distinctly different pattern of variability at Debre Zeit. This did not include the range of variation, which is 0.84 pd to 2.34 pd for the first and 0.70 pd to 1.42 pd for the second basal internodes. But wider GCV difference was recorded for the trait between the two internodes; 7.64 for the first and 11.63 for the second. The variation in heritability was so wide; 21.32 for the first and 62.90 for the second to finally create big difference in the genetic advancement potential of the strengths between the two adjacent internodes. Genetic advance as percent of means was very low (7.25%) for the basal internode but moderately valuable (18.96%) for the internode above it.

5.1.3.3. Lodging index

Log (x+1) transformation of data of lodging index narrowed linear relationships observed between predicted means and residuals and amended CV in F-test from 31.41% to 19.95% at Akaki and from 22.52% to 14.20% at Debre Zeit. The level of significance was high, which is at $P < 1\%$ at Akaki and $P < 0.1\%$ both at Debre Zeit and the combined data and level of significance was similar both for the untransformed & transformed data for all the three cases. However, transformation at Debre Zeit minimized the explanatory effect of the difference observed among the RILs (R^2 was lowered from 58% to 14.4%).

PCV was high (23.64% at Akaki and 20.86% at Debre Zeit) but GCV was moderate and more comparable between the sites (15.16% at Akaki and 16.31% at Debre Zeit). As a trait, inheritance of lodging was considerably high but showed huge difference between the two locations; 41.13% at Akaki and 61.14% at Debre Zeit. Consequently, high level of potential genetic advance as % of mean was recorded; 20% at Akaki and 26.22% at Debre Zeit. As per the expectation of high variability in these RILs, for which mainly the crossing program was organized, the existing variability (about 15% GCV) can be considered very high in lodging index. This was in contrast to minimum and very low variability in lodging index revealed in the study among the earlier interspecific *E. tef x E. pilosa* cross progenies (Tefera *et al.,* 2003b).

5.1.3.6. Panicle length and Spikelet per panicle

Variability of the trait between the sites was significant ($p < 0.1\%$). Range of values for panicle length was more than double of the lower limit; 12.80 to 32.00 with mean of 21.13 in Akaki and 20.67 to 48.93 with mean of 29.15 at Debre Zeit. It can be mentioned that panicle length together with spikelet per panicle uniquely showed consistently comparable and higher GCV and PCV, heritability and genetic advance between the locations. Hence, values for panicle length can be narrowed that PCV is about 17%; GCV 15%; heritability 80% and genetic advance as % of means < 30%. In the combined analysis also these four variability parameters showed consistently lower values may be due to interaction effects between genotypes and locations.

Range of values for spikelet per panicle seems exaggerated may be due to nature of the trait to exhibit huge numeral. It was 146.33 to 492.07 with mean of 251.00 at Akaki and 214.20 to 771.66 with mean of 415.56 at Debre Zeit. As stated in the description of panicle length results, here also, comparable consistence of the following variability parameters necessitate assignment of single approximation to values of each of the parameters over the locations to provide a more general summary of results obtained.

Figure 4. Panicle phenotypic appearances of parental species at field level:
E. pilosa (PI-223259), *E. tef* (DZ-01-974) and *E. pilosa* (PI-222988) [from left to right]

Values of PCV, GCV, heritability and genetic advance as % of means were about 27%, 21%, 60% and 35%, respectively. The PCV, GCV and genetic advance that is the ultimate return of heritable variation are the second largest values recorded, next to grain yield, over all the traits considered in this study; except biomass, which is slightly greater in genetic advance only in one of the sites. Similar results were obtained for both traits by other study (Tefera *et al.,* 2003a).

5.1.3.7. Tiller number

Tiller number is the only trait that showed very low variability. Ranges of values recorded for tillers number were 2.80 to 7.20 at Akaki and 5.93 to 12.13 at Debre Zeit. It showed moderate to high PCV but very low GCV (< 5%). Hence, the considerably wide range of variation observed could predominantly explain the unrepeatable source of variability, PCV. The genetic gain is so little to mention not only for absence of variability but also for its very low heritability in general. In addition, no single variability parameter tends to reveal some consistent variation for the trait throughout the analysis. The result opposes to a similar study on wheat; tillers per plant showed significant and positive genotypic as well as phenotypic correlation with grain yield per plant (Saleem *et al.,* 2006).

5.1.3.8. Shoot biomass

Biomass is about everything for which most traits of an organism tend to exert their contributions. Its values were taken /weighted/ in field just after harvest; at harvest maturity moisture content. The only huge value is attached to it and the range of variation thereby tends to go over. Its value ranged from 367 to 633 with mean value of 470 at Akaki and 300 to 933 with mean value of 575 at Debre Zeit.

Drawing more attention could be differences in PCV, GCV and heritability between the sites. PCV at Akaki was relatively low (10.97%) while at Debre Zeit high (22.61%). Consequently, GCV at Akaki was very low (6.55%) while at Debre Zeit about high (18.69%) or relatively very high. More surprisingly, heritability at Akaki (35.62%) is about half that of its analogue recorded at Debre Zeit (68.33%). All the variations accumulated to provide low genetic gain (8.03%) at Akaki while considerably high (31.76%) at Debre Zeit. F-test also revealed that variability between the locations with respect to this trait was significant ($p < 0.1\%$), which was actually obvious even from observation of general growth conditions in the experimental fields.

5.1.3.9. Grain yield

To a narrower range, grain yield is also expected to be influenced by many other traits like the biomass. Though the data on grain yield was normal, some semicircular relationship was obtained in plotting predicted means versus residuals at Debre Zeit for which log transformation was made. Relationship between predicted means and residuals was somehow linear at Akaki for which arcsine transformation was made. In both cases, the heterogeneity of error variance was moderately amended and coefficient of variability was drastically reduced from > 35% to < 15%.

