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Appendix

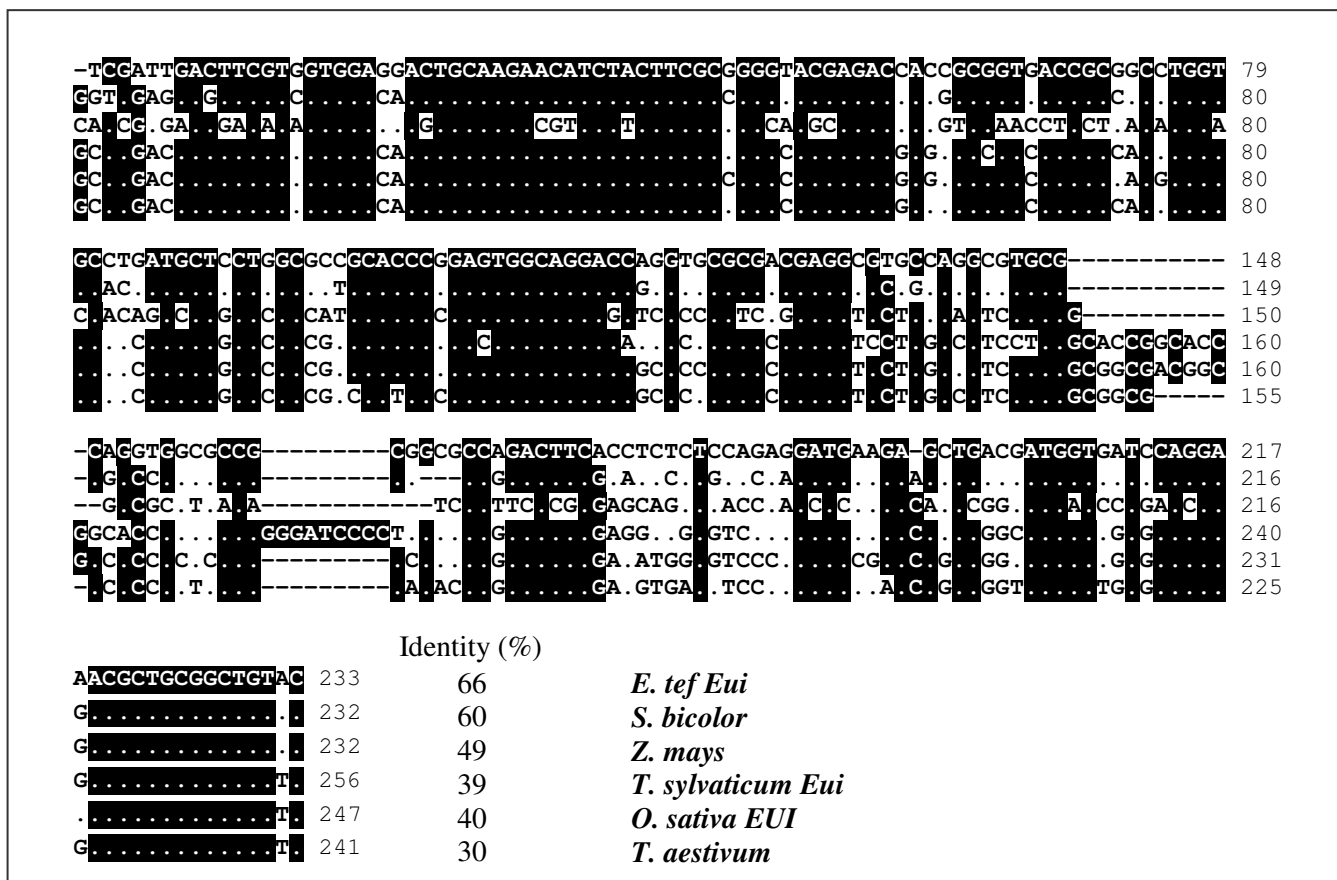
A

TGCGGCAGCGTGAAGAAGGCGTCCATTTCGAGTGGAGTCTCGGAATCCTCAAACACTACTGCAG
CAGCAGCAGCAGTAGTAGTAGTCTCCTCCTAGTCAATCAGAGAGAGAGAGAGAGAGAGAGAG
AGAGAGAGAGAGAGAGGCCAAGCCAGCTGCCCGTGATGGTGGTGGTAGCGCAGGCGCAGGCGC
AGGCGCAGATAGAAGTAGAAGCAGATGAGCCGCCGAGCAGCTTGAGGTGGTGGTGGTTCGAC
GCGGCCCGTCTGAGCGGGCTGAGTGACATCCCGGCCAGTTTTTGTGGCCGGAGGAGGAGAG
CCCAGCGCCTGACGCGGCGGAGGAGGAGCTGGACGTTCCCTCTGATCGACCTCTCCGGCGACG
CGTCGGAGGTGGTCCGTCAGGTGCGTGAGGCCTGCGAGGCGCACGGCTTCTCCAGGTGGTG
AACCACGGCATCGACGCCGGCCTCGTGGCGGAGGCGCACCGCTGCATGGACGCCTTCTTCAC
GCTGCCGCTGCCGGAGAAGCAGCGCGCCAGCGCCAGCCCGGCGACTGCTGCGGCTACGCCA
GCAGCTTCACGGGCCGCTTCGCCAGCAAGCTGCCATGGAAGGAGACGCTCTCCTTCCGGGCC
AAGGCCAAGGCCACCGATGATGATGATGATGATGTGGTGGGCTACTACGTCAGCAAGCTGGG
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GGAGACGCTGGGCACGGGCCCGCATTGCGACCCACCTCCCTCACCATCCTGCACCAGGACC
ACGTCGCCGGCCTCCAGGTCTTCGCCGCCGGCCGGTGGCTCTCCATCCGCCCGCACGCCCCAG
GCCTTCGTCGTCAACATCGGCGACACCTTCATGGCGCTCTCCAACGGCCGGTACAAAAGTTG
CCTGCACAGGGCGGTGGTCAACAGCAGCGTCCCGCGGAGGTCCCTGGCCTTCTTCTCTGCC
CGGAGATGGACAAGCTCGTCACGCTCCCGCGCAGCTTCTTCTGATCTGCCCGGAGACAAC
CAAAGGAGGCGCCCCTACCCGACTTCACGTGGCGCACCCCTGCTCGAATTCACGCAGAAGCA
CACAGGGCCGACATGAAGACGCTCGAGGTCTTCTCCAAGTGGCTCCGCCATGGCCAGGACAA
GGTAGCGCTACCTCCCTATGCTAGTTATTCTCTCCATACCAATATGTAATGTAATGTAATG
AATGTAGTCATCCATGACCGCCTGTTCTGTTCAAAAAAAAAAAGTCGACATCGATACGCGTGG
TCCGCCTCCTTTGGTTGTCTCC

