ANNUAL SCIENTIFIC PROGRESS REPORT
(July 1, 2001 to June 30, 2002)

A. Title of Project: Genetic Basis for Tef Improvement in Ethiopia

B. Names and Signature of Principal Investigators Contributing to this Report:

Hailu Tefera: _____

Mark Sorrells: _____

C. Executive Summary:

The overall objective of the McKnight Foundation's Collaborative Crop Research Program in tef is to increase the yield potential of tef through genetic manipulations, and to train tef researchers. In Ethiopia, five separate field-trial activities were carried out this year; two of them were yield trials, two were related to generation advancement of segregating populations, and one was a crossing scheme. From the combined analysis of variance of early and late set experiments, genotype, location and their interaction effects were significant for almost all traits. We, therefore, compromised our selection between mean values of grain yield across locations and at specific locations. Accordingly, eight promising genotypes each from the early set and late set trials were selected for further evaluation in the Pre-national Variety Trial for 2002/03 season. Twenty recombinant inbred lines (RILs) were selected from the cross DZ-01-2785 x *E. pilosa* (30-5) to be included in the Preliminary Yield Observation at Debre Zeit. From the segregating populations of two crosses designed for improving seed quality, a total of 126 homozygous lines were selected to be included in Preliminary Yield Observations and Pre-National Variety Trials in 2002/03. In the hybridisation work, fourteen crosses successfully set hybrid seeds, out of which one was hybrid sterile. Of the remaining 13 crosses, nine and five crosses are now in the F_2 and F_3 segregating population stages, respectively.

At Cornell, a genetic linkage map of tef was generated using 251 loci obtained from 162 RILs of an inter-specific cross of Kaye Murri x *E. pilosa (30-5)*. The total map length was 2410.8 cM spread over 30 linkage groups. The goal of this work is to have a genetic map that covers most of the tef genome, provide a link to comparative genetic information from other cereals and to identify loci attributing to lodging resistance. Using this linkage map and field data from Ethiopia, highly significant QTLs were identified for several agronomic traits such as days to maturity, days to heading, grain yield, shoot biomass, plant height, culm length, panicle length, panicle weight, panicle seed weight and culm diameter ($P<0.01$ and % R^2 up to 24%).

Pertaining to training, the two PhD students, Mr. Aderajew Haddis and Mr. Solomon Chanyalew, have continued their work in Ethiopia at the Addis Ababa University and Alemaya University, respectively. One M.Sc student (Mr. Fisseha Werede) in Ethiopia will soon be defending his thesis at Alemaya University. The M.Sc student at Cornell (Ms. Elizabeth Graznak) will complete her thesis for the M.Sc degree and prepare a publication on her studies over the next two months. Four research staff received training on participatory research methods, in Nairobi, Kenya, on 9-13 December 2001. The Advisory Committee (AC) convened seven times. Major issues discussed and salient proceedings of these meetings are summarized in the report.

Abbreviations used in this report:
RZ = Rice cDNA clone; BCD = Barley cDNA clone; CDO = Oat cDNA; TCD = Tef cDNA, WG = Wheat Genomic clone; CSU = Maize cDNA, DM = Wheat EST-SSRs; ISSR = Inter-Simple Sequence Repeat amplification; RIL = Recombinant inbred line(s); LG = Linkage group; RFLP = Restriction Fragment Length Polymorphism; EST = Expressed Sequence Tags; SSR = Simple Sequence Repeats; PCR = Polymerase Chain Reaction; QTL = Quantitative Trait Loci; PAGE = poly acrylamide gel electrophoresi; sES = Early Set; LS = Late Set; DZBS = Debre Zeit Black Soil; DZLS = Debre Zeit Light Soil; ANOVA = Analysis of Variance; DZARC = Debre Zeit Agricultural Research Center.

D. Overall Objectives of the Project:

The growing population of Ethiopia, which is now estimated to be 65 million, poses an increasing demand for tef. Increasing tef productivity in the various agro-ecologies of Ethiopia is therefore one of the primary goals of the National Tef Research Program. The overall objectives of the research and training program are a) genetic improvement of tef to increase its yield potential, b) improve lodging resistance, c) develop a genetic link between tef and model crop species through the use of comparative genetic analyses, and d) upgrade the knowledge of tef researchers through long and short-term trainings.

E. Research Progress:

E.1. Genetic Improvement Studies in the Field (Ethiopia)

E.1.1. Advanced observation of early and late maturing tef lines

Two separate sets of performance evaluation trials, early (ES) and late sets (LS) were carried out. The objectives of these trials were to evaluate the performance and adaptability of tef genotypes at different locations and identify superior genotypes for further evaluation. For the ES, 47 genotypes plus a standard (DZ-Cr-37) and local checks were tested at Debre Zeit black soil (DZBS) and light soil (DZLS), Denbi, Alemtena, Melkassa, Holetta, Mekelle and Adet. For the LS, 46 genotypes plus two standard checks (DZ-01-974 and DZ-01-358) and a local check were tested at DZBS, DZLS, Denbi, Holetta, Adet, Mekelle, Akaki and Chefe Donsa. The test genotypes included germplasm lines and recombinant inbred lines of various crosses promoted from previous evaluation trials. The design used in both cases was 7x7 simple lattice design with two replications on standard plots ($4m^2$). Data from Mekelle were not included in the combined ANOVA because of their high level of coefficients of variation.

Mean values of the test genotypes for grain yield at individual locations and combined over locations together with the results from analysis of variance (ANOVA) are given in Tables 1 and 2 for the early and late set trials, respectively. Results of the ANOVA for other agronomic traits of individual locations are summarized in Table 3.

For the early set (ES) trials, significant differences ($P<0.05$) for grain yield were observed at Melkassa, DZBS, DZLS and Adet. While for the late set (LS) trials, significant differences ($P<0.05$) for grain yield were observed at all locations except Alemtena and DZLS. In both sets, genotypic differences were not observed at Alemtena for all traits. Also non-significant in most cases were genotypic differences for shoot biomass and lodging index. In the ES trials, some test genotypes gave better yields than the checks but not in the LS. In both cases, however, the differences from the checks were not statistically significant. The highest and lowest mean location yields were obtained at Holetta and Mekelle, respectively, for both sets of trials. From the combined ANOVA, genotype, location and their interactions effects were significant for almost all traits. We, therefore, compromised our selection between mean

values of grain yield across locations and at specific locations. Accordingly, eight promising genotypes each from the ES and LS trials were selected for further evaluation in the Pre-national Variety Trial for 2002/03 season.

Mean values across locations for the agronomic traits other than grain yield are given in Tables 4 and 5 for ES and LS trials, respectively. Generally, the mean values of the ES were higher in shoot biomass, grain yield, plant height, panicle length, and lodging index than the LS. On the other hand, their heading and maturity times were earlier indicating that classifications of the test genotypes were correct.

E.1.2. Development of recombinant inbred line (RILs) from an interspecific cross of DZ-01-2785 x *E. pilosa* (30-5): Generation advancement to F_4, F_5 and F_6

The development of RILs from this specific cross has now reached to F_8. It was originally planned to backup the mapping populations previously used in the linkage-map construction. Because we have seen very useful segregations and the presence of transgressive segregants in the previous interspecific RILs, we continued using RILs of this cross for variety development too. Last year 400 RILs were planted for evaluation. On the basis of their field performance and crude evaluation of yield potential, 21 lines were selected for early-set groups, to be included in the Preliminary Yield Observation at Debre Zeit.

E.1.3. Evaluation of F_3 segregating populations from two crosses of tef

Hybridisation breeding of selected genotypes has been successfully utilized in tef improvement program. Two targeted crosses were made with the objective of improving the seed quality of one variety (DZ-01-974) and one advanced genotype (DZ-01-2356); both were crossed with DZ-01-196, donor of seed quality characteristics. These crosses, we believe, are very essential in producing high yield and exceptionally high-quality seeds for the eastern-central highlands where quality demands by the farmers override grain yield because of their urban-market proximity.

Using greenhouse, off-season and main-season nurseries, these crosses have now reached to F_7 generation, which is more than sufficient to fix homozygousity in tef. Selection was based not only agronomic data (close to the recipient parents) but also on visual assessment of seed characteristics (close to the donor parent), mainly colors and size. From the DZ-01-974 x DZ-01-196 cross, 60 and eight lines, respectively, were selected and included in the 2002/03 late-set groups of Preliminary Yield Observation and Pre-National Variety Trial. From the cross between DZ-01-196 x DZ-01-2356, 45 and 13 lines, respectively, were included in similar trials of early-set groups.

E.1.4. Crossing tef lines

Eighteen cross combinations were attempted. Eighteen parental lines composed of two released varieties (DZ-01-974 and DZ-Cr-37), twelve germplasm selections, three cultivars and one accession of the wild *E. pilosa* (accession PI219588) were included in the hybridisation scheme. DZ-01-974 was involved in 15 of the cross combinations. Fourteen crosses successfully set hybrid seeds, out of which one [(DZ-01-974 x *E. pilosa* (accession PI219588)] was hybrid sterile. All the four crosses that failed to set hybrid seeds were between tef genotypes and therefore there is no prior reason to assume other than a miss in the crossing technique. Of the remaining 13 crosses, nine and five crosses are now in the F_2 and F_3 segregating population stages, respectively.

E.2. Molecular Genetic Studies at Cornell

E.2.1. Construction of a genetic map of tef

Materials and methods:
Plant material: A recombinant inbred lines (RILs) derived from a cross of *E. tef* cv. Kaye Murri and *E. pilosa* cv. 30-5 were used for construction of tef genetic map. One hundred and sixty two RILs were grown at three locations in Ethiopia in the summer/fall of 1999 and at eight locations in Ethiopia during the summer/fall of 2000. These 162 RILs were used to obtain genotypic scores.

DNA markers: RFLP anchor probes derived from rice, barley, oat and wheat were used in this mapping effort. In addition, we requested maize anchor set from University of Missouri-Columbia and finger millet probes from Dr. Katrien Devos at John Innes Center, UK. We used several publicly available rice, wheat and maize microsatellites for analysing the tef parental lines. We obtained 21 EST-derived SSR primer pairs from Dr. Wayne Powell. We designed 15 ISSR primers based on known SSR motifs (Kantety et al., 1995) and purchased a set of 100 ISSR primers from the biotechnology center at the University of British Columbia, Canada. All of these markers were PCR amplified according to their specific conditions and the amplicons were analysed using 4% denaturing poly acrylamide gel electrophoresis (PAGE) and silver staining of the products. Nusieve agarose gels (4%) were used to analyse some of the SSR products.

Mapping: There were a total of 251 loci, including 129 RFLP markers (82 anchor probes, 47 Tef cDNAs), 26 EST-SSR markers and 96 ISSR markers. MapManager QTX was used to construct tef map at a threshold of LOD = 3.0. The command 'ripple' was used to order markers within a linkage group.