For grain yield, significance of variability by genotype, by location and even in their interaction was to the level of < 0.1%. Consequently, range of variation was about six folds (10.10 to 66.41) with mean of 25.88 at Akaki; and about 29 folds (7.09 to 206.34%) with mean of 66.70 at Debre Zeit. Accordingly, the highest of all traits in PCV and GCV was also recorded for this trait; 39.65 and 32.18% at Akaki, and 55.35% and 51.47% at Debre Zeit. Heritability was high (65.88% at Akaki and 86.47% at Debre Zeit) to boost potential for genetic gain to 53.71% and 98.40%, respectively, to a maximum. Very similar results were obtained by other studies (Tefera *et al.,* 2003a; Tefera *et al.,* 2003b). Seed yield is a complex character conditioned by the interaction of various growth and physiological processes throughout the life cycle of the plant (Ercan *et al.,* 2002).

5.1.3.10. 100-Seed weight

Seed weight was one of the two traits for which variability was not significant at Akaki. At Debre Zeit and in the combined, high difference (p < 0.1%) was obtained. High difference (p <0.1%) was also revealed between the locations with respect to this trait. Though not significant, the range of variability was more than double (0.012 to 0.029) at Akaki; while extended to 0.013 to 0.034 at Debrez Zeit. PCV (13.84%) was moderate but GCV (5.01%) was too low at Akaki while higher PCV (21.42%) and moderate GCV (16.43%) was obtained at Debre Zeit. Heritability and genetic advance as % of mean between the locations showed huge difference: 13.10%, 3.73% at Akaki and 58.84%, 25.90% at Debre Zeit, respectively. 100-seed weight and tiller number showed low heritability as well as low genetic advance (the former trait mainly at Akaki) indicating the prevalence of non-additive gene action thereby restricting the scope for improvement through selection (Babu *et al.,* 2004).

5.1.4. Transgressive segregants

This part presents data which showed transgressive variation beyond the better parent. For example, for lodging index, if any, RILs that showed significantly low index than the lower parent were screened out but for grain yield RILs in the upper zone were screened just for checking results in the desired direction. Mean comparisons of all the traits discussed hear can be referred to for details from the table in the appendix.

At Akaki, no transgressive segregant were obtained for culm diameter and strength, plant height, shoot biomass, days to heading, maturity and 100-seed weight. Progenies transgressed for lodging, panicle length, spikelet per panicle and grain yield. Seven RILs only from cross-2 for lodging index as revealed by log transformation; two RILs for panicle length; one RIL for spikelet per panicle and three RILs for grain yield, showed the effect. No RIL showed the transgression from cross-1 for the lodging index and grain yield.

At Debre Zeit, however, considerably different outputs were recorded for many traits. Days to maturity, plant height, panicle length, spikelet per panicle and 100-seed weight showed neatly different output as opposed to the case at Akaki. Two RILs for days to maturity, four RILs for plant height and two RILs for 100-seed weight showed the effect. However, no transgression was identified for grain yield. Only lodging index showed consistency in transgression across the sites; a total of 23 RILs transgressed at Debre Zeit; more interesting was to see three RILs transgressed at both sites. The transgression suggests presence of additive gene action for those traits that showed the effect; either those favorable additive alleles are brought by both parents, and/or that complementary interaction occur between alleles of different origins (Tefera *et al.,* 2003b).

5.1.5. Cross-1 versus cross-2

To compare performance of the two crosses progenies, checks were considered as reference lines as they were common to both families. In days to maturity, RILs obtained from cross-1 (DZ-01-974 x PI-223259) were by far earlier maturing over cross-2 (DZ-01-974 x PI-222988). At Akaki, quncho was significantly late in maturity over 29 lines most of them (18) were from cross-1; DZ-Cr-37 was later than 24 RILs; 15 of them were from cross-1. At Debre Zeit, however, most of the RILs from both crosses were significantly earlier maturing over the check cultivars.

In culm characteristics, most of the RILs among the highest yielding lines were from RIL2. RILs‟ culms were not thicker than quncho but few RILs showed thicker culm over DZ-Cr-37; most of them were from cross-2. In culm strength, quncho was among the most rigid culms but DZ-Cr-37 showed lower rigidity than RIL2-126 and RIL1-84 at Akaki.

With respect to more quantitative traits like grain yield, plant height, panicle length and spikelet per panicle, most of the RILs that gave comparable or higher yield than the checks were progenies obtained from cross-2 implying potential of obtaining more variability by alternating parental accessions in future breeding efforts. Quncho was among the highest yielding cultivars for most of such traits. In plant height, four RILs from cross-2 and quncho represent the longest lines at Akaki but at Debre Zeit only quncho was the longest but three RILs of cross-2 showed longer plants over DZ-Cr-37.

In panicle length, RIL2-148 and RIL2-126 at Akaki and together with RIL2-47 and RIL2-118 at Debre Zeit showed significantly higher yield over DZ-Cr-37; six RILs (RIL1-62, RIL2-180, RIL2-126, RIL2-172, RIL2-36 and RIL1-77) at Akaki but only RIL2-126 at Debre Zeit showed the same effect for spikelet per panicle. The pattern for grain yield was different. No RIL outsmarted DZ-Cr-37 but RIL2-188 was over quncho at Debre Zeit. For 100-seed weight RIL2-33 outsmarted quncho at Akaki while no RIL exceeded the checks at Debre Zeit.