B

RQREEGVHSSGVSESSNSLQOQQQ***SSS*SIREREREREREREREPSQLPVMVVVAQAQAO
AQIEVEADEPPQOLEVVVFDAARLSGLSDIPAQFLWPEEESPTPDAAEEELDVPPLIDLSDA
SEVVRQVREACEAHGFFQVVNHGIDAGLVAEAHRCMDAFFTLPLPEKQRAQRQPGDCCGYAS
SFTGRFASK**LPWKET**LSFRAKAKATDDDDDDVVGYVSKLGEAYRRHGEVYGRYCSEMSRLS
LEIMEVLGESLGVGRRCFRDFQDNDSIMRL**NYPPCORP**METLGTGP**HCD**PTSLTILHQDH
VAGLQVFAAGRWLSIRPHAQAFVFNIGDTFMALSNGRYKSLHRAVNVSSVPRRSLAFFLCP
EMDKLVTLPPQLLPDLPGDNQRRRPYPDFTWRTLLLEFTQKHTGPT*RRSRSSPTGSAMARTR
*RYLPYASYSLHTNM*CNVMNVVIHDRLFCSKKKVDIDTRGPPPLVVS

Figure A.1 (A) *E. tef* *GA20ox1* full coding region (nucleotide sequence) and (B) deduced amino acid residues of *E. tef* *GA20ox1* sequence with 482 aa with conserved domains



indicated (bold and underlined). Conserved domains include (i) the consensus sequence **NYYPXCXXP** of 2-oxoglutarate dependent dioxygenase (2ODDs) for binding the common co-substrate; ii) sequence **LPWKET**, which binds to the GA substrates, and iii) three histidine residues **HCD** for binding Fe²⁺.

C

GCTGCCGTGGAAGGAGACGCTCTCCTTCGGCCACCGCGACGTCGTGGAGTACTTCACATCCA
CCCTCGGCAGCGACTTCAAACCCCTAGG**GTAACATAAACTGTTGAAATAGCTAGCTTCGCT**
ACGTTTTTTTTTGTACGTACAAGAGATCGGTCATCGGAGAGCTTTTACAATGACTAATGCAC
CGATCGAGCCATGCATGGACGCAGGGAGGTGTTCCGAGACTACTGCCAATCGATGAAGGAGG
TGTCGCTGGCGATCATGGAGGTGCTGGGCGCGAGCCTGGGCGTGGGGAGGCGCTACTGCAGG
GACTTCTTCGCCGACGGCTGCTCCATCATGAGGTGCAACTACTACCCGCCGTGCCCGGAGCC
GGACCGGACGCTGGGCACGGGGCCCCACTGCGACCCGGCGGCCACACCCCTTTGCTCCAGG
ACGACGