

## Genotyping-by-sequencing reasserts the close relationship between *tef* and its putative wild *Eragrostis* progenitors

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Table S1. Germplasm class information and origin of materials used in the experiment. IPS: Institute of Plant Sciences; m a.s.l.: meter above sea level; MoA: Ministry of Agriculture; USDA: United States Department of Agriculture.

Common/scientific name	Germplasm origin		Altitude (m a.s.l.)	Reference
	Location	Coordinates		
<b>1. Tef cultivars</b>				
<i>Ada</i>	Debre Birhan, North Shewa	9°41'N, 39°32'E	2750	(Ebba 1975)
<i>Addissie</i>	Debre Zeit, East Shewa	8°42'N, 39°5'E	2000	(Ebba 1975)
<i>Adoensis</i>	Nekemte, Wollega	9°1'N, 36°30'E	2400	(Ebba 1975)
<i>Balami</i>	Debre Zeit, East Shewa	8°42'N, 39°5'E	2000	(Ebba 1975)
<i>Beten</i>	Debre Zeit, East Shewa	8°42'N, 39°5'E	2000	(Ebba 1975)
<i>Bunninye</i>	Nejo, Wellega	9°30'N, 35°30'E	2000	(Ebba 1975)
<i>Burssa</i>	Harar, East Hararghe	9°21'N, 42°8'E	1856	(Ebba 1975)
<i>Curati</i>	Damota, Gojam	10°33'N, 36°35'E	2400	(Ebba 1975)
<i>Dabbi</i>	Bahir Dar, Gojam	10°33'N, 38°27'E	1840	(Ebba 1975)
<i>Denkeye</i>	Harar, East Hararghe	9°21'N, 42°8'E	1856	(Ebba 1975)
<i>Dschanger</i>	Unknown			(Ebba 1975)
<i>Enatite</i>	Debre Zeit, East Shewa	8°42'N, 39°5'E	2000	(Ebba 1975)
<i>Fesho</i>	Wolisso, West Shewa	8°35'N, 38°0'E	2200	(Ebba 1975)
<i>Gofarie</i>	Jimma, Keffa	7°35'N, 36°45'E	1750	(Ebba 1975)
<i>Gommadie</i>	Agaro, Keffa	7°47'N, 36°36'E	1870	(Ebba 1975)
<i>Gorradie</i>	Haramaya, East Hararghe	9°24'N, 42°26'E	2100	(Ebba 1975)
<i>Hamrawe-murri</i>	Ameressa, East Hararghe	9°23'N, 42°7'E	1860	(Ebba 1975)
<i>Hatalla</i>	Harar, East Hararghe	9°21'N, 42°8'E	1856	(Ebba 1975)
<i>Janno</i>	Damota, Gojam	10°43'N, 37°2'E	2310	(Ebba 1975)
<i>Karadebie</i>	Ghimbi, Wollega	9°9'N, 35°37'E	2100	(Ebba 1975)
<i>Kaye-murri</i>	Hidabu-Gensay, Wollega	9°31'N, 35°28'E	2000	(Ebba 1975)
<i>Keyagachem</i>	Debre Zeit, East Shewa	8°42'N, 39°5'E	2000	(Ebba 1975)
<i>Manya</i>	Debre Zeit, East Shewa	8°44'N, 39°0'E	2100	(Ebba 1975)
<i>Purpurea</i>	Unknown			(Ebba 1975)
<i>Rosea</i>	Debre Zeit, East Shewa	8°42'N, 39°5'E	2000	(Ebba 1975)
<i>Rubicunda</i>	Unknown			(Ebba 1975)
<i>Shewa-gemerra</i>	Shewa-Gemerra, Keffa	7°1'N, 35°50'E	2743	(Ebba 1975)
<i>Trotteriana</i>	Damota, Gojam	10°44'N, 35°45'E	2480	(Ebba 1975)