Herewith, it is also valuable to compare RILs with the check cultivars to earmark potentials of the RILs for the future of the crop, tef. Some RILs showed either higher or comparable performance for many of the traits. More than 25% of the RILs showed significant earliness over both of the checks. In culm diameter, quncho remained among the thickest RILs; but DZ-cr-37 was outsmarted by some RILs. However, most RILs showed no significant rigidity over the checks; which was absolutely true for quncho, but first culm strength at Akaki showed that RIL2-126 and RIL1-84 were rigid over DZ-cr-37.

Plant height showed promising future to develop dwarf tef cultivars; compared to DZ-cr-37, a number of RILs were shorter. In panicle length, quncho was the highest but a few RILs showed higher values over DZ-cr-37. The same trend was revealed for spikelet per panicle; six RILs at Akaki but only two at Debre Zeit outsmarted DZ-cr-37. Very different result between the locations was recorded for 100-seed weight; RIL2-62 was heavier than quncho at Akaki but both

checks were among the heaviest seeds at Debre Zeit. In grain yield, check cultivars were among the highest yielding lines at Akaki and for the combined data; only quncho was outsmarted by RIL2-118 at Debre Zeit. For lodging index, no RIL showed significantly lower value than the check cultivars.

5.2. Associations of traits

5.2.1. Estimates of correlation coefficients

In the 13 traits for which significant difference was observed, analysis of all (78) bivariate association was done. About 60-90% of the bivariate showed significant (P < 5%) phenotypic association and the remaining 10-40% insignificant. Genotypically also, the general pattern of strength in association among most pairs of the traits was similar, which may imply considerable effect of both the inherent characteristics and the outside environments. The result also indicated that all the associations were positive. That is, though some of the associations are insignificant or very low, all the 13 traits tend to complement each other.

To emphasis more important associations in line with the objective of the crossing, traits like grain yield and the most undesirable agronomic trait, lodging, are given due attention for the present discussion. These traits are expected to be outputs of cumulative effects of most of the other traits (Vidya and Oommen, 2002); controlled by many variables (Virginia, 2003); quantitative in nature and is poly-genetically controlled (Izge *et al.,* 2006); and hence may also provide generalized statements-within for associations of other traits. Other very strong associations observed include: days to heading and days to maturity ($r_g > 0.85$); panicle length and spikelet per panicle ($r_g > 0.8$); panicle length and plant height ($r_g > 0.85$); plant height and days to maturity ($r_g > 0.8$). This is consistent with results of other studies (Tefera *et al.*, 2003a; Virginia, 2003; Chanyalew, 2006).

Genotypic correlation coefficient closer to one was revealed for associations of some traits. Sometimes correlation coefficients greater than one can be found and considered strong (Saleem *et al.,* 2006). Majority of such coefficients were observed for association of culm strength with some other traits. Accordingly, at Akaki, first culm strength showed this effect when correlated with shoot biomass, days to heading and days to maturity while second culm strength with 100-seed weight and days to maturity. 100-seed weight also showed this effect with plant height and days to maturity. At Debre Zeit, the phenomenon was reflected by fewer bivariate; only second culm strength with plant height, 100-seed weight, days to heading, maturity, panicle length and spikelet per panicle.

Correlation between different traits is generally due to the presence of linked genes and epistatic effect of different genes (Saleem *et al.,* 2006). Relationships between genotypic and phenotypic correlation coefficients did not follow some pattern. The dual nature of phenotypic correlation makes it clear that the magnitude of genetic correlation cannot be determined from phenotypic correlation (Saleem *et al.,* 2006).

NB: Test of significance was done for phenotypic correlation. For genotypic association discussion was done by comparing the correlation coefficients relative to each other.

Table 5a. Phenotypic (above the diagonal) and genotypic (below the diagonal) coefficients of correlation among 13 traits in 79 lines of the *E .tef* x *E. pilosa* crosses at Akaki

Trait	FCD	SCD	FCS	SCS	LG	PH	GY	SB	SW	DH	DM	PL	SP
FCD	*	0.90**	0.56**	0.44**	0.16	0.63**	0.17	0.10	0.27*	0.52**	0.57**	0.71**	0.70**
SCD	0.97	*	0.58**	0.47**	0.19	0.65**	0.23*	0.17	0.26*	0.53**	0.59**	0.73**	0.70**
FCS	0.77	0.81	*	0.48**	0.08	0.49**	0.25*	0.42**	0.19	0.56**	0.53**	0.52**	0.35**
SCS	0.57	0.61	0.48	*	0.90**	0.55**	0.27*	0.25**	0.31**	0.51**	0.57**	0.51**	0.35**
LG	0.21	0.24	0.05	0.90	*	0.37**	0.21	0.10	0.24*	0.30**	0.38**	0.30**	0.19
PH	0.75	0.76	0.71	0.77	0.49	*	0.45**	0.33**	0.30*	0.51**	0.63**	0.90**	0.54**
GY	0.30	0.41	0.52	0.69	0.53	0.64	*	0.67**	0.14	0.17	0.34**	0.35**	0.14
SB	0.25	0.28	1.01	0.62	0.26	0.48	0.93	*	0.09	0.20	0.13	0.24*	0.04
SW	0.88	0.79	0.35	1.06	0.90	1.03	0.67	0.40	*	0.33*	0.27*	0.28*	0.21
DH	0.68	0.68	1.05	0.85	0.45	0.64	0.35	0.44	1.02	*	0.69**	0.60**	0.45**
DM	0.77	0.80	1.01	1.03	0.67	0.83	0.44	0.27	0.83	0.91	*	0.66**	0.44**
PL	0.87	0.87	0.74	0.70	0.38	0.93	0.52	0.38	0.95	0.76	0.86	*	0.70**
SP	0.91	0.95	0.46	0.57	0.36	0.65	0.24	0.10	0.77	0.68	0.59	0.84	*

FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, PL=Panicle length, SP=spikelet per panicle, SBM=Shoot biomass, Yld=grain yield, SWT=100-seed weight DH= days to heading, DM=days to maturity, PH=plant height, LI=lodging index

Table 5b. Phenotypic (above the diagonal) and genotypic (below the diagonal) coefficients of correlation among 13 traits in 79 lines of the *E. tef* x *E. pilosa* crosses at Debre Zeit

Trait	FCD	SCD	FCS	SCS	LG	PH	GY	SB	SW	DH	DM	PL	SP
FCD		0.93**	0.35**	0.13	0.01	0.68**	0.34**	0.46**	0.23*	0.48**	0.53**	0.63**	0.52**
SCD	1.01	*	0.42**	0.19	0.05	0.69**	0.29**	0.43**	0.22*	0.54**	0.57**	0.65**	0.58**
FCS	0.56	0.78	*	0.40**	0.12	0.50**	0.34**	0.35**	0.25*	0.52**	0.50**	0.51**	0.38**
SCS	0.12	0.18	0.42	*	0.77**	0.43**	0.33**	0.32*	0.42**	0.24*	0.41**	0.26*	0.18
LG	-0.02	0.03	0.29	0.94	*	0.33**	0.17	0.25*	0.32**	0.15	0.32**	0.20	0.14
PH	0.85	0.82	1.06	0.53	0.43	*	0.57**	0.78**	0.45**	0.66**	0.80**	0.84**	0.65**
GY	0.49	0.39	0.63	0.46	0.25	0.62	*	0.79**	0.59**	0.34**	0.50**	0.42**	0.46**
SB	0.85	0.69	1.11	0.53	0.44	0.96	0.92	*	0.59**	0.50**	0.75**	0.64**	0.47**
SW	0.36	0.31	0.69	0.73	0.45	0.59	0.83	0.99	*	0.40**	0.52**	0.34**	0.44**
DH	0.78	0.80	1.20	0.33	0.24	0.81	0.44	0.69	0.56	*	0.74**	0.72**	0.68**
DM	0.76	0.75	1.10	0.53	0.39	0.88	0.58	0.88	0.71	0.83	*	0.75**	0.59**
PL	0.82	0.81	1.15	0.33	0.25	0.89	0.48	0.83	0.43	0.90	0.87	*	0.70**
SP	0.79	0.86	1.00	0.24	0.18	0.81	0.60	0.72	0.70	0.97	0.78	0.93	*

FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, PL=Panicle length, SP=spikelet per panicle, SBM=Shoot biomass, Yld=grain yield, SWT=100-seed weight DH= days to heading, DM=days to maturity, PH=plant height, LI=lodging index

5.2.1.1. Associations with lodging index

Phenotypically, lodging index was found associated with second culm strength, plant height, days to heading and maturity, panicle length and 100-seed weight at Akaki. However, only the association with second culm strength was very strong (0.90); all others showed r_p below 0.40. The same pattern of the association trend was also observed at Debre Zeit, but the association with panicle length was nullified and with biomass turned-out significant though weak. The trait culm strength at the second internode slightly narrowed down the huge difference in the degree of association of lodging index with itself from 0.90 to 0.77 at this location.

Genotypically, the association between lodging index and second culm strength was the maximum (about 0.9). The association of most other traits with lodging index was also substantially high including plant height, grain yield, 100-seed weight, and day to maturity mainly at Akaki and except culm diameter and spikelet per panicle at Debre Zeit. From this result, one may be confident with the consistently strong association of lodging index with second culm strength; no study is found to be compared with. The obvious association of lodging index with that of the other traits like plant height, days to maturity and panicle length is in line with results of many studies including recent once (Chanyalew, 2006).

Irrespective of its relatively highly quantitative nature, the trait that showed list association with most other traits was lodging index. It showed very little association with culm diameter and first culm strength. This may contradict with the obvious logic if not explained by lack of objectivity for collecting the data and/or the scale of indexing during data collection, and the design and management of the field experiment most of which might have reduced the lodging index.

5.2.1.2. Associations with grain yield

Phenotypically, at Akaki, grain yield was found associated with shoot biomass (r_p = 67%) and culm characters, days to maturity and panicle length; with coefficients aggregated around 0.25-0.40. It showed no association with lodging index, 100-seed weight, days to heading and spikelet per panicle. At Debre Zeit, however, grain yield was found significantly associated with all other traits except lodging index. Strength of association was maximum for biomass (r_p = 0.79) and for

days to heading and maturity, panicle length, spikelet per panicle and 100-seed weight aggregated to around 0.4-0.6. Substantial association was also recorded with the culm characters; their r_p aggregated around 30-35%. Strong positive association with spikelet per panicle and biomass revealed that the two traits were most important grain yield attributes (Teklu and Tefera, 2005).

Genotypic association of grain yield with other traits was more than the phenotypic association. The highest was recorded with shoot biomass followed by 100-seed weight. Associations with plant height and panicle length were also considerably high. Uniquely and as opposed to other studies (Teklu and Tefera, 2005), spikelet per panicle showed the lowest genotypic association at Debre Zeit. Shoot biomass showed consistently highest association with grain yield. Biological yield had the highest positive direct effect on grain yield (Surek and Beser, 2003).