Results and discussion

DNA marker polymorphism:
RFLP analysis: A total of 347 probes were surveyed on the tef parental lines, Kaye Murri and *E. pilosa*, digested with 11 restriction enzymes. In addition, survey (or mapped enzyme) information obtained from Texas Tech University was used for mapping TCD clones and some anchor probes. The maize anchor probes were not successful in hybridising to tef DNA. Eighty-eight of the maize genomic probes such as, BNL, UMC and ASG clones did not produce enough hybridisation signal so they could not be used for further analysis. We obtained 40 millet probes from Dr. Katrien Devos but they were unsuccessful in hybridisation like the maize genomic clones. We re-obtained some problematic millet probes from Dr. Devos but they didn't produce good hybridisation signal to be useful for mapping in tef. Although the millet probes were originated from finger millet, which is related to tef, they did not hybridise to tef DNA. This indicates that genomic clones from even closely related grasses may not be useful for generating tef map.

The cDNA clones originated from barley, oat, rice and wheat were successful in hybridising to tef DNA. We surveyed 169 probes from this collection and obtained 59% (100) polymorphism with at least one enzyme. Seventy-five of these probes were used for genotyping the RILs. In addition, we hybridised 40 maize cDNA probes (CSU) and 70% of the probes were successful with 12 probes being polymorphic on the tef parents. All of these probes are currently being used to genotype the RILs.

In summary, cDNA probes from other graminaceous species were successful in hybridising tef DNA where as the genomic clones from maize and finger millet did not hybridise well. Most of the grass anchor probes produced good hybridisation signal on tef DNA when compared to maize clones (CSU) presumably due to their earlier selection criteria based on their hybridisation signal to DNA of several plant species on "garden blots".

PCR analysis:

EST-SSR markers: A touchdown PCR approach was found to be the best for amplifying tef DNA template using EST-SSR primer pairs derived from other graminaceous species. PCR conditions for SSR-ESTs included a first denaturation at 94 °C for 5 min, followed by 10 cycles of denaturation at 94 °C for 45 s, annealing at 58 °C for 60 s with a decrement of 0.5 °C / cycle to reach a final annealing temperature of 53 °C, and extension at 72 °C for 90 s, followed by 30 cycles of denaturation at 94 °C for 45 s, annealing at 53 °C for 60 s, and extension at 72 °C for 90 s, with a final extension at 72 °C for 7 min. A suffix of "a-c" was added to the marker name when multiple polymorphism was scored.

Twenty one simple sequence repeats derived from expressed sequence tags (EST-SSRs) derived from wheat and 180 consensus EST-SSR primer pair combinations derived from barley, maize, rice, and wheat were surveyed for amplification of tef DNA. A total of 77 primer pairs detected polymorphism among tef parental lines (Table 6). The size or the type of repeat motif in the original EST did not correlate with the polymorphism in tef. The length of the microsatellite in the original EST sequences ranged from 18 to 36 bases.

ISSR markers: ISSR technique involves amplification of the DNA between two oppositely oriented SSRs that are separated at a distance amplifiable by taq polymerase using single primer designed based on a SSR motif. Several primers can be designed based on a single SSR motif. Primers with different specificity can be designed by the addition of 2 to 3 strict or degenerate bases at the 5' or 3' end. ISSR technique produces gel patterns that are similar to AFLP patterns and results in a high number of markers in a short time.

We surveyed 115 ISSR primers and selected 23 primers that resulted in multiple polymorphic bands per primer. The number of bands amplified per primer ranged from 15 to 97 (Table 7). The number of bands scored per primer ranged from 1 to 12 with an average of 4.2 polymorphic bands/primer. A total of 96 loci were scored on the population using the 23 primers. The ISSR bands were designated with the primer number along with a suffix letter (a through l).

Tef linkage map:

Originally we generated genotypic information using some of the grass anchor probes and all the PCR-based markers. The genotypic data generated in our lab was combined with the data obtained from Texas Tech University and generated a map using 319 markers. This initial map had 43 linkage groups with some linkage groups exclusively based on Cornell or Texas Tech markers only. When markers from both data sources were present in a linkage group, they were not interspersed with each other and rather they were clustered together in two areas of that linkage group. The confidence of linkage between Cornell and Texas markers was low with a LOD value below 3.0 for most of the junctions.

In order to confirm the RILs identity and accuracy of the data between the two labs, we used twelve tef and grass anchor probes with the same enzyme combination as the one Texas Tech lab used and obtained genotypic data on our mapping filters. A comparison of the data

indicated that there were several discrepancies between the two data sets. In general, the data between the two groups were different enough that the markers never co-mapped and in most cases were present in different linkage groups. Therefore we decided to omit all of the data we included from Texas Tech and we produced data in our lab for the rest of the grass anchor probes and tef cDNA clones. Originally, Texas Tech lab has used 79 tef cDNAs for mapping but we could only amplify 41 of them in our lab. These 41 tef cDNA clones were used for mapping presented in this report.

The tef map was constructed using the 251 loci obtained by genotyping the RILs. The map consists of 30 linkage groups with a total length of 2410.8 cM. The number of markers in each linkage group ranged from 3 to 20. The length of each linkage group ranged from 25 cM to 251.7 cM with an average of 80.4 cM per linkage group. The linkage groups were named based on the order of their total length (Figure 1).

Tef is an allotetraploid with 20 haploid chromosomes. The identification of the homeologous linkage groups is important for a more accurate representation of the map. In order to identify homeologous groups we need multiple adjacent markers with multiple loci mapped on different linkage groups. We identified 28 markers with multiple loci on the map. Nine such markers had multiple loci mapped on the same linkage group indicating that these genes are duplicated, share a common motif/sequence, or a member of a gene family. Of the remaining 19 markers, six had additional loci that were unlinked and 13 had multiple loci mapped on different linkage groups. Although there is some evidence, it is difficult to say with confidence on which linkage groups are homeologous in this map.

A second probe-enzyme combination was used to find out if the second polymorphism will identify a homeologous group. For example, TCD99 and TCD197 were mapped with two different enzymes but they map to the same linkage group. We believe that some of the smaller linkage groups may join together when additional markers are added to the map thus bringing the number of linkage groups close to the expected number of 20. However, several more markers need to be mapped before we can identify all the homeologous groups.

E.2.2. QTL Analysis

Materials and methods

Population construction: A recombinant inbred lines consisting of 181 individuals were developed from a cross between Kaye Murri and *Eragrostis pilosa* accession 30-5 at the Debre Zeit Agricultural Research Center (DZARC). The original population of 400 F_2 individuals was advanced in the glasshouse using the single seed decent method and the F_9 generation was bulked for phenotypic evaluation and mapping. Based on genotypic data collected at Texas Tech University and phenotypic data collected in Ethiopia in 1999, the population was further reduced and a total of 162 RILs were chosen for a second set of field trials in 2000.

The cultivar Kaye Murri is as described by Ebba (1975) and the accession (30-5) of *Eragrostis pilosa* was obtained from Holetta Agricultural Research Center, Ethiopia. Kaye Murri is a tall, thick culmed, late maturing variety with a long compact panicle. The lemma color is red and the seed color is white. *E. pilosa* has many weedy characteristics compared to cultivated tef, such as thin culms, prostrate growth habit and short loose panicles. In contrast

to Kaye Murri it has red/brown seeds and a greyish colored lemma. *E. pilosa* is tetraploid, which allows for a relatively successful crossing with cultivated tef.

Field trials: Field-testing was carried out in Ethiopia at three different locations in 1999 and eight locations in 2000. In 1999, 181 lines were planted in four replicates each, in complete randomised block design (CRBD) at three locations (Akaki, Alemtena, and Debre Zeit Black Soil). In 2000, 162 lines were planted in two replicates at each of eight locations (Akaki, Alemtena, Debre Zeit Black Soil, Debre Zeit Light Soil, Denbi, Melkasa, Chefe, and Holetta). The 2000 planting scheme also followed a CRBD. The seeds were broadcast-sown in 1 x 2 meter plots. The eight locations were chosen based on their wide range of environmental conditions, allowing for a diverse set of environments. These eight locations fit into three major and seven minor agroecologies that have been documented in Ethiopia for tef (Simane et al., 1997). These locations are as follows: i) the humid zone (C1) in the western regions of Ethiopia, ii) the wet semi-arid (C2) region in the central part of the country, iii) the dry semi-arid region also known as the Northern Rift Valley (C3).

Trait Data: Twenty-four phenotypic traits were evaluated on the 162 F_{10} RILs of the Kaye Murri x *E. pilosa* population during the 2000 growing season at the majority of the eight locations (Table 8). Sixteen of these traits were evaluated on 181 F_9 RILs at three locations during the 1999 growing season. Ten plants per line were randomly selected at physiological maturity and the following measurements were taken: (1) *Days to heading* was evaluated as the number of days from planting until 50% of the plants in the plot produced their panicles (when the panicle emerges from the leaf sheath), (2) *Days to maturity* was measured as the number of days from planting to the day when 50% of the plants in the plot reached physiological maturity, (3) *Panicle weight* was measured as the weight in grams of the panicle, (4) *Panicle seed weight* was measured as the weight in grams of the seeds harvested from one primary panicle, (5) *100 seed weight* was measured as the weight in milligrams of 100 seeds, (6) *Culm length* was measured as the length in centimetres from the crown to the base of the panicle, (7) *Culm diameter of the 1st internode* was measured using a calliper and was determined as the width at the middle of the first internode up from the base of the plant, (8) *Culm diameter of the 2nd internode* was also measured using a calliper and was determined as the width at the middle of the second internode up from the base of the plant, (9) *Peduncle length* was measured in centimetres as the distance between the top of the last internode and the bottom of the panicle (node where the first panicle branch starts), (10) *Panicle length* was measured in centimetres from the base of the panicle to the tip, (11) *Plant height* was determined as the combined total length of the culm plus the panicle, (12) *Number of internodes* was the total number of internodes on the plant, (13) *1st Internode length* was measured as the length in centimetres of the culm section from the crown up to the base of the first node, (14) *2nd Internode length* was measured as the length in centimetres of the culm section from the top of the first node up to the base of the second node, (15) *Grain yield* was measured as the total weight in grams of all the seed harvested from each plot, (16) *Lodging index* was determined based on the formula from Caldicott and Nutall (1979), who described the lodging index as the sum of the product of each scale of lodging (0-5) and its percentage divided by five, (17) *Lemma color* in this population has been classified in to eight categories. The four main categories are purple (p=6), red (r=5), grey (g=7) and yellowish white (yw=8). The second group is classified as variegated. The four sub groupings are as follows: V(g+r)=(1) Variegated, grey lemma with red tips and margins, V(g+p)=(2) Variegated, grey lemma with purple tips and margins, V(p+y)=(3) Variegated, yellowish white lemma with purple tips and margins, and V(r+y)=(4) Variegated, yellowish white lemma with red tips and margins, (18) *Panicle form* was determined to consist of four

types (loose = 1, fairly loose = 2, very loose = 3, and compact = 4), (19) *Crown diameter* was measured using a calliper and was determined as the width in centimetres around the middle portion of the crown, (20) *Shoot biomass* was determined as the weight in grams of the remaining plant biomass after harvest, (21 & 22) *Rind penetrometer resistance of the 1st and 2nd Internodes* were measured as the force in pounds required to puncture a 5cm long section cut from the first and second internodes (ten randomly chosen plants were collected at physiological maturity and tests were performed on the main tiller. Two separate sections were cut 5 cm in length and 5cm up from the base of each internode), (23 & 24) *Crushing strength of the 1st and 2nd internodes* were measured as the force in pounds required to crush, to the point of bending, a cut stem section. The same 10 plants and stems used for the puncture resistance tests were used for this measurement. Stem sections were measured and cut to be 5cm in length and cut 10cm up from the base of each internode. The sections were then dried at air temperature for 4 weeks and then measured.

QTL analysis: The genetic map described in section E.2.1 above was used for QTL mapping using Qgene 3.06n.1 (Nelson, 1997). Single point analysis and interval mapping were performed with Qgene to analyse the phenotypic data from each of the trials. In order to determine accurate significance for each trait permutation testing was performed with Qgene to set experiment-wise significance thresholds for each of the traits at each location using1,000 permutations across all the 30 linkage groups.

Results and discussion

Table 9 depicts yield and yield related QTLs and Table 10 presents QTLs associated with morphological characteristics related to plant height. All QTLs presented here are significant at $p<.001$ and have LOD scores with values that are equal to or are higher than the 95% LOD threshold determined using 1,000 permutations. There are three linkage groups (6, 8 and 15), which contain the majority of identified QTLs. On linkage group 6 the TCD95 marker was significant for both yield and plant height related traits (panicle seed weight, culm length, plant height, grain yield and shoot biomass). Heading date was correlated with a DuPont Microsatellite, DM1654c on linkage group 6. Also on linkage group 6 panicle weight was highly correlated with RZ214 which is just 8cM from DM165c. An important rice marker, RZ962d, is located on linkage group 8 and was significant for heading date, panicle weight, culm diameter at 2nd internode, panicle length, plant height, number of internodes and shoot biomass. This marker may be a very important marker for selection purpose, as it appears to play a role in controlling yield as well as plant height.

CDO470 on linkage group 15 may also prove effective for controlling plant morphological traits as it was significantly correlated to heading and maturity dates as well as culm length and plant height. Markers associated with shoot biomass showed the highest numbers with 6 markers each on different linkage groups. Two different markers, I547b and RZ962d on linkage groups 11 and 8 respectively, were significant for culm diameters at the 1st and 2nd internodes, respectively. Unfortunately, no markers were found that directly correlate with lodging resistance. However, it is known in tef that the incidence of lodging increases with taller plants so the markers associated with morphological traits such as plant height, culm length and culm diameter may prove quite effective for reducing lodging.

F. Proceedings of the First International Tef Workshop:

Despite the importance of tef in Ethiopian agriculture and a reasonably large body of research results, the information has not been brought into one volume. Neither was the research progresses discussed in a scientific forum specific to tef. This happened for the obvious, but not surprising, reason that tef, because of its local importance, did not for decades enjoy

international funding and support. In an earnest intent to remedy the situation, the competitive research grant obtained from the McKnight Foundation (since 1995) under the Collaborative Crop Research Program has made it possible, for the first time, to organize an International Workshop on Tef Genetics and Improvement in Addis Ababa, Ethiopia, from 16-19 October 2000. The objectives were to review past and current research progresses, document the available information in tef research, and share the research experiences of other crops. The workshop brought together scientists from the National Tef Research Program and resource scientists from Ethiopia, USA, Great Britain, Austria, Guinea and Mexico.

The proceeding, which can be considered as a milestone contribution in the history of tef research, appeared in January 2001 under the title "Narrowing the Rift: Tef Research and Development". The total number of pages is 326. It presents 28 papers categorized in five sections: General, genetics and breeding (from conventional methods to biotechnological approaches), crop management, utilization and technology transfer, and experiences from other crops. The last section provides recent scientific advancements on other cereals that may be relevant and applicable to tef research in the future. Tef being categorized in the so-called group of "Orphan crops", the title part "Narrowing the Rift" implies two things: Firstly, tef has now attracted international attentions, and secondly, what the frontiers of science can achieve in high-profile crops such as rice, maize and wheat can potentially be transferred to tef. One or more scientists who are specialists in the subject area have contributed each paper in this proceeding; staff from DZARC authored/co-authored 15 articles. An attempt was made to put together the information in such a way that it may be useful to researchers, extension workers, teachers, students and policy makers. Nevertheless, because the final print did not come out to an acceptable standard, we are in the process of re-printing it for distribution to an international audience.

G. Training Progress:

Training is one of the major components of the project designed to upgrade the qualified manpower need of the National Tef Research Program. For the trainings leading to PhD degree, Mr. Aderajew Haddis and Mr. Solomon Chanyalew were selected to be trained at the Addis Ababa University and Alemaya University, respectively. Mr. Aderajew Haddis has started his study in April 2001 under the supervision of Professor Endashaw Bekele of Addis Ababa University. He has now completed his first season field-experiments at Debre Zeit and Melkassa Centers. Mr. Solomon Chanyalew has been accepted by Alemaya University, and has completed a one-semester course work and thesis proposal writing under the title "*Variation and associations among yield and yield related traits in interspecific and intraspecific crosses and molecular genetic characterization of parents and recombinant inbred lines of tef* (*Eragrostis tef*). His graduate advisory committee includes Prof. Harjit Singh, Dr. Hailu Tefera, Dr. Habtamu Zelleke and Prof. Mark Sorrells. The M.Sc research work of Mr. Fisseha Werede, Alemaya University, which was conducted under the supervision of Dr. Hailu Tefera, has been completed. The thesis will be presented for an open defence sometime in October 2002.

Elizabeth Graznak (M.Sc. candidate at Cornell) has continued with her statistical analyses on morphological trait data on the RILs generated by Dr. Hailu Tefera. The population was created from a cross between *E. pilosa* (30-5), one of the progenitors of tef, and Kaye Murri a high performing and elite cultivar. With the help of staff at the Tef Research Program, the population was evaluated at eight different locations ranging from high altitudes such as at Chefe Donsa and Holetta (2400 m), to lowland areas in Melkasa and Alemtena (1600 m). In May, Ms. Graznak took a leave of absence so that she could start a job on a farm while the tef

map is completed. Now that the map is complete, she has nearly finished the analyses. Over the next two months Ms. Graznak will complete her thesis for the M.S. degree and prepare a publication on her studies.

Getachew Belay, Fassil Kelemework (Debre Zeit), Solomon Chanyalew (Melkassa) and Getachew Hruy (Mekelle) participated in a workshop on *'Participatory Research Methods'* held in Nairobi, Kenya, on 9-13 December 2001. Participants generally evaluated the workshop as 'very successful'. We believe that the experience gained is of immense value for the Participatory Plant Breeding approach the project is to pursue in the 2002-2006 period.

The Principal Investigator of the project, Dr. Hailu Tefera, stayed at Cornell University from October 1, 2001 to March 31, 2002. His notable activities included the following: 1) Trained and worked on microsatellite (SSR) markers to enrich the tef genetic map. 2) Developed work plan for the renewal proposal in collaboration with his project counterpart, Mark Sorrells, and in consultation with Rebecca Nelson, program Director of CCRP. 3) Participated in the Grantees Conference, in Mexico, and made presentations in the conference that included conference report, work plan for the period July 2002 – June 2006, and Intellectual Property Rights (IPR) plan for the project. 4) Participated in a meeting co-ordinated by Roz Naylor of Stanford University, and held at Granlibakken Conference Center, Tahoe City, California, in March 21-22, 2002. The objective of the meeting was to discuss on paper presentation to an international conference on agricultural biotechnology, which yielded the following paper: Naylor, R.; Falcon W.; Nelson, R.; Jahn, M.; Goodman, R.; Kalazich, J.; Senguba, T.; and Hailu Tefera (2002). Integrating New Genetic Technologies in the Improvement of Orphan Crops in Least Developed Countries. Proceedings of the 6th International Conference on **Agricultural Biotechnologies: New Avenues for Production, Consumption and Technology Transfer**. Ravello (Italy), July 11 to 14, 2002. *(http://www.economia.uniroma2.it/conferenze/icabr/abstract/Naylor.htm)*

H. Institutional or Additional Support:
Fund has been obtained from the Ethiopian government to support the National Tef Research Program activities at 12 centers in the country. The National Tef Research Program is one of the research budget receiving programs of the Ethiopian Agricultural Research Organization.

I. Activities of Partnership Advisory Committee:
From July1, 2001 through June 30, 2002 the Advisory Committee (AC) convened seven times. Major issues discussed and salient proceedings of these meetings are summarized below. Mere notifications by the PI to the AC or vice versa, in the regular updates on the project are not included.

July 24, 2001
Only administrative issues were deliberated.

September 15, 2001
The AC deliberated on the nomination procedures of participants for the African Grantees workshop in Nairobi on Participatory Research Methodologies, and the PI's financial and technical reports of the project. The PI was given the responsibility to make the selection of participants for the workshop.

The PI gave an overall presentation of financial and technical aspects of the project both at EARO and Cornell University. The presentation was based on the Annual Technical Reports

submitted to MF. The AC held a thorough discussion on the achievements made and the problems encountered so far. AC members expressed their appreciation to the overall work done and the scientific contributions of the project. AC members, however, also made some recommendations that would facilitate the budget utilization of the project.

December 06, 2001
The AC approved the four nominees by the PI and who would participate in the MF-CCRP training workshop on "Participatory Research Methodologies", held in Nairobi, Kenya. After careful deliberations, the AC also nominated the individuals who would participate in the MF-CCRP conference, "building strong partnerships for food security", held March 9-13, 2002 in Puerto Vallarta, Mexico.

February 25, 2002
This AC meeting was convened primarily for its feedbacks (suggestions and comments) on the project renewal proposal for the coming four years (June 2002-June 2006). The proposal contains a work plan due for submission to the Oversight Committee (OC) of the McKnight Foundation - Collaborative Crop Research Program (MF-CCRP) for approval. AC members read the renewal proposal prepared by Drs. Hailu Tefera and Mark Sorrells. The Acting PI (Dr. Getachew Belay) singled out the new research areas included in the renewal proposal. Comments/suggestions of AC members were immediately communicated to the PI, who at the time was at Cornell University, for his considerations before the final submission of the renewal proposal.

April 30, 2002
The PI briefed the AC about his six-month stay at Cornell University, and reported on his research visit, Grantees conference and the renewal proposal. Specifically, the PI reminded the AC that the M.Sc training component of the renewal proposal requires critical decision with regard to its effective implementation and budget utilization. The AC made thorough discussion on this aspect and recommended the PI and the Secretary to come up with an action plan, particularly regarding fields of study and training places. The AC also discussed the contract renewal of the postdoc/research associate in the project, which comes to an end on July 7, 2002. Before doing so, however, the AC advised the PI to present performance report of the postdoc, and his personal recommendations to AC members.

June 13, 2002
The AC discussed matters related to the publication of the proceeding of the First International Tef Workshop. The AC recognized the proceedings as a milestone contribution from the project. However, the final print was not up to the expected standard; the major ones are poor paper-quality, and layout error of the cover page. The AC also did not believe that enough copies have been printed, and therefore advised for the printing of additional 300 copies. The remaining printed copies shall be distributed to relevant institutions, authors and workshop participants.

The PI presented four possible places for an MSc training of the project together with the cost breakdown. After a thorough deliberation, Wageningen University, The Netherlands, was chosen. The PI also presented the activity report of the postdoc/research associate, together with his letter of recommendation addressed to AC chairman and Acting Director General of EARO, Dr. Abera Debelo. However, the absence of an evaluation format (similar to the one used for other EARO employees) had put the AC in a difficult position to reach to a conclusion. Therefore, the PI was advised to use, where appropriate, the evaluation format for

contract employees of The National Seed Industry Agency and present the case for a meeting to be held before June 27, 2002.

June 25, 2002
The agendum related to the contract renewal of the postdoc/research associate was deliberated in the absence of Dr. Getachew Belay who is currently holding the position. After reviewing a) Dr. Getachew's technical report, b) the PI's evaluation and recommendation, c) support by the Center Manager of Debre Zeit Agricultural Research Center, and d) availability of fund in EARO's project account and the possibility of extending its use until June 30, 2003, the AC agreed to extend the employment contract for one year.

The AC also deliberated and agreed on the selection of candidates for training in one each of the areas of breeding/genetics, agronomy and extension (participatory breeding). It has also been agreed to follow EARO's procedure and standard format for the selection of candidates both at Center and EARO levels from the project participating Centers (Debre Zeit, Holetta, Melkassa, Adet and Mekelle). The PI will inform the AC the selected individuals for the trainings. In the discussion it was also emphasized that only individuals who are working on tef research and who will continue to work on the same after training should be considered for this opportunity.

Table 1. Mean values for grain yield (kg/ha) of tef genotypes tested in advanced observation of Early Maturing Tef Lines in 2001/02 season at eight locations (Boldface= promoted lines).

No	Cross/Genotype	Alemtena	Melkassa	Mekelle	Denbi	DZLS	DZBS	Holetta	Adet	MEAN
1	DZ-Cr-37	1118	1568 a-i	767	2108	3093 a-h	2295 b-d	3056	2028 b-j	2004 a-i
2	Local Check	1164	1345 c-m	860	1641	2864 a-k	2136 b-g	2884	2713 ab	1951 b-l
3	**DZ-01-443**	**1336**	**1178 g-m**	**1358**	**2380**	**3136 a-h**	**3086 a**	**3393**	**2074 b-j**	**2243 a**
4	DZ-01-1276	1196	1119 i-m	915	2444	3300 a-d	2715 ab	3056	2559 a-e	2163 a-c
5	DZ-01-667	1321	1205 f-m	782	2216	2426 d-l	2028 b-g	2690	2215 a-i	1860 d-n
6	DZ-01-147	1550	1079 g-m	580	2209	3123 a-h	1946 c-g	2751	2644 a-c	1985 a-j
7	DZ-01-1225	1206	1565 a-i	957	1916	3058 a-i	1989 b-g	3272	2618 a-c	2073 a-e
8	**DZ-01-1629**	**1360**	**1529 a-k**	**800**	**2643**	**2410 e-l**	**2236 b-f**	**3461**	**2085 b-j**	**2066 a-e**
9	DZ-Cr-377 (RIL 10)	998	1273 d-m	635	1313	2174 i-l	2070 b-g	2903	2338 a-h	1713 j-n
10	DZ-Cr-377 (RIL 38)	1420	1618 a-g	628	2015	2404 e-l	1736 c-g	3326	2900 a	2006 a-i
11	DZ-Cr-377 (RIL 42)	1246	1386 c-m	1002	2263	2578 a-l	1896 c-g	3278	2342 a-h	1999 a-i
12	DZ-Cr-377 (RIL 44)	1160	1483 a-m	656	2288	3181 a-h	1700 c-g	3204	2613 a-d	2035 a-h
13	DZ-Cr-377 (RIL 46)	1535	1770 a-c	644	1934	2479 c-l	2129 b-g	2856	2086 b-j	1929 b-m
14	DZ-Cr-377 (RIL 205)	1338	1599 a-i	884	1925	2338 g-l	2201 b-f	3363	2521 a-g	2021 a-i
15	DZ-Cr-377 (RIL 275)	1013	1020 lm	602	2508	1865 l	1926 c-g	2840	2270 a-i	1755 h-n
16	DZ-Cr-377 (RIL 309)	1015	1536 a-j	605	2076	2361 g-l	1830 c-g	2317	1692 h-f	1679 l-n
17	**DZ-Cr-376 (RIL 40)**	**1209**	**1596 a-i**	**935**	**2536**	**2994 a-g**	**2020 b-g**	**2574**	**2645 a-c**	**2064 a-f**
18	**DZ-Cr-376 (RIL 67)**	**1411**	**1404 c-m**	**935**	**2758**	**2720 a-l**	**2076 b-g**	**2411**	**2543 a-f**	**2032 a-h**
19	DZ-Cr-376 (RIL 153)	1094	1471 a-m	631	1816	3288 a-e	1964 c-g	2785	1855 e-j	1863 d-n
20	DZ-Cr-376 (RIL 198)	1220	1519 a-k	919	2021	2114 j-l	1981 b-g	2460	1764 h-j	1750 h-n
21	**DZ-Cr-376 (RIL 47)**	**1469**	**1699 a-e**	**744**	**2534**	**3211 a-g**	**1956 c-g**	**2864**	**2864 a**	**2168 ab**
22	**DZ-Cr-376 (RIL 392)**	**1294**	**1903 ab**	**914**	**2539**	**2734 a-l**	**2149 b-g**	**3253**	**1989 b-j**	**2097 a-d**
23	DZ-Cr-375 (RIL 62)	1054	1268 e-m	964	2090	2395 f-l	1651 d-g	3031	1436 j	1736 i-n
24	DZ-Cr-375 (RIL 239)	1380	1003 m	380	2470	2719 a-l	1889 c-g	2776	1612 h-j	1779 f-n
25	DZ-Cr-375 (RIL 263)	1621	1013 m	993	1629	2019 kl	1499 e-g	2820	1986 b-j	1697 k-n
26	DZ-Cr-379 (F_4 sel 15)	1268	1569 a-i	781	2356	2931 a-j	2251 b-e	2559	1725 h-j	1930 b-m
27	DZ-Cr-379 (F_4 sel 25)	1230	1480 a-m	692	2260	3388 ab	1908 c-g	2832	1872 e-j	1958 b-l
28	**DZ-Cr-379 (F_4 sel 31)**	**1353**	**1614 a-h**	**926**	**2188**	**2465 d-l**	**2438 bc**	**3435**	**1671 h-j**	**2011 a-i**
29	DZ-Cr-379 (F_4 sel 34)	1109	1754 a-d	764	2299	3021 a-i	1808 c-g	2406	1836 e-j	1874 d-m

No	Cross/Genotype	Alemtena	Melkassa	Mekelle	Denbi	DZLS	DZBS	Holetta	Adet	MEAN
30	DZ-Cr-379 (F_4 sel 51)	1166	1601 a-i	1041	1958	2510 b-l	1665 d-g	2512	1667 h-j	1765 g-n
31	DZ-Cr-379 (F_4 sel 13)	1399	1398 c-m	775	2278	3193 a-h	2191 b-f	3352	1816 f-j	2050 a-g
32	DZ-Cr-379 (F_4 sel 14)	1393	1130 h-m	992	1815	2784 a-k	1955 c-g	3324	2349 a-h	1968 a-k
33	**DZ-Cr-379 (F_4 sel 19)**	**941**	**1411 c-m**	**2811**	**1803**	**2640 a-l**	**1783 c-g**	**2343**	**1684 h-j**	**1652 mn**
34	DZ-Cr-379 (F_4 sel 22)	1253	1500 a-l	1049	2268	3364 a-c	1759 c-g	2747	2118 b-j	2007 a-i
35	DZ-Cr-379 (F_4 sel 24)	1421	1939 a	1003	2126	2860 a-k	1718 c-g	3047	2032 b-j	2018 a-i
36	DZ-Cr-379 (F_4 sel 36)	1183	1454 b-m	591	2050	2448 d-l	1915 c-g	3146	1936 c-j	1840 d-n
37	DZ-Cr-379 (F_4 sel 37)	1194	1720 a-e	1132	1781	2940 a-j	1756 c-g	2708	1456 j	1836 d-n
38	DZ-Cr-379 (F_4 sel 38)	1374	1050 k-m	710	1949	2868 a-k	1950 c-g	2571	2057 b-j	1816 d-n
39	DZ-Cr-379 (F_4 sel 42)	1240	1531 a-k	809	2124	2316 h-l	1645 d-g	2907	2084 b-j	1832 d-n
40	DZ-Cr-379 (F_4 sel 44)	1054	1208 f-m	764	2024	3406 a	2093 b-g	2556	1807 f-j	1864 d-n
41	DZ-Cr-379 (F_4 sel 48)	1693	1346 c-m	946	1743	2838 a-k	1415 g	3236	1779 g-j	1874 d-n
42	DZ-Cr-380 (F_4 sel 53)	1069	1143 g-m	828	1589	2398 f-l	1946 c-g	2263	1849 e-j	1635 n
43	DZ-Cr-380 (F_4 sel 54)	1218	1673 a-f	661	2555	3093 a-h	2211 b-f	2958	2059 b-j	2053 a-f
44	DZ-Cr-380 (F_4 sel 61)	1188	1146 g-m	452	2303	2359 g-l	1476 fg	2860	2135 b-j	1740 i-n
45	DZ-Cr-380 (F_4 sel 63)	1513	1060 j-m	537	2340	2675 a-l	1798 c-g	2913	2081 b-j	1864 d-n
46	DZ-Cr-380 (F_4 sel 64)	1380	1705 a-c	791	2221	2415 d-l	1828 c-g	2561	1876 d-j	1847 d-n
47	DZ-Cr-359 (F_4 sel 74)	1058	1484 a-m	1027	2274	2521 a-l	1759 c-g	2592	1585 ij	1787 e-n
48	DZ-Cr-381 (F_4 sel 68)	1473	1193 f-m	411	1979	2748 a-k	1848 c-g	2420	1973 b-j	1755 h-n
49	DZ-Cr-384 (F_4 sel 80)	1404	1588 a-i	1034	2098	3260 a-f	1538 d-g	2413	1741 h-j	1884 c-n
	Mean	1271	1425	804	2136	2743	1954	2863	2073	1909
	CV (%)	20.40	13.67	33.34	18.41	13.00	15.67	15.04	14.46	16.85
	SEM	259.37	194.81	268.143	393.12	356.63	306.28	430.45	299.71	321.67
	LSD (0.05)	NS	391.70	NS	NS	717.10	615.80	NS	602.60	223.6

Table 2. Mean values for grain yield (kg/ha) of tef genotypes tested in advanced observation of late maturing tef lines in 2001/02 season at ten locations (Boldface= promoted lines).

No	Cross/Genotype	Alemtena	Melkassa	Mekelle	Denbi	DZLS	DZBS	Holetta	Adet	Akaki	Chefe Donsa	Mean
1	DZ-01-974	1348	1768 ab	492 a-f	2163 a-i	2885	3285 bc	3973 a-c	2978 a-c	2384 a-f	705	2198 a
2	Local Check	1678	1721 a-c	574 a-c	1488 f-k	2725	2615 c-i	2835 f-j	2635 a-g	1269 g-h	1234	1877 d-c
3	DZ-Cr-358	1288	1476 b-h	441 a-g	2575 a-d	2440	4011 a	3230 a-g	2544 a-h	2628 ab	1513	2215 a
4	Balami	1531	850 ij	490 a-f	2044 a-i	1596	2510 d-j	2612 f-i	1729 gh	1943 a-g	923	1623 c-o
5	Enatite	1648	1263 b-j	433 a-g	2080 a-i	3565	2921 c-g	3228 a-g	2703 a-f	2568 a-d	1451	2186 a-b
6	**Gofarie**	**1113**	**1309 b-j**	**523 a-e**	**2058 a-i**	**2456**	**3285 bc**	**2713 f-j**	**3078 ab**	**1544 e-h**	**1350**	**1943 b-h**
7	Janno	1291	1235 b-j	300 c-i	1370 h-k	2113	2015 i-l	2906 e-j	1634 h	1591 e-h	956	1587 n-o
8	DZ-01-146	1163	1414 b-i	579 a-c	1901 b-j	2405	3633 a-b	3213 a-g	3321 a	2598 a-c	1419	2164 a-c
9	DZ-Cr-46	1306	1170 b-j	435 a-g	1710 b-k	2815	2558 d-j	2989 c-j	2627 a-g	1981 a-g	1183	1877 d-l
10	DZ-01-1193	1215	833 i-j	520 a-e	1634 d-k	1905	2519 d-j	2070 jk	2360 b-h	1771 b-g	1195	1602 m-o
11	**DZ-01-1717**	**1373**	**1393 b-j**	**568 a-d**	**2866 a**	**2620**	**2981 b-f**	**3472 a-f**	**2333 b-h**	**2829 a**	**1459**	**2189 a**
12	DZ-01-348	1180	1646 a-f	614 a-b	2329 a-g	2746	2650 c-i	3350 a-g	2327 b-h	2006 a-g	1210	2006 a-f
13	DZ-Cr-377 (RIL 78)	1133	1096 d-j	359 a-i	1085 gk	2014	1843 g-l	3217 a-g	2579 a-h	1593 e-h	888	1580 n-o
14	DZ-Cr-377 (RIL 153)	1199	1413 b-i	514 a-e	2306 a-h	2909	3009 b-f	3092 a-i	3320 a	2188 a-g	1046	2100 a-d
15	**DZ-Cr-377 (RIL 351)**	**1194**	**1395 b-i**	**372 a-i**	**2019 a-g**	**2071**	**2359 e-k**	**3934 a-d**	**2808 a-e**	**1753 b-g**	**1046**	**1895 d-k**
16	DZ-Cr-377 (RIL 276)	1069	1059 e-j	362 a-i	1694 c-k	2344	2134 i-l	3089 b-i	2378 a-l	1745 b-g	1510	1738 g-o
17	DZ-Cr-377 (RIL 357)	1281	1051 fj	338 a-i	1741 b-k	1686	1770 k-l	3907 a-e	2230 b-l	2016 a-g	1310	1733 g-o
18	DZ-Cr-377 (RIL 43)	1019	1090 d-j	228 e-i	1859 b-g	1739	2226 g-l	3605 a-f	1978 d-h	1765 b-g	1064	1657 j-o
19	DZ-Cr-377 (RIL 60)	1080	1219 b-j	386 a-i	1784 b-k	2589	2559 d-j	3468 a-f	2602 a-g	1579 e-h	1164	1843 d-n
20	DZ-Cr-377 (RIL 105)	923	985 g-j	376 a-i	1744 b-k	1980	2190 h-l	3328 a-g	2205 b-h	1825 b-g	890	1645 k-o
21	**DZ-Cr-377 (RIL 58)**	**1170**	**1004 g-j**	**500 a-e**	**1440 g-k**	**1990**	**2434 e-k**	**3970 a-c**	**2509 a-h**	**1671 c-g**	**1178**	**1786 f-n**
22	DZ-Cr-377 (RIL 317)	1170	1120 c-j	285 c-i	1603 e-k	2174	2538 d-j	3239 a-g	2204 b-h	1848 b-g	1180	1736 g-o
23	DZ-Cr-377 (RIL 318)	1603	1298 b-j	415 a-i	1226 i-k	2233	2188 i-l	2716 f-j	2337 b-h	1508 e-h	850	1637 k-o
24	DZ-Cr-377 (RIL 320)	1158	1179 b-j	326 b-i	2321 a-g	2075	2304 f-k	3563 a-f	2482 a-l	2090 a-g	935	1843 d-n
25	**DZ-Cr-377 (RIL 352)**	**1161**	**1315 b-j**	**540 a-d**	**2115 a-i**	**2568**	**2644 c-i**	**4113 a**	**2355 b-l**	**1481 f-h**	**869**	**1916 c-j**
26	DZ-Cr-377 (RIL 145)	1549	1274 b-j	436 a-g	1618 e-k	1863	2181 i-l	3251 a0g	2276 b-l	1859 b0g	904	1721 n-o
27	DZ-Cr-379 (RIL 356)	1049	1400 b-i	311 b-i	2081 a-i	2084	2484 d-j	3571 a-f	2801 a-e	2004 a-g	853	1864 d-m
28	DZ-Cr-379 (F_4 sel 16)	1420	1741 ab	350 a-i	2644 a-b	2669	3035 b-e	3138 a-i	2766 a-e	2009 a-g	840	2061 a-e

No	Cross/Genotype	Alemtena	Melkassa	Mekelle	Denbi	DZLS	DZBS	Holetta	Adet	Akaki	Chefe Donsa	Mean
29	DZ-Cr-381 (F_4 sel 71)	1120	1254 b-j	288 c-i	2535 a-e	2120	2939 c-g	3332 a-g	2636 a-g	2126 a-g	858	1921 c-g
30	DZ-Cr-376 (RIL 136)	1670	1301 b-j	116 h-i	2329 a-g	2234	2566 d-i	2188 h-k	1881 e-h	1613 e-h	820	1672 i0o
31	DZ-Cr-376 (RIL 159)	885	1198 b-j	169 g-i	1929 a-j	1799	1971 i-l	2135 i-k	2299 b-l	1699 b-g	736	1482 o
32	**DZ-Cr-376 (RIL 229)**	**1209**	**2084 a**	**185 f-i**	**2425 a-f**	**2560**	**2551 d-j**	**2860 fg**	**2251 b-l**	**1839 b-g**	**826**	**1879 d-l**
33	DZ-Cr-376 (RIL 313)	1224	1580 a-g	378 a-i	1804 b-k	2463	2509 d-j	2771 fg	2338 b-l	1690 b-g	943	1770 f-n
34	DZ-Cr-376 (RIL 332)	1123	1561 a-g	312 b-i	2108 a-i	2075	2326 e-k	2705 fg	2331 b-l	1910 a-g	886	1734 g-o
35	DZ-Cr-376 (RIL 32)	1649	1696 a-d	322 b-i	2444 a-e	2191	2548 d-j	3179 a-h	2439 a-l	1869 b-g	899	1923 c-i
36	**DZ-Cr-375 (RIL 38)**	**1239**	**1670 a-e**	**425 a-g**	**1664 c-k**	**2406**	**2398 e-k**	**4015 ab**	**2888 a-d**	**2430 a-e**	**791**	**1992 a-j**
37	DZ-Cr-375 (RIL 77)	1358	1561 a-g	262 d-i	1996 a-j	2919	2544 d-j	2938 d-j	1805 f-l	1616 e-h	909	1791 f-n
38	DZ-Cr-375 (RIL 82)	1143	1671 a-d	284 c-i	1975 a-j	2568	2510 d-j	3112 a-i	1928 e-h	2013 a-g	1316	1852 d-m
39	DZ-Cr-375 (RIL 91)	1351	1536 a-h	330 a-i	1769 b-k	2250	2441 e-k	3299 a-g	2111 c-h	1758 b-g	801	1765 f-m
40	DZ-Cr-375 (RIL 107)	1344	1595 a-g	347 a-i	2100 a-i	2863	2909 c-h	3424 a-g	1872 e-h	1806 b-g	974	1923 c-i
41	DZ-Cr-375 (RIL 120)	1191	1654 a-f	419 a-h	1418 g-k	2474	2614 c-i	2593 f-j	2441 a-h	1650 d-g	859	1731 g-o
42	DZ-Cr-375 (RIL 152)	1380	1234 b-j	405 a-i	1280 i-k	2375	2400 e-k	3475 a-f	2040 c-l	1818 b-g	935	1734 g-o
43	DZ-Cr-375 (RIL 164)	931	936 h-j	504 a-e	2011 a-j	1916	2013 i-l	3100 a-i	2654 a-g	1815 b-g	866	1675 i-o
44	DZ-Cr-375 (RIL 248)	1248	1514 a-h	404 a-i	1895 b-j	1873	2433 e-k	2706 f-j	2344 b-l	1500 e-h	1046	1696 h-o
45	DZ-Cr-375 (RIL 252)	1068	1270 b-j	370 a-i	2238 a-h	2248	2408 e-k	2411 g-j	2013 d-l	1316 gh	908	1625 l-o
46	DZ-Cr-375 (RIL 260)	1029	1434 b-i	390 a-i	2293 a-h	2233	2318 e-k	3158 a-h	1989 d-l	1705 b-g	775	1732 j-o
47	DZ-Cr-375 (RIL 290)	1036	770 j	108 i	923 k	1885	1598 l	1350 k	792 i	733 h	419	961 p
48	**DZ-Cr-375 (RIL 371)**	**1095**	**1408 b-i**	**451 a-g**	**1773 b-k**	**2324**	**2458 d-k**	**3220 a-g**	**2905 a-d**	**1906 a-g**	**856**	**1839 e-n**
49	DZ-Cr-375 (RIL 377)	1088	1313 b-j	639 a	2600 a-c	2895	3173 b-d	2738 f-j	2979 a-c	2328 a-f	1146	2090 a-e
	Mean	1238	1346	391	1939	2325	2541	3112	2388	1861	1014	1817
	CV (%)	18.56	18.30	31.82	19.61	19.60	11.41	13.25	16.03	20.40	33.99	18.5
	SEM	229.85	246.37	124.52	380.22	455.64	289.87	412.21	382.95	379.62	344.73	336.00
	LSD (0.05)	NS	495.40	250.40	764.50	NS	582.80	828.80	270.80	763.30	NS	208.8

Table 3. Results from ANOVA of six agronomic traits for the advanced observations of early and late maturing tef lines at individual locations.

Location	SB (kg/ha)		DTH		DTM		Pht (cm)		PL (cm)		LI	
	Early	Late	Early	Late	Early	Late	Early	Late	Early	Late	Early	Late
Akaki	-	***	-	**	-	NS	-	***	-	NS	-	**
Alemtena	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
DZBS	NS	***	***	***	***	***	***	***	***	***	**	NS
DZLS	NS	NS	***	***	***	***	**	***	***	NS	NS	***
Denbi	NS	*	***	***	NS	**	***	***	***	***	***	NS
Holetta	NS	***	***	**	***	***	**	***	***	***	NS	***
Melkassa	*	*	**	***	*	*	NS	NS	*	***	NS	***
Adet	NS	***	***	***	***	***	***	NS	*	NS	-	NS
Mekelle	NS	**	-	***	-	**	-	NS	-	-	-	-
Chefe Donsa	-	NS	-	***	-	***	-	***	-	**	-	*
Combined												
Genotype (G)	*	***	***	***	***	***	***	***	***	***	***	***
Location (L)	***	***	***	***	***	***	***	***	***	***	***	***
G x L	NS	***	***	***	***	***	***	***	**	***	***	***

*, **, *** = $p<0.05$, 0.01 and 0.001, respectively.
NS= non-significant
SB= Shoot biomass; DTH= Days-to-head; DTM= Days-to-mature; Pht= Plant height; PL= Panicle Length; LI= Lodging index

Table 4. Mean values for other agronomic traits of tef genotypes tested in advanced observation of early maturing tef lines in 2001/02 season at eight locations (Boldface= promoted lines).

No.	Cross/Genotype	SB	DTH	DTM	Pht	PL	LI
1	DZ-Cr-37	9268	42	88	88	33	79
2	Local Check	9821	44	90	85	32	79
3	**DZ-01-443**	**9910**	**46**	**93**	**88**	**34**	**78**
4	DZ-01-1276	9857	46	93	92	38	82
5	DZ-01-667	9411	46	95	92	35	77
6	DZ-01-147	10053	48	92	95	35	75
7	DZ-01-1225	9196	46	93	89	36	81
8	**DZ-01-1629**	**9607**	**43**	**88**	**86**	**32**	**79**
9	DZ-Cr-377 (RIL 10)	9250	46	88	80	32	73
10	DZ-Cr-377 (RIL 38)	10161	43	89	86	31	73
11	DZ-Cr-377 (RIL 42)	9536	45	87	87	34	76
12	DZ-Cr-377 (RIL 44)	9911	43	86	86	31	80
13	DZ-Cr-377 (RIL 46)	9911	43	87	88	33	83
14	DZ-Cr-377 (RIL 205)	9232	44	88	88	30	76
15	DZ-Cr-377 (RIL 275)	10250	46	90	91	34	73
16	DZ-Cr-377 (RIL 309)	8804	43	86	81	30	73
17	**DZ-Cr-376 (RIL 40)**	**9446**	**44**	**88**	**84**	**32**	**74**
18	**DZ-Cr-376 (RIL 67)**	**10571**	**46**	**88**	**97**	**38**	**74**
19	DZ-Cr-376 (RIL 153)	8625	42	83	86	29	78
20	DZ-Cr-376 (RIL 198)	9375	46	91	90	31	76
21	**DZ-Cr-376 (RIL 47)**	**9821**	**44**	**86**	**83**	**32**	**76**
22	**DZ-Cr-376 (RIL 392)**	**9443**	**43**	**87**	**84**	**28**	**83**
23	DZ-Cr-375 (RIL 62)	9000	41	83	76	27	81
24	DZ-Cr-375 (RIL 239)	9875	42	84	76	25	82
25	DZ-Cr-375 (RIL 263)	9375	41	84	77	27	85
26	DZ-Cr-379 (F_4 sel 15)	9196	41	86	81	30	81
27	DZ-Cr-379 (F_4 sel 25)	9643	41	86	85	33	81
28	**DZ-Cr-379 (F_4 sel 31)**	**10589**	**44**	**87**	**82**	**29**	**81**
29	DZ-Cr-379 (F_4 sel 34)	9661	43	86	87	34	80
30	DZ-Cr-379 (F_4 sel 51)	8589	43	85	82	30	82
31	DZ-Cr-379 (F_4 sel 13)	9554	44	87	84	32	77
32	DZ-Cr-379 (F_4 sel 14)	9911	43	88	78	31	80
33	**DZ-Cr-379 (F_4 sel 19)**	**8250**	**43**	**85**	**80**	**27**	**80**
34	DZ-Cr-379 (F_4 sel 22)	9357	45	87	84	32	80
35	DZ-Cr-379 (F_4 sel 24)	9232	43	85	83	31	86
36	DZ-Cr-379 (F_4 sel 36)	9000	42	87	85	32	87
37	DZ-Cr-379 (F_4 sel 37)	9768	44	85	81	32	81
38	DZ-Cr-379 (F_4 sel 38)	9500	44	88	86	34	79
39	DZ-Cr-379 (F_4 sel 42)	9357	42	88	87	32	82
40	DZ-Cr-379 (F_4 sel 44)	10125	43	86	83	32	78
41	DZ-Cr-379 (F_4 sel 48)	9268	42	87	84	30	80
42	DZ-Cr-380 (F_4 sel 53)	8857	42	88	80	31	84
43	DZ-Cr-380 (F_4 sel 54)	9804	44	87	84	31	79
44	DZ-Cr-380 (F_4 sel 61)	8518	40	86	80	28	80

Table 4. Contd.

No.	Cross/Genotype	SB	DTH	DTM	Pht	PL	LI
45	DZ-Cr-380 (F_4 sel 63)	9036	41	85	82	28	80
46	DZ-Cr-380 (F_4 sel 64)	8429	41	86	82	30	80
47	DZ-Cr-359 (F_4 sel 74)	8446	44	85	82	29	76
48	DZ-Cr-381 (F_4 sel 68)	10357	44	87	81	32	81
49	DZ-Cr-384 (F_4 sel 80)	9554	45	86	85	33	81
	Mean	9467	43	87	85	32	79
	CV (%)	17.5	4.7	4.2	8.3	11.0	9.4
	SEM	443	0.54	1.0	1.9	0.9	2.1
	LSD (0.05)	32.51	3.9	7.2	13.8	6.8	14

SB= Shoot biomass; DTH= Days-to-head; DTM= Days-to-mature; Pht= Plant height; LI=Lodging index

Table 5. Mean values for other agronomic traits of genotypes tested in advanced observation of late maturing tef lines in 2001/02 season at ten locations (Boldface= promoted lines).

No.	Cross/genotype	SB	DTH	DTM	Pht	PL	LI
1	DZ-01-974	10028	45	97	82	32	75
2	Local Check	9625	48	100	82	30	76
3	DZ-Cr-358	9722	48	103	83	32	75
4	Balami	9056	51	51	90	37	76
5	Enatite	9625	48	46	81	33	74
6	**Gofarie**	**9819**	**48**	**106**	**82**	**33**	**72**
7	Janno	9139	49	102	85	33	66
8	DZ-01-146	10375	47	104	80	32	73
9	DZ-Cr-46	9972	49	103	83	32	72
10	DZ-01-1193	9361	50	97	79	30	73
11	**DZ-01-1717**	**9681**	**47**	**104**	**84**	**35**	**77**
12	DZ-01-348	10125	45	92	80	31	74
13	DZ-Cr-377 (RIL 78)	10167	48	104	81	32	69
14	DZ-Cr-377 (RIL 153)	9597	43	100	82	33	77
15	**DZ-Cr-377 (RIL 351)**	**9458**	**44**	**101**	**80**	**30**	**78**
16	DZ-Cr-377 (RIL 276)	9181	49	100	81	31	74
17	DZ-Cr-377 (RIL 357)	9278	45	**101**	**79**	**30**	**70**
18	DZ-Cr-377 (RIL 43)	8833	**46**	**102**	**77**	**31**	**75**
19	DZ-Cr-377 (RIL 60)	9801	45	100	82	31	73
20	DZ-Cr-377 (RIL 105)	9486	47	103	80	30	70
21	**DZ-Cr-377 (RIL 58)**	**10917**	**48**	**104**	**83**	**31**	**75**
22	DZ-Cr-377 (RIL 317)	9250	45	100	78	30	72
23	DZ-Cr-377 (RIL 318)	10694	49	105	86	34	72
24	DZ-Cr-377 (RIL 320)	10069	46	100	79	28	68
25	**DZ-Cr-377 (RIL 352)**	**10431**	**47**	**101**	**84**	**33**	**71**
26	DZ-Cr-377 (RIL 145)	8833	44	102	77	29	74
27	DZ-Cr-379 (RIL 356)	9500	45	102	84	32	74
28	DZ-Cr-379 (F_4 sel 16)	9986	48	102	85	32	71
29	DZ-Cr-381 (F_4 sel 71)	9069	42	98	76	27	82
30	DZ-Cr-376 (RIL 136)	7764	43	94	72	25	77
31	DZ-Cr-376 (RIL 159)	8472	45	99	81	30	75
32	**DZ-Cr-376 (RIL 229)**	**8694**	**44**	**95**	**80**	**30**	**76**
33	DZ-Cr-376 (RIL 313)	9069	47	94	80	30	73
34	DZ-Cr-376 (RIL 332)	9292	45	97	82	31	68
35	DZ-Cr-376 (RIL 32)	9403	47	98	80	29	75
36	**DZ-Cr-375 (RIL 38)**	**9694**	**47**	**105**	**83**	**30**	**78**
37	DZ-Cr-375 (RIL 77)	8097	43	96	69	25	77
38	DZ-Cr-375 (RIL 82)	8389	44	96	80	28	76
39	DZ-Cr-375 (RIL 91)	8153	42	94	74	27	81
40	DZ-Cr-375 (RIL 107)	8319	43	95	79	29	73
41	DZ-Cr-375 (RIL 120)	8306	44	96	78	28	70
42	DZ-Cr-375 (RIL 152)	9347	42	97	80	29	79

Table 5. Contd.

No.	Cross/genotype	SB	DTH	DTM	Pht	PL	LI
43	DZ-Cr-375 (RIL 164)	8722	48	99	73	27	71
44	DZ-Cr-375 (RIL 248)	8708	44	99	71	27	80
45	DZ-Cr-375 (RIL 252)	8028	46	96	78	30	77
46	DZ-Cr-375 (RIL 260)	8056	41	100	78	27	79
47	DZ-Cr-375 (RIL 290)	5222	42	95	64	24	47
48	**DZ-Cr-375 (RIL 371)**	**8667**	**44**	**100**	**77**	**29**	**82**
49	DZ-Cr-375 (RIL 377)	9597	46	99	86	32	73
	Mean	9206	46	100	80	30	74
	CV (%)	15.7	4.9	4.5	8.9	12.5	12.4
	SEM	341	0.53	1.05	1.66	0.89	2.29
	LSD (0.05)	28.36	4.4	8.7	13.7	7.4	18

SB= Shoot biomass; DTH= Days-to-head; DTM= Days-to-mature; Pht= Plant height; LI=Lodging index

Table 6. The polymorphic EST-SSRs that have been mapped in this study. The source species of the EST sequence, repeat motif and the primer pair are shown.

SSR-EST	Species	Repeat	5' Primer	3' Primer
DuPw004	Wheat	$(AC)_{13}$	GGTCTGGTCGGAGAAGAAGC	TGGGAGCGTACGTTGTATCC
DuPw124	Wheat	$(ACT)_{7}$	AGCCAAGCCAGTCCAAGC	ACGCGAGAAGGATTATTTGG
DuPw135	Wheat	$(ACATG)_{5}$	CGCTTCTCTTGTCTTGTCCC	CATGGTGAAGACGGTGACG
DuPw165	Wheat	$(AACAGC)_{5}$	TAGGTCTCGACAACAAGCCG	TCACCACTTGGAGGTTACTGC
DuPw210	Wheat	$(AAG)_{6}$	CGATTTGGATTCTTCCGC	AGAGCCTTTGAAGAGCAGGG
DuPw216	Wheat	$(AAG)_{9}$	ACAAACCTCTCCCTCTCACG	ATGATGATTCAGCGAGTCGG
DuPw217	Wheat	$(AAG)_{12}$	CGAATTACACTTCCTTCTTCCG	CGAGCGTGTCTAACAAGTGC
SC6CR	Rice	$(GGT)_{7}$; $(CGG)_{6}$	CCCTTCGCCGAATCCAGC	TTGTCGCAGCACGGCCACG
SC296W	Wheat	$(CAGT)_{4}$; $(AGG)_{8}$	TACACCAAGGCGGAGTCTGT	TCAGTAGAACCATAACGCAACG
SC1082W	Wheat	$(CTT)_{11}$	CCGCTTCTCGTGCTTCTT	AGTCGCAGTTGGAGCAGA

Table 7. A summary of markers obtained using 23 ISSR primers. The PCR conditions and the reaction constituents were the same for all primers with the only exception of annealing temperature. An average of 61 bands were obtained using each primer.

ISSR Primer	Primer Sequence (5'-3')	Ann. Temp (ºC)	Number of Bands		
			Total	Polymorphic	Mapped
I545	$(CA)_6RY$	45	61	8	7
I546	$(CA)_6RG$	45	65	6	4
I547	$(CA)_6R$	45	70	8	6
I548	$(GT)_6YR$	45	49	4	2
I549	$(GT)_6AY$	45	59	6	5
I550	$(AGC)_4Y$	45	85	4	3
I615	$(AGC)_4AY$	45	81	2	1
I617	$(AGC)_4GR$	45	55	1	1
I618	$(GCT)_4Y$	45	80	2	2
I809	$(AG)_8G$	52	67	4	4
I810	$(GA)_8T$	52	73	5	2
I811	$(GA)_8C$	52	69	6	5
I812	$(GA)_8A$	52	71	4	4
I813	$(CT)_8T$	52	24	2	2
I814	$(CT)_8A$	52	15	1	1
I836	$(AG)_8YA$	52	79	10	9
I840	$(GA)_8YT$	52	46	5	3
I841	$(GA)_8YC$	52	81	6	5
I842	$(GA)_8YG$	52	97	8	7
I843	$(CT)_8RA$	52	27	1	0
I844	$(CT)_8RC$	52	29	1	1
I856	$(AC)_8YA$	52	60	1	1
I857	$(AC)_8YG$	52	50	1	1
Total			1393	96	77

Table 8. QTL analysis trait descriptions and trial locations

Trait	Description	Year trait data collected	Locations trait data collected
Head	Days to Heading	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
Mat	Days to Maturity	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
PanWt	Panicle Weight (cm)	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
PSW	Panicle Seed Weight (gm)	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
100SW	100 Seed Weight (mg)	2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
CulmLen	Culm Length (cm)	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
CD1	Culm Diameter 1st Internode	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
CD2	Culm Diameter 2nd Internode	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
PedLen	Peduncle Length	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
PanLen	Panicle Length	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
PlHt	Plant Height = (CulmLen + PanLen)	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
NumInt	Number of Internodes	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
IntLen1	1st Internode Length (cm)	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
IntLen2	2nd Internode Length (cm)	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
GnYld	Grain Yield (gm)	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
Lodg	Loding Index	1999 & 2000	AK, AL, DZBS, DZLS, DE, CH, HO
Lem	Lemma Color	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
PanFm	Panicle Form	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
CrDia	Crown Diameter (mm)	2000	AK, DZBS, CH
ShBio	Shoot Biomass (gm)	1999 & 2000	AK, AL, DZBS, DZLS, DE, MEL, CH, HO
RPR1	Rind Penetrometer Resistance 1st Internode (lbs)	2000	DZLS
RPR2	Rind Penetrometer Resistance 2nd Internode (lbs)	2000	DZLS
Crush1	Crushing Strength 1st Internode (lbs)	2000	DZLS
Crush2	Crushing Strength 2nd Internode (lbs)	2000	DZLS

Akaki (AK), Alemtena (AL), Debre Zeit Black Soil (DZBS), Debre Zeit Light Soil (DZLS), Denbi (DE), Melkasa (MEL), Chefe Donsa (CH), Holetta (HO)

Table 9. Yield and yield related component QTLs detected in Kaye Murri x *E. pilosa* RIL population [Akaki 2000, Akaki 99, Alemtena 2000, Alemtena 99, Debre Zeit Black Soil 2000 (DZBS2), Debre Zeit Black Soil 99 (DZBS99)]

LOD > 99% experiment-wise threshold level

QTL	LG	Peak marker	Interval	Increased effect	SIM/ SP	Akaki 2000		Akaki 99		Alemtena 2000		Alemtena 99		DZBS 2000		DZBS 99	
						LOD	R2	LOD	R2	LOD	R2	LOD	R2	LOD	R2	LOD	R2
Days to heading																	
head6.1	6	DM165c	RZ252-RZ386	KM	SIM									3.1	9.1%		
head8.1	8	RZ962d	RZ962d-TCD270a	KM	SIM	4.4*	13.60%			2.9	9.16%			3.1	9.70%		
					SP	5.49*	24.25%	3.56	16.64%	3.82*	17.58%			3.45	16.01%		
head15.1	15	CDO470	I814a-I842c	KM	SIM					3.2	14.65%						
Days to maturity																	
mat3.1	3	I550b	I547c-I550b	KM	SIM									3.1	9.23%		
					SP									2.23	20.39%		
mat12.1	12	RZ144	RZ836a-RZ144	KM	SIM							4.0*	11.63%				
					SP							2.93	16.29%				
mat15.1	15	CDO470	I814a-I550c	KM	SIM									3.1	14.23%		
					SP									3.06	18.22%		
Panicle Weight																	
panwt6.1	6	RZ214	RZ252-RZ386	KM	SIM												
					SP												
panwt8.1	8	RZ962d	RZ962d-TCD270a	KM	SIM												
					SP												
Panicle Seed Weight																	
psw2.1	2	TCD197 b-DraI	OsPaLb-TCD197-BamHI	KM	SIM											3.5	10.29%
					SP											3.24	14.01%
psw6.1	6	DM165c	RZ252-DM165c	KM	SIM												
pswUN.1	UN	TCD278	I811b-BCD880	KM	SIM											3.8	11.08%
					SP											2.33	24.04%
Grain Yield																	
gnyld2.1	2	TCD197	OsPALb-	KM	SIM												

		b-DraI	I836h														
					SP												
gnyld6.1	6	TCD95	RZ386-CDO20	KM	SIM											3.2	9.42%
					SP											2.92	16.40%
gnyldUN.1	UN	I841e	RZ476-I545b	KM	SIM									4.5*	12.88%		
Lodging																	
lodg9.1	9	TCD230d	TCD230b-RZ742a	KM	SIM									3.5	10.86%		
					SP									2.6	10.12%		
lodg23.1	23	TCD182	I809a-RZ819b	KM	SIM					3.2	13.21%						
					SP					3.27	17.75%						

Table 9. Continued [Debre Zeit Light Soil (DZLS), Denbi, Melkassa, Chefe, Holetta]

LOD > 99% experiment-wise threshold level

QTL	LG	Peak marker	Interval	Increased effect	SIM/ SP	DZLS		Denbi		Melkassa		Chefe		Holetta	
						LOD	R2	LOD	R2	LOD	R2	LOD	R2	LOD	R2
Days to heading															
head6.1	6	DM165c	RZ252-RZ386	KM	SIM										
head8.1	8	RZ962d	RZ962d-TCD270a	KM	SIM							3.4	10.77%		
					SP							4.35	19.76%		
head15.1	15	CDO470	I814a-I842c	KM	SIM										
					SP										
Days to maturity															
mat3.1	3	I550b	I547c-I550b	KM	SIM										
					SP										
mat12.1	12	RZ144	RZ836a-RZ144	KM	SIM										
					SP										
mat15.1	15	CDO470	I814a-I550c	KM	SIM										
					SP										
Panicle weight															
panwt6.1	6	RZ214	RZ252-RZ386	KM	SIM									3.4	9.88%
					SP									1.7	8.81%
panwt8.1	8	RZ962d	RZ962d-TCD270a	KM	SIM			3.3	10.33%						
					SP			2.8	13.28%						
Panicle Seed Weight															
psw2.1	2	TCD197 b-DraI	OsPaLb-TCD197-BamHI	KM	SIM										
					SP										
psw6.1	6	DM165c	RZ252-DM165c	KM	SIM									3.4	9.80%
pswUN.1	UN	TCD278	I811b-BCD880	KM	SIM										
					SP										