<i>Tullu-Nasy</i>	Nasy, Nejo, Wollega	9°40'N, 35°25'E	2400	(Ebba 1975)
<i>Viridis</i>	Unknown			(Ebba 1975)
<i>Zuccagniana</i>	Damota, Gojam	10°44'N, 35°45'E	2480	(Ebba 1975)
<b>2. Improved varieties</b>				
DZ-01-1285 ( <i>Koye</i> )	Debre Zeit Res. Center	8°45'N, 38°59'E	1900	(MoA 2014)
DZ-01-196 ( <i>Manya</i> )	Debre Zeit Res. Center	8°45'N, 38°59'E	1900	(MoA 2014)
DZ-01-2675 ( <i>Dega Tef</i> )	Debre Zeit Res. Center	8°45'N, 38°59'E	1900	(MoA 2014)
DZ-01-354 ( <i>Enatite</i> )	Debre Zeit Res. Center	8°45'N, 38°59'E	1900	(MoA 2014)
DZ-01-787 ( <i>Wellonkomi</i> )	Debre Zeit Res. Center	8°45'N, 38°59'E	1900	(MoA 2014)
DZ-01-899 ( <i>Gimbichu</i> )	Debre Zeit Res. Center	8°45'N, 38°59'E	1900	(MoA 2014)
DZ-01-99 ( <i>Asgori</i> )	Debre Zeit Res. Center	8°45'N, 38°59'E	1900	(MoA 2014)
DZ-Cr-387 ( <i>Quncho</i> )	Debre Zeit Res. Center	8°45'N, 38°59'E	1900	(MoA 2014)
DZ-Cr-438 ( <i>Kora</i> )	Debre Zeit Res. Center	8°45'N, 38°59'E	1900	(MoA 2014)
DZ-Cr-44 ( <i>Menagesha</i> )	Debre Zeit Res. Center	8°45'N, 38°59'E	1900	(MoA 2014)
<b>3. Mutant line</b>				
GA10	IPS, University of Bern			(Tadele 2013)
<b>4. Wild <i>Eragrostis</i> species</b>				
<i>E. acutiflora</i>	Brazil	Not available		(USDA 2015)
<i>E. acutiglumis</i>	Brazil			(USDA 2015)
<i>E. aethiopica</i>	South Africa			(USDA 2015)
<i>E. airoides</i>	Brazil			(USDA 2015)
<i>E. bahiensis</i>	Brazil			(USDA 2015)
<i>E. barbonodis</i>	South Africa			(USDA 2015)
<i>E. bicolor</i>	South Africa			(USDA 2015)
<i>E. capensis</i>	Zimbabwe			(USDA 2015)
<i>E. cilianesis</i>	USA			(USDA 2015)
<i>E. cilindriflora</i>	South Africa			(USDA 2015)
<i>E. congesta</i>	Zimbabwe			(USDA 2015)
<i>E. curvula</i>	South Africa			(USDA 2015)
<i>E. dielsii</i>	Australia			(USDA 2015)
<i>E. echinochloidea</i>	South Africa			(USDA 2015)
<i>E. eriopoda</i>	Australia			(USDA 2015)
<i>E. ferruginea</i>	Papua New Guinea			(USDA 2015)
<i>E. heteromera</i>	South Africa			(USDA 2015)
<i>E. humidicola</i>	Kenya			(USDA 2015)
<i>E. intermedia</i>	South Africa			(USDA 2015)
<i>E. lehmanniana</i>	South Africa			(USDA 2015)
<i>E. lugens</i>	Uruguay			(USDA 2015)
<i>E. mexicana</i>	Uruguay			(USDA 2015)
<i>E. nigra</i>	India			(USDA 2015)
<i>E. nindensis</i>	South Africa			(USDA 2015)
<i>E. nutans</i>	India			(USDA 2015)
<i>E. obtusa</i>	South Africa			(USDA 2015)
<i>E. pallens</i>	South Africa			(USDA 2015)
<i>E. papposa</i>	Tunisia			(USDA 2015)
<i>E. patentipilosa</i>	South Africa			(USDA 2015)
<i>E. pectinacea</i>	Canada			(USDA 2015)
<i>E. pilosa</i>	France			(USDA 2015)

<i>E. plana</i>	Lesotho	(USDA 2015)
<i>E. rigidior</i>	South Africa	(USDA 2015)
<i>E. samentosa</i>	South Africa	(USDA 2015)
<i>E. superba</i>	South Africa	(USDA 2015)
<i>E. tenella</i>	Sierra Leone	(USDA 2015)
<i>E. tremula</i>	Nigeria	(USDA 2015)
<i>E. trichodes</i>	USA	(USDA 2015)
<i>E. trichopora</i>	South Africa	(USDA 2015)
<i>E. viscosa</i>	Zimbabwe	(USDA 2015)

Table S2. Summary of the ApeKI *Eragrostis* GBS.