Genotypic association of grain yield with lodging index was considerably high (r_g=0.53) at Akaki though it was the least (r_g=0.25) compared to associations with other traits at Debre Zeit. The weak association of grain yield with lodging index may not require unique explanation over the other traits. In small plots, as in experimental fields, yield may easily be secured from lodged plants without loss that would come due to lodging otherwise. In tef production at wide plots of land, grain yield loss due to lodging may be high during harvesting for mechanical reasons and due to post maturity climatic hazards like rainfall.

In a casual route of associations with grain yield, high lodging by no means can be a cause for high grain yield rather to reduced grain yield and hence it is logical to consider grain yield always as causal variable. To elaborate, high lodging index due to high yield; the reducing effect of lodging on grain yield is partly of post physiological mechanism. Low grain yield and shorter plant height was recorded at Akaki that might have contributed to the weak association between grain yield and lodging index there; effects could be rather more of environmental.

5.2.2. Path-analysis

The correlation studies taken alone are often misleading and the actual dependence of grain yield on the correlated yield component characters needs confirmation, which can easily be untangled and unraveled by path coefficient analysis (Izge *et al.,* 2006). Path analysis was also used in other crops to evaluate interspecific crosses (Diz *et al.,* 1994). In contrast to the exclusive positive association between the 13 traits, partitioning it in to direct and indirect effect exposed negative relationships also. Here, only the genotypic effects are included. As path analysis via SPAR software could not provide test for significance, more relevance was given to effects with values greater than 0.5 (Tefera, 1988).

5.2.2.1. Path-analysis for lodging

The only consistently strong direct effect on lodging index was exerted by second culm strength, which is positive. At Akaki, strong positive effect of all other traits on lodging index was revealed indirectly through second culm strength. At this location, considerable negative direct effect on lodging index (around 0.5) was also recorded by first culm strength. Days to heading, days to maturity and shoot biomass showed similar effect indirectly through first culm strength. Effect of all other traits on lodging index was weak.

Table 6a. Direct (shaded diagonal) and indirect effects of 12 traits on lodging index of 79 lines of the *E. tef* x *E. pilosa* crosses at Akaki

	FCD	**SCD**	**FCS**	**SCS**	**PH**	**GY**	**SB**	**SW**	**DH**	**DM**	**PL**	**SP**	**r_g**
FCD	-0.08	0.04	-0.35	***0.78***	-0.13	-0.08	0.05	-0.01	-0.15	0.03	0.11	-0.06	**0.21**
SCD	-0.08	0.05	-0.37	***0.85***	-0.13	-0.10	0.05	-0.01	-0.15	0.03	0.11	-0.06	**0.24**
FCS	-0.06	0.04	**-0.45**	***0.67***	-0.12	-0.13	0.19	-0.00	-0.23	0.04	0.10	-0.03	**0.05**
SCS	-0.04	0.03	-0.22	**1.38**	-0.13	-0.17	0.12	-0.01	-0.19	0.04	0.09	-0.04	**0.90**
PH	-0.06	0.03	-0.32	***1.06***	-0.17	-0.16	0.09	-0.01	-0.14	0.03	0.12	-0.04	**0.50**
GY	-0.02	0.02	-0.24	***0.95***	-0.11	-0.25	0.17	-0.01	-0.08	0.02	0.07	-0.02	**0.53**
SB	-0.02	0.01	**-0.46**	***0.86***	- 0.08	-0.23	0.19	-0.00	-0.10	0. 01	0.05	-0.01	**0.26**
SW	0.07	0.04	-0.16	***1.46***	-0.17	-0.17	0.08	-0.01	-0.23	0.03	0.12	-0.05	**0.90**
DH	-0.05	0.03	**-0.48**	***1.17***	-0.11	-0.09	0.08	-0.01	-0.22	0.03	0.10	-0.05	**0.45**
DM	-0.06	0.04	**-0.46**	***1.42***	-0.14	-0.11	0.05	-0.01	-0.20	0.04	0.11	-0.04	**0.67**
PL	-0.07	0.04	-0.34	***0.97***	-0.16	-0.13	0.07	-0.01	-0.17	0.03	0.13	-0.06	**0.38**
SP	-0.07	0.04	-0.21	***0.79***	-0.11	-0.06	0.02	-0.01	-0.15	0.02	0.11	-0.07	**0.36**

Residual = -0.0053

FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, PL=Panicle length, SP=spikelet per panicle, PH=plant height, SB=Shoot biomass, GY=grain yield, SWT=100-seed weight, DH= days to heading, DM=days to maturity, r_g=genotypic correlations for lodging index

However, at Debre Zeit, strong positive direct effect was recorded for panicle length in addition to the second culm strength. Effect of all other traits on lodging was strong and positive through panicle length. Plant height, days to maturity, spikelet per panicle showed strong negative direct effect on lodging index. Almost all other traits also showed strong indirect effect through these three traits. The indirect effect of most traits on lodging index was strong and positive except for culm diameter, panicle length and spikelet per panicle. Indirect effect of most other traits through most other traits on lodging index was generally very low (< 0.3). Traits like panicle length, plant height and spikelet per panicle can be proposed at Debre Zeit; main traits that showed high direct and indirect effect there.