Grain yield																
gnyld2.1	2	TCD197 b-DraI	OsPALb-I836h	KM	SIM			3.8*	11.14%							
					SP			2.84	12.38%							
gnyld6.1	6	TCD95	RZ386-CDO20	KM	SIM	3.9*	11.31%	3.2	9.30%							
					SP	2.47	14.06%	2.72	15.39%							
gnyldUN.1	UN	I841e	RZ476-I545b	KM	SIM											
Lodging																
lodg9.1	9	TCD230 d	TCD230b-RZ742a	KM	SIM											
					SP											
lodg23.1	23	TCD182	I809a-RZ819b	KM	SIM											
					SP											

Table 10. Morphological and plant height related QTLs detected in Kaye Murri X *E. pilosa* RIL population [Akaki 2000, Akaki 99, Alemtena 2000, Alemtena 99, Debre Zeit Black Soil 2000 (DZBS2), Debre Zeit Black Soil 99 (DZBS99)]

LOD > 99% experiment-wise threshold level

QTL	LG	Peak marker	Interval	Increased effect	SIM/ SP	Akaki 2000		Akaki 99		Alemtena 2000		Alemtena 99		DZBS 2000		DZBS 99	
						LOD	R2	LOD	R2	LOD	R2	LOD	R2	LOD	R2	LOD	R2
Culm length																	
culmlen6.1	6	TCD95	RZ386-CDO20	KM	SIM			4.2*	12.22%								
					SP			4.28*	23.38%								
culmlen15.1	15	CDO470	I814a-I550c	KM	SIM			4.3*	19.41%								
					SP			3.8*	22.42%								
Culm Diameter 1st Internode																	
culmdia-1st11.1	11	I547b	I841a-I549c	KM	SIM											3	26.24%
Culm Diameter 2nd Internode																	
culmdia-2nd8.1	8	RZ962d	RZ962d-TCD270a	KM	SIM												
					SP												
Peduncle Length																	
pedlen24.1	24	RZ698c	RZ413a-RZ698c	E. pilosa	SIM												
					SP												
Panicle length																	
panlen6.1	6	TCD95	RZ386-TCD248	KM	SIM			3.5	10.37%								
panlen8.1	8	RZ962d		KM	SIM												
					SP												
Plant height																	
plht6.1	6	TCD95	RZ386-CDO20	KM	SIM			4.6*	13.25%								
					SP			3.7*	20.58%								
plht8.1	8	RZ962d	RZ962d-TCD270a	KM	SIM												
					SP												
plht15.1	15	CDO470	I814a-I550c	KM	SIM			4.5*	20.01%								
					SP			3.45	20.56%								
Number of Internodes																	
numofint8.1	8	RZ962d	RZ962d-	KM	SIM	3.4*	10.59%										

			TCD270a														
					SP	2.95	13.85%										
2nd Internode Length																	
2ndIntlen2.1	2	TCD197 b-DraI	OsPALb-I836h	KM	SIM							3.4	9.95				
					SP							3.3	14.24%				
Shoot biomass																	
shbio2.1	2	RZ876	TCD52a-OsPALa	KM	SIM												
					SP												
shbio3.1	3	TCD503	I856a-RZ519b	KM	SIM							3.3	9.77%				
					SP							3.05	12.85%				
shbio5.1	5	RZ588	RZ123-RZ588	E. pilosa	SIM							3.1	9.72%				
					KM							2.48	10.89%				
shbio6.1	6	TCD95	RZ214-TCD248	KM	SIM			3.8*	11.23%								
					SP			1.63	9.63%								
shbio6.2	6	RZ252	RZ252-RZ214	KM	SIM					3.4	9.94%						
					SP					2.67	17.24%						
shbio8.1	8	RZ962d		KM	SIM												
					SP												
shbio27.1	27	I842b	I548d-I842b	KM	SIM												
					SP												

Table 10. Continued [Debre Zeit Light Soil (DZLS), Denbi, Melkassa, Chefe, Holetta]

LOD > 99% experiment-wise threshold level

QTL	LG	Peak marker	Interval	Increased effect	SIM/ SP	DZLS		Denbi		Melkassa		Chefe		Holetta	
						LOD	R2	LOD	R2	LOD	R2	LOD	R2	LOD	R2
Culm length															
culmlen6.1	6	TCD95	RZ386-CDO20	KM	SIM			3.5	10.10%	3.7	10.77%				
					SP			3.78	20.71%	3.25	18.08%				
culmlen15.1	15	CDO470	I814a-I550c	KM	SIM					4.7*	20.65%				
					SP					4.34*	24.85%				
Culm Diameter 1st Internode															
culmdia-1st11.1	11	I547b	I841a-I549c	KM	SIM										
Culm Diameter 2nd Internode															
culmdia-2nd8.1	8	RZ962d	RZ962d-TCD270a	KM	SIM			3.2	9.97%						
					SP			3.38*	15.70%						
Peduncle length															
pedlen24.1	24	RZ698c	RZ413a-RZ698c	E. pilosa	SIM			4.4*	15.33%						
					SP			4.18*	19.44%						
Panicle length															
panlen6.1	6	TCD95	RZ386-TCD248	KM	SIM					3.1	9.16%				
panlen8.1	8	RZ962d		KM	SIM			3.2	10.18%						
					SP			3.22	15.04%						
Plant height															
plht6.1	6	TCD95	RZ386-CDO20	KM	SIM			3.8	11.10%	4.4*	12.55%				
					SP			2.84	16.02%	3.17*	17.67%				
plht8.1	8	RZ962d	RZ962d-TCD270a	KM	SIM			3.5	11.07%						
					SP			3.4	15.79%						
plht15.1	15	CDO470	I814a-I550c	KM	SIM					4.3*	19.02%				
					SP					3.7*	21.62%				
Number of Internodes															

numofint8.1	8	RZ962d	RZ962d-TCD270a	KM	SIM					3.4	10.65%				
					SP					3.99*	18.29%				
2nd Internode Length															
2ndIntlen2.1	2	TCD197 b-DraI	OsPALb-I836h	KM	SIM										
					SP										
Shoot biomass															
shbio2.1	2	RZ876	TCD52a-OsPALa	KM	SIM			4	11.71%						
					SP			2.95	13.88%						
shbio3.1	3	TCD503	I856a-RZ519b	KM	SIM										
					SP										
shbio5.1	5	RZ588	RZ123-RZ588	E. pilosa	SIM										
					KM										
shbio6.1	6	TCD95	RZ214-TCD248	KM	SIM										
					SP										
shbio6.2	6	RZ252	RZ252-RZ214	KM	SIM										
					SP										
shbio8.1	8	RZ962d		KM	SIM			3.1	9.82%						
					SP			2.95	13.88%						
shbio27.1	27	I842b	I548d-I842b	KM	SIM									3.1	15.43%
					SP									2.85	25.31%

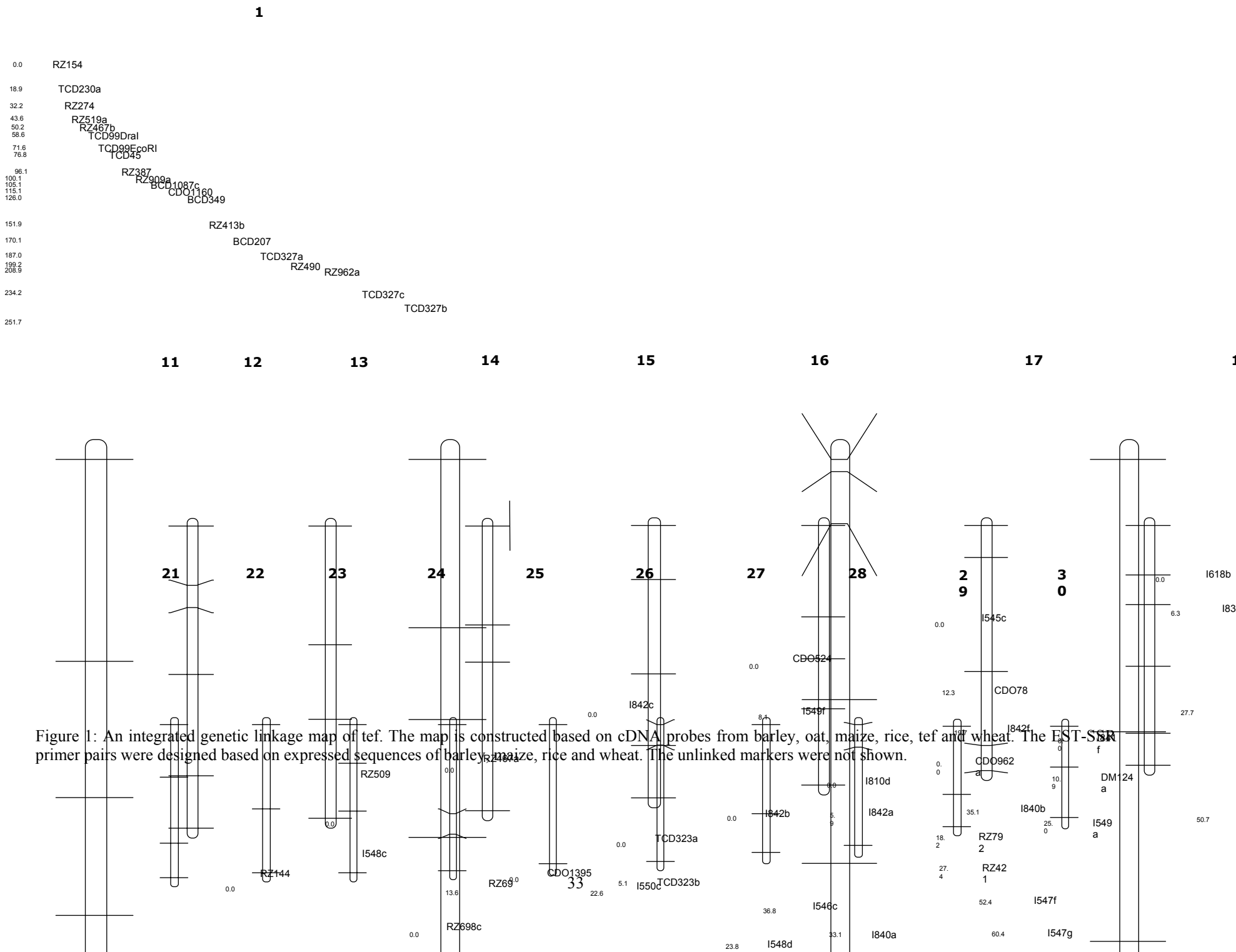

Figure 1: An integrated genetic linkage map of tef. The map is constructed based on cDNA probes from barley, oat, maize, rice, tef and wheat. The EST-SSR primer pairs were designed based on expressed sequences of barley, maize, rice and wheat. The unlinked markers were not shown.

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