GBS statistics	Number
• Samples sequenced (total)	95 + BLANK
• Reads in the plate (total)	237,134,465
• Mean read count	2,491,878
• Good barcoded reads	144,938,479
• Low-quality reads	92,198,148
• Failed samples	3

Table S3. Number of read counts and mapping rate to the tef genome.

Common/scientific name	Read counts (in millions of reads)	Mapping rate (%)
<b>1. Tef species</b>		
<i>Ada</i>	3.15	94.2
<i>Addissie</i>	3.20	93.6
<i>Adoensis</i>	2.92	94.0
<i>Balami</i>	4.05	93.9
<i>Beten</i>	3.07	93.7
<i>Bunninye</i>	2.53	94.1
<i>Burssa</i>	2.38	93.7
<i>Curati</i>	2.09	93.5
<i>Dabbi</i>	3.14	94.0
<i>Denkeye</i>	3.35	94.3
<i>Dschanger</i>	2.33	94.5
<i>Enatite</i>	2.83	94.3
<i>Fesho</i>	3.02	93.9
<i>Gofarie</i>	3.55	93.9
<i>Gommadie</i>	3.34	93.5
<i>Gorradie</i>	2.57	94.2
<i>Hatalla</i>	2.41	93.4
<i>Karadebie</i>	2.41	94.2
<i>Kaye-murri</i>	1.74	94.3
<i>Keyagachem</i>	2.39	94.2
<i>Manya</i>	2.56	93.9
<i>Purpurea</i>	2.35	93.4
<i>Rosea</i>	2.58	93.9
<i>Rubicunda</i>	2.61	93.7
<i>Shewa-gemerra</i>	2.89	93.8
<i>Trotteriana</i>	2.94	93.8
<i>Tullu-Nasy</i>	2.05	93.9
<i>Viridis</i>	2.12	94.3
<i>Zuccagniana</i>	2.52	93.3
DZ-01-1285 ( <i>Koye</i> )	2.49	94.0
DZ-01-196 ( <i>Manya</i> )	2.33	93.8
DZ-01-2675 ( <i>Dega Tef</i> )	2.86	93.9
DZ-01-354 ( <i>Enatite</i> )	3.29	93.9
DZ-01-787 ( <i>Wellonkomi</i> )	2.52	94.4
DZ-01-899 ( <i>Gimbichu</i> )	2.73	94.0
DZ-01-99 ( <i>Asgori</i> )	2.99	94.6
DZ-Cr-387 ( <i>Quncho</i> )	2.87	93.9
DZ-Cr-438 ( <i>Kora</i> )	2.42	93.7
DZ-Cr-44 ( <i>Menagesha</i> )	2.17	93.9
GA10 (mutant line)	3.14	94.0