Table 6b. Direct (shaded diagonal) and indirect effects of 12 traits on lodging index of 79 lines of the *E. tef* x *E. pilosa* crosses at Debre Zeit

	FCD	**SCD**	**FCS**	**SCS**	**PH**	**GY**	**SB**	**SW**	**DH**	**DM**	**PL**	**SP**	**r_g**
FCD	0.39	-0.19	0.13	0.16	***-0.68***	0.14	0.03	-0.001	0.09	***-0.77***	***1.28***	***-0.68***	***-0.02***
SCD	0.39	-0.19	0.18	0.24	***-0.66***	0.11	0.02	-0.001	0.09	***-0.76***	***1.25***	***-0.74***	***0.03***
FCS	0.22	-0.15	0.22	***0.56***	***-0.85***	0.18	0.04	-0.002	0.14	***-1.11***	***1.78***	***-0.87***	***0.29***
SCS	0.05	-0.03	0.09	**1.33**	*-0.42*	0.13	0.02	-0.002	0.04	***-0.54***	***0.51***	*-0.21*	***0.94***
PH	0.33	-0.15	0.24	***0.70***	**-0.80**	0.18	0.03	-0.001	0.09	***-0.89***	***1.38***	***-0.70***	***0.43***
GY	0.19	-0.07	0.14	***0.62***	**-0.50**	0.29	0.03	-0.002	0.05	***-0.59***	***0.75***	***-0.52***	***0.27***
SB	0.33	-0.13	0.25	***0.70***	***-0.77***	0.27	0.04	-0.002	0.08	***-0.89***	***1.29***	***-0.62***	***0.44***
SW	0.14	-0.06	0.15	***0.97***	**-0.47**	0.24	0.04	-0.002	0.06	***-0.72***	***0.67***	***-0.61***	***0.45***
DH	0.35	-0.15	0.27	**0.45**	***-0.65***	0.13	0.02	-0.001	0.15	***-0.84***	***1.40***	***-0.84***	***0.24***
DM	0.30	-0.14	0.24	**0.71**	***-0.71***	0.17	0.03	-0.002	0.10	**-1.01**	***1.36***	***-0.68***	***0.39***
PL	0.32	-0.15	0.26	0.44	***-0.71***	0.14	0.03	-0.001	0.10	***-0.88***	**1.55**	***-0.81***	***0.25***
SP	0.31	-0.16	0.22	0.32	***-0.65***	0.17	0.03	-0.002	0.11	***-0.79***	***1.45***	**-0.87**	**0.18**

Residual = 0.242

FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, PL=Panicle length, SP=spikelet per panicle, PH=plant height, SB=Shoot biomass, GY=grain yield, SWT=100-seed weight DH= days to heading, DM=days to maturity, r_g=genotypic correlation of lodging index

5.2.2.1. Path analysis for grain yield

In contrast to the path analysis result of lodging index, which was directly effected by or manifested through only some of the traits, effects for grain yield were scattered among most of the traits. All except 100-seed weight at Akaki and days to maturity showed considerable direct effects. Direct effects of first culm strength and days to heading were negative. Effect of days to maturity was distributed only indirectly through most other traits. Direction (+/-) of direct effects by culm diameter, second culm strength, lodging index, plant height and biomass alternated between the sites. In some cases, environment affects both the traits simultaneously in same direction or some time in different directions (Saleem *et al.,* 2006). It was also interesting to see effects directly and/or indirectly on grain yield by all other traits, which may explain the highly quantitative nature of the trait.

Table 7a. Direct (shaded diagonal) and indirect effects of 12 traits on grain yield of 79 lines of the *E. tef* x *E. pilosa* crosses at Akaki

	FCD	SCD	FCS	SCS	LI	PH	SB	SW	DH	DM	PL	SP	rg
FCD	**-0.58**	***0.56***	***-1.67***	***3.56***	***-0.99***	***-0.82***	0.21	0.10	***-0.67***	0.12	***0.87***	***-0.51***	***0.30***
SCD	***-0.57***	**0.58**	***-1.76***	***3.85***	***-1.12***	***-0.83***	0.24	0.09	0.13	***-0.67***	***0.88***	***-0.53***	***0.41***
FCS	**-0.45**	**0.47**	**-2.17**	***3.03***	-0.24	***-0.78***	***0.86***	0.04	***-1.03***	0.16	***0.75***	-0.26	**0.52**
SCS	-0.33	0.36	***-1.05***	**6.28**	***-4.20***	***-0.84***	***0.53***	0.12	***-0.83***	0.16	***0.71***	-0.32	**0.69**
LI	-0.12	0.14	-0.11	***5.63***	**-4.68**	***-0.54***	0.22	0.10	***-0.45***	0.11	0.38	-0.20	**0.53**
PH	-0.44	0.44	***-1.55***	***4.85***	***-2.31***	**-1.09**	0.41	0.11	***-0.63***	0.13	***0.93***	-0.36	**0.64**
SB	-0.14	0.16	***-2.19***	***3.90***	***-1.21***	***-0.52***	**0.85**	0.04	-0.44	0.04	0.39	-0.06	**0.93**
SW	**0.51**	**0.46**	***-0.75***	***6.65***	***-4.23***	***-1.12***	0.34	0.11	***-1.01***	0.13	***0.96***	-0.43	**0.67**
DH	-0.40	0.39	***-2.27***	***5.30***	***-2.13***	***-0.69***	0.38	0.11	**-0.99**	0.15	***0.76***	-0.38	**0.35**
DM	**-0.45**	**0.47**	***-2.18***	***6.44***	***-3.14***	***-0.90***	0.23	0.09	***-0.90***	**0.16**	***0.86***	-0.33	**0.44**
PL	***-0.51***	***0.50***	***-1.61***	***4.40***	***-1.79***	***-1.01***	0.33	0.10	***-0.75***	0.14	**1.01**	**-0.47**	**0.52**
SP	***-0.53***	***0.55***	***-1.00***	***3.60***	***-1.69***	***-0.71***	*0.09*	*0.08*	***-0.67***	*0.09*	***0.85***	**-0.56**	**0.24**

Residual = -0.099
FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, PL=Panicle length, SP=spikelet per panicle, PH=plant height, LI=lodging index, SB=Shoot biomass, SWT=100-seed weight DH=days to heading, DM=days to maturity, r_g=genotypic correlation of lodging index

At Akaki, relatively broader range of very strong effects for almost all other traits was shown directly and indirectly through culm diameter, lodging index and plant height. No strong effect was recorded directly by and indirectly through 100-seed weight at this site.