**2. Wild *Eragrostis* species**

<i>E. acutiflora</i>	1.62	63.6
<i>E. acutiglumis</i>	1.60	56.0
<i>E. aethiopica</i>	2.31	93.4
<i>E. airoides</i>	2.81	73.5
<i>E. bahiensis</i>	2.13	77.8
<i>E. barbonodis</i>	2.18	80.5
<i>E. bicolar</i>	2.53	77.6
<i>E. capensis</i>	2.08	75.2
<i>E. cilianensis</i>	1.80	69.7
<i>E. cilindriflora</i>	2.03	68.4
<i>E. congesta</i>	2.69	79.8
<i>E. curvula</i>	3.09	79.0
<i>E. dielsii</i>	2.76	69.3
<i>E. echinochloidea</i>	1.80	77.0
<i>E. eriopoda</i>	1.94	89.3
<i>E. ferruginea</i>	2.81	93.4
<i>E. heteromera</i>	2.16	67.8
<i>E. himidicola</i>	2.30	57.2
<i>E. intermedia</i>	2.05	80.1
<i>E. lehmanniana</i>	2.66	91.5
<i>E. lugens</i>	2.09	92.7
<i>E. mexicana</i>	2.41	83.1
<i>E. nigra</i>	2.96	73.3
<i>E. nindensis</i>	3.06	82.1
<i>E. nutans</i>	2.23	81.7
<i>E. obstua</i>	2.16	91.3
<i>E. pallens</i>	2.35	77.5
<i>E. papposa</i>	2.16	57.2
<i>E. patentipilosa</i>	1.94	82.3
<i>E. pectinacea</i>	2.80	75.5
<i>E. pilosa</i>	3.10	94.5
<i>E. plana</i>	1.93	82.7
<i>E. rigidior</i>	2.23	76.6
<i>E. samentosa</i>	2.50	78.6
<i>E. superba</i>	2.85	78.8
<i>E. tenella</i>	2.55	78.7
<i>E. tremula</i>	3.08	73.5
<i>E. trichopora</i>	3.13	68.5
<i>E. viscosa</i>	2.60	80.0

Table S4. Number of SNPs detected on individual pseudomolecules and SNP density. \*The number of SNPs listed here is obtained after filtering the raw SNPs detected per pseudomolecule by allelic state (biallelic), coverage (60%), and minor allele frequency (MAF  $\geq$  0.05).

<b>Pseudo-chromosome</b>	<b>Sequence length (bases)</b>	<b>No. of SNPs*</b>	<b>SNP Mb<sup>-1</sup></b>
<b>Chr1</b>	73,017,089	17,226	236
<b>Chr2</b>	55,089,357	12,951	235
<b>Chr3</b>	58,718,112	14,563	248
<b>Chr4</b>	43,964,424	11,540	262
<b>Chr5</b>	19,121,838	3,234	169
<b>Chr6</b>	34,025,776	8,777	258
<b>Chr7</b>	26,054,076	5,639	216
<b>Chr8</b>	20,774,635	3,748	180

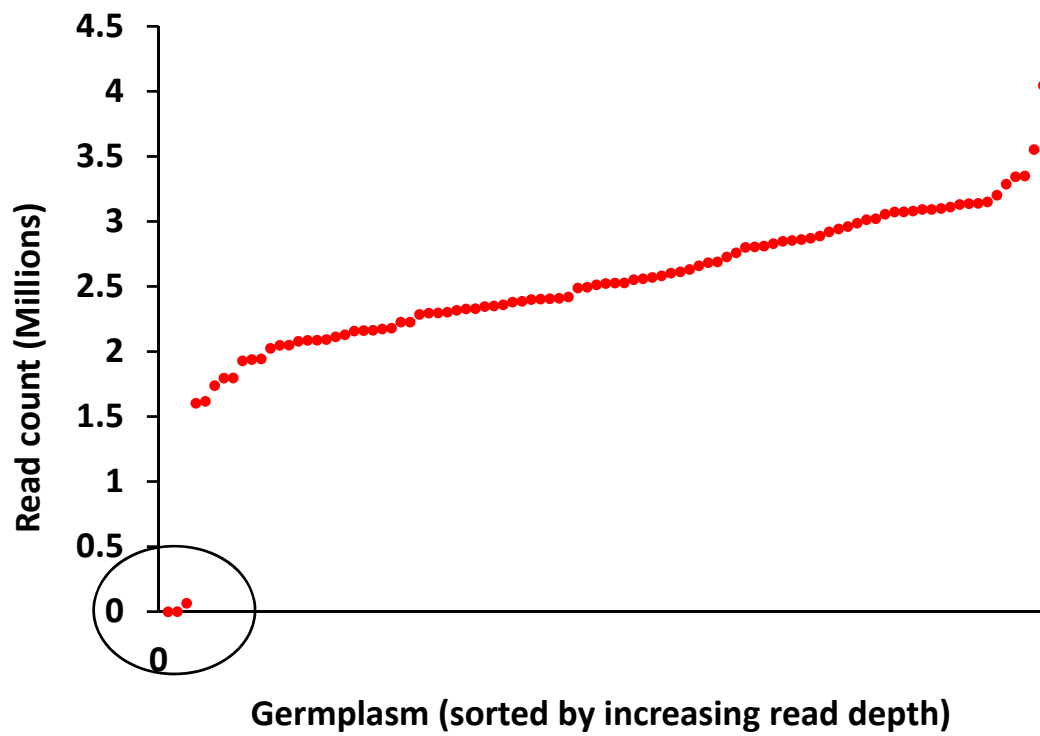


Figure S1. Mean sequencing depth (expressed as read count per germplasm) of the ApeKI Eragrostis library generated by the GBS protocol. The number of read counts per individual germplasm is shown in order of increasing number of reads generated. Three (*E. trichodes*, *Hamrawi-murri* and *Jano*) of the 95 samples were excluded from further analysis due to very low read counts and are indicated by red points inside the circle.

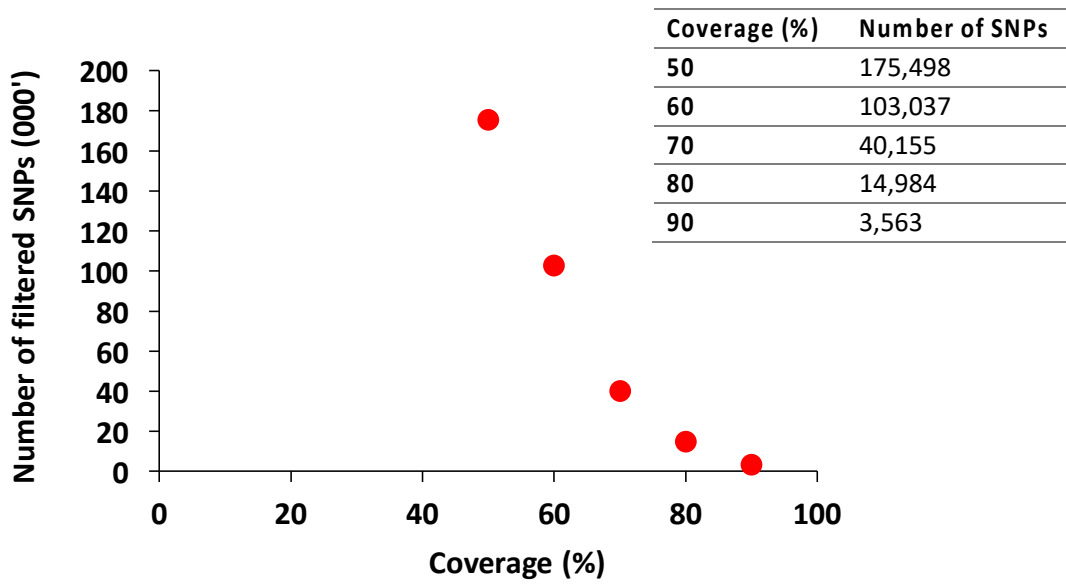


Figure S2. SNP coverage statistics. We filtered the raw SNP dataset using ranges of coverages as a cutoff. By coverage we mean the number of sites (SNPs) based on the proportion of missing data defined to be 50, 60, 70, 80, and 90. The number of SNPs retained is plotted against the corresponding coverage. The number of filtered SNPs dramatically decreases as the coverage increases (in other words as the amount of missing data is reduced).



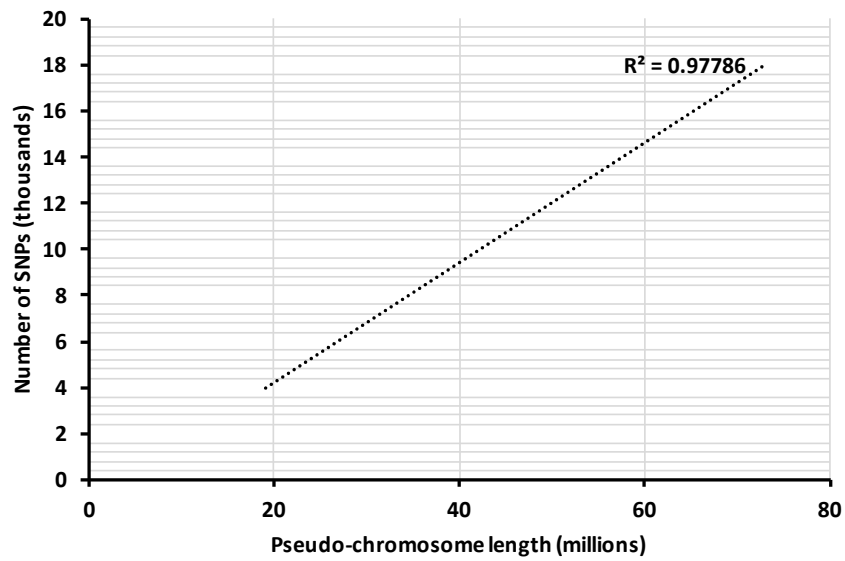


Figure S3. SNP number vs. pseudomolecule length. The number of SNPs positively and linearly increases with pseudo-chromosome length. The strength of correlation is measured by the correlation coefficient ( $R^2$ ) and is 0.978.

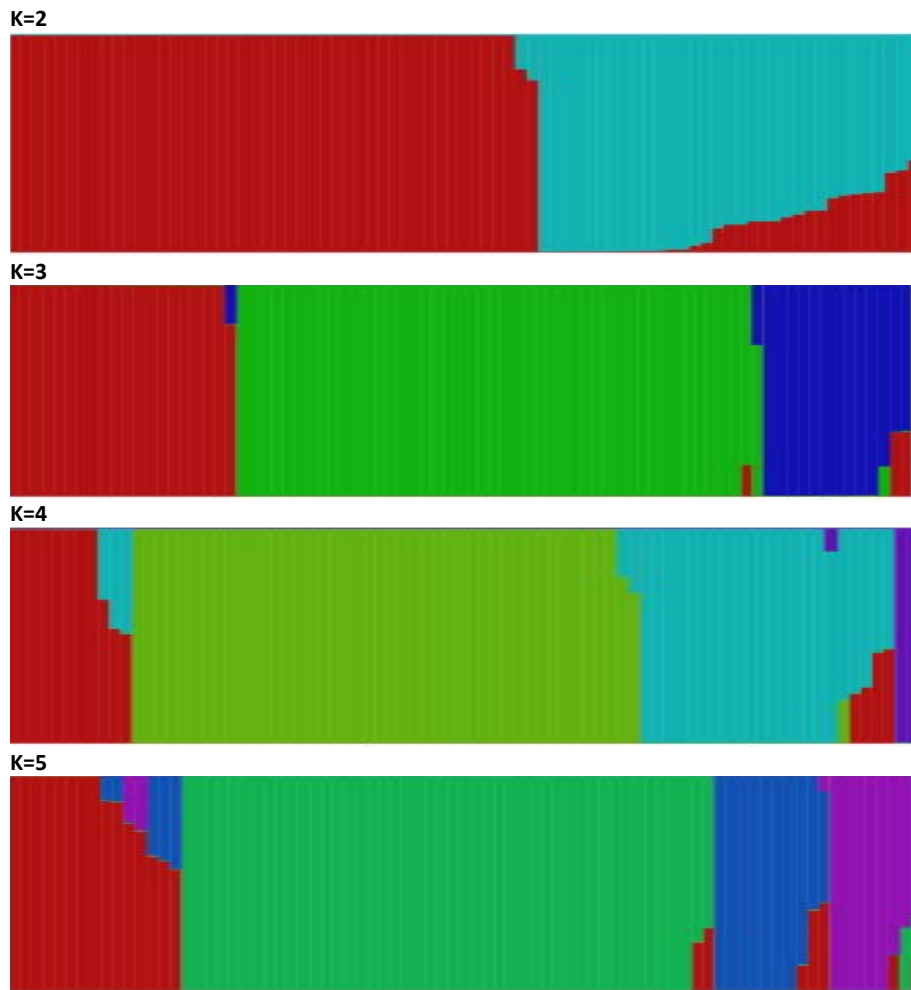


Figure S4. Population structure at different (K) clustering levels. We used fastStructure, an algorithm for inferring population structure from large SNP genotype data. Estimation of the most probable number of clusters (K), was based on four independent runs and K ranging from 2 to 5.

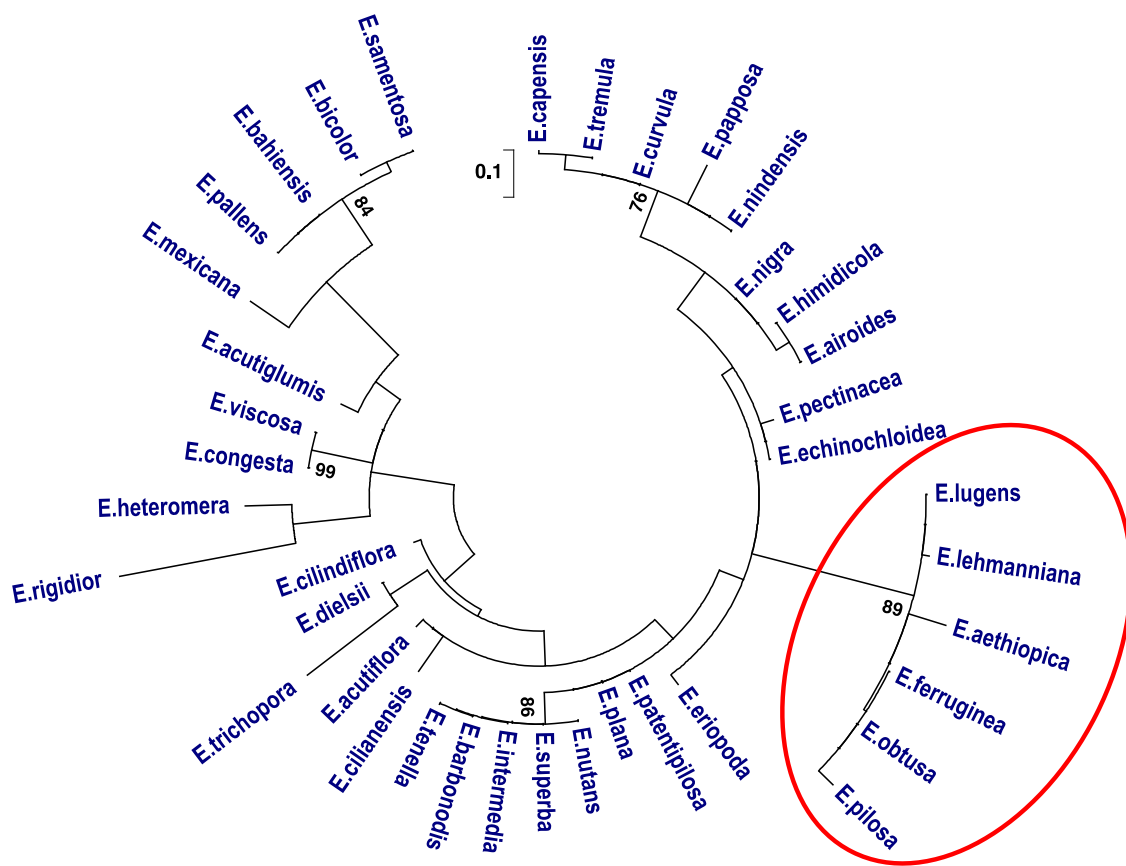


Figure S5. Phylogenetic tree of the wild *Eragrostis* species. Very little is known about the intraspecific relationships among the wild *Eragrostis* species, thus it was difficult to make sense of their grouping pattern displayed on the phylogenetic tree shown above. We subsampled these species and inferred a separate tree to visualize their relationships. The species that showed grouping with the tef species are clustered into one clade (red circle).

## References

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