At Debre Zeit, effect of lodging index on grain yield was shown directly and indirectly through plant height, panicle length and shoot biomass. Effects through lodging index were considerable only for second culm strength. Relatively very strong indirect effect of most traits was observed through culm diameter except lodging index. With the exception of second culm strength, lodging index and days to maturity, the traits showed strong indirect effect through most other traits.

Table 7b. Direct (shaded diagonal) and indirect effects of 12 traits on grain yield of 79 lines of the *E. tef* x *E. pilosa* crosses at Debre Zeit

	FCD	SCD	FCS	SCS	LI	PH	SB	SW	DH	DM	PL	SP	r_g
FCD	**4.32**	***-6.35***	***-0.87***	-0.06	-0.02	***1.50***	***-1.11***	0.28	-0.35	0.05	***1.70***	***1.14***	**0.49**
SCD	***4.35***	**-6.31**	***-1.23***	-0.09	0.02	***1.45***	***-0.91***	0.24	-0.35	0.05	***1.67***	***1.25***	**0.39**
FCS	***2.42***	***-4.95***	**-1.56**	-0.20	0.20	***1.89***	***-1.46***	***0.53***	**-0.53**	0.07	***2.38***	***1.46***	**0.63**
SCS	***0.52***	*-1.16*	***-0.66***	**-0.47**	***0.64***	***0.93***	***-0.69***	***0.56***	-0.15	0.03	***0.68***	0.35	**0.46**
LI	-0.10	-0.21	**-0.46**	-0.44	**0.68**	***0.76***	***-0.57***	0.35	-0.11	0.03	***0.52***	0.26	**0.25**
PH	***3.66***	***-5.17***	***-1.66***	-0.25	0.29	**1.77**	***-1.26***	**0.46**	-0.36	0.06	***1.84***	***1.18***	**0.62**
SB	***3.65***	***-4.38***	***-1.74***	-0.25	0.30	***1.70***	**-1.31**	***0.77***	-0.31	0.06	***1.72***	***1.04***	**0.92**
SW	***1.57***	***-1.95***	***-1.07***	-0.34	0.31	***1.05***	***-1.30***	**0.78**	-0.29	0.05	***0.89***	***1.02***	**0.83**
DH	***3.37***	***-5.03***	***-1.88***	-0.16	0.16	***1.44***	***-0.90***	0.43	**-0.45**	0.05	***1.86***	***1.41***	**0.44**
DM	***3.30***	***-4.72***	***-1.71***	-0.25	0.27	***1.56***	***-1.16***	***0.55***	-0.37	0.06	***1.81***	***1.14***	**0.58**
PL	***3.56***	***-5.09***	***-1.79***	-0.17	0.17	***1.58***	***-1.09***	0.33	-0.40	0.06	**2.07**	***1.36***	**0.48**
SP	***3.39***	***-5.42***	***-1.57***	-0.11	0.12	***1.44***	***-0.94***	***0.54***	-0.43	0.05	***1.93***	**1.46**	**0.60**

Residual=0.573
FCD=first culm diameter, SCD=second culm diameter, FCS=First culm strength, SCS=second culm strength, PL=Panicle length, SP=spikelet per panicle, PH=plant height, LI=lodging index, SB=Shoot biomass, SWT=100-seed weight DH= days to heading, DM=days to maturity, r_g=genotypic correlations of lodging index

5.2.3. Principal component Analysis

In the analysis made to estimate the relative contribution of the traits studied towards the overall phenotypic variation among the 79 lines, the first three principal components with eigenvalues of greater than unity explained about 68% of the total variation. The first principal component (PC_1) alone explained about 45% of the entire variability at Akaki. The second and third principal components (PC_2 and PC_3) explained about 12% and 11%, respectively, of the entire variability among the lines. Similarly, PC_1, PC_2 and PC_3 each explained 48%, 14% and 9%, respectively, of the entire variability at Debre Zeit.

Plant height, panicle length, days to maturity and days to heading chiefly accounted for about 45% of the gross variability among the lines. Culm diameter at Akaki and shoot biomass at Debre Zeit also contributed largely to the huge variability in PC_1.

Table 8. Eigenvector, eigenvalue and variability explained by first three principal components for the 14 traits of the 79 lines of *E. tef x E. pilosa*

	Akaki			**Debre Zeit**		
	PC_1	**PC_2**	**PC_3**	**PC_1**	**PC_2**	**PC_3**
Eigenvalue	6.33	1.64	1.50	6.75	1.93	1.62
Variability explained (%)	**45.2**	**11.7**	**10.7**	**48.2**	**13.8**	**9.0**
Cumulative variability explained (%)	**45.2**	**56.9**	**67.6**	**48.2**	**62.0**	**71.0**
	Eigenvector					
First culm diameter	**0.32**	**0.31**	-0.04	0.28	**0.34**	-0.03
Second culm diameter	**0.33**	0.25	-0.04	0.29	**0.33**	-0.12
First culm strength	0.28	0.01	-0.1 9	0.23	0.05	-0.23
Second culm strength	0.29	**-0.32**	**0.39**	0.19	**-0.48**	**-0.41**
Lodging index	0.18	**-0.41**	**0.53**	0.13	**-0.52**	**-0.37**
Plant height	**0.34**	-0.04	-0.08	**0.36**	0.02	-0.02
Grain yield	0.17	**-0.46**	**-0.40**	0.25	-0.22	**0.49**
Shoot biomass	0.14	**-0.47**	**-0.48**	**0.31**	-0.14	**0.32**
Days to heading	**0.30**	0.04	0.08	**0.30**	0.12	-0.05
Days to maturity	**0.31**	-0.02	0.12	**0.34**	-0.03	-0.04
Panicle length	**0.35**	0.11	-0.06	**0.33**	0.13	0.02
Spikelet per panicle	0.28	**0.32**	0.01	0.29	0.14	0.06
Tiller number	-0.13	-0.13	0.28	-0.01	-0.29	**0.45**
100-seed weight	0.16	-0.04	0.16	0.23	-0.28	0.16

The second and third PCs, around 12% and 10% of the variation, were largely originated from lodging index and second culm strength. Culm diameter also considerably contributed to PC_2. Large contribution by the traits grain yield, shoot biomass and spikelet per panicle was observed at Akaki. Not little to escape was the contribution of grain yield and shoot biomass to PC_3.

It was interesting to see such moderately to highly consistent result between the two sites. It may also be possible to attach such major amount of gross variation to major differences between the two species *(E. tef and E. pilosa)* from the traits considered in this study for which plant height, panicle length and days to heading and maturity could be prior to mention.

6. Conclusion and Recommendation

In this section, attention was given to cases that showed consistency in all the conditions attempted by the study. The study revealed presence of large amount of variation. When elaborated, the amount of difference due to environmental effects and/or error factors than intrinsic ones became more only for few of the traits like tiller number and culm strength. For most of the traits, the variability did not show huge gap from phenotype to genotype revealing prominence of the genetic components in determining traits product and hence appropriate to draw breeders‟ attention. The existence of significant genotype x location interaction demand testing the RILs in much more environments to represent tef growing agro-ecological conditions.

Heritability of majority of the traits was moderately high to very high for the sites considered. Growing duration, plant height, panicle length and grain yield were such traits; exhibited values > 65%. Still considerably high heritability was also observed for most other traits. Such strong inherent feature of most of the traits considered in this study implied efficiency for selection in crop improvement as far as the required amount of variability exists.

Those variability and heritability parameters were computed to provide moderately high to very high genetic gain for some traits. The potential genetic gain for spikelet per panicle and grain yield was very high. These two complementing traits can best be used in the improvement of grain yield among the lines. Considerably high genetic advance could also be attained through working with most other traits including plant height, panicle length and lodging index. The case for lodging index can be promising when compared to the persisting problem (lack of variability) that has been reported for decades for the species, *E. tef*.

Relating single trait to lodging index would not be a satisfactory method of assessing lodging resistance. The relationship between lodging index and second culm strength opened a point of new attention for further investigation as it showed consistently strong positive association in all the conditions considered by this study; not only directly but also indirectly via all other traits. The mystery may also revolve around traits like plant height, panicle length and length of growing period for they contributed maximum to the gross variability among the lines.

The weak direct effect of length of growing period on grain yield may contradict with its sufficiency for good grain-filling may be due to unfavorable match between critical growth stages and climatic conditions like moisture shortage late in the growing season. Potential of genotypes is expressed only in conducive environment. Conversely, the negative effect of days to heading on grain yield may explain the time extended before flowering so that seed-setting period would have been confounded.

The association of grain yield with most other traits may be a common scenario and reveals complexity of the trait. Its improvement directly or indirectly may require dealing with many traits. The maximum variability recorded for grain yield may have also reflected immense variability within for vast majority of traits of tef that are not considered in this study. Future studies need to consider more specific traits that would be pivotal for grain yield improvement.

Lodging is more dependent on grain yield than the reverse and it would be more logical to explain the effect of grain yield on lodging. However, effect of grain yield on lodging index was weak. Plant height was assumed to be the main intervening trait in between. It showed positively strong association with grain yield. This contradicts with the physiological mechanism such that dry matter partitioning increases one at the expense of the other. Perhaps the trait plant height might have been viewed excluding the length containing the grain (the panicle length) or traits like spikelet per unit length of panicle and seed-weight should be given more attention. This would be one entry point in reducing the contradicting desire from lodging and grain yield.

Shorter seed-filling period accompanied by higher lodging index usually results in reduced grain yield. However, perhaps for the general suitability of Debre Zeit environment for tef production, high grain yield was obtained compared to the other site. This phenomenon may not alter the selection criteria for improvement of the crop between the sites as the effect of one over the other was similar though the magnitude may vary.

Data collected on panicle form, growth habit, lemma color and basal stalk color showed that majority of the RILs did not neatly fix for such observable traits though the RILs showed predominance of single characteristics. This may imply that more quantitative traits (as of the traits used in this study) would take considerably longer generation to get characteristically fixed. Hence to use the phrase „recombinant inbred line" may not be fully appropriate at the seventh filial generation. High chromosome number increases segregating units and upon crossing obtaining inbred lines may take longer generation. Studies followed to observe shattering behavior revealed considerable variability among the RILs. Data on stand-count was tested for significance and showed variation. These features should account for some of the existing variability mainly on grain yield.

E. pilosa shall not dilute desired characteristics of tef. Further studies on the nutritional quality and other characters of candidate interspecific RILs in relation to desirable characteristic features of tef, and to extend the knowledge to other crops" improvement programs especially within the conventional breeding procedures whereby manipulation /the crossing and subsequent segregations/ tend to mix-up different genomes without clear limit, is empirical. Otherwise, the study demonstrated availability of genetic variability for a number of heritable traits in the RILs for exploitation through selection and presence of promising inbred RILs for further breeding; verified the importance of *E. pilosa* in diversifying the germplasm pool for tef breeding.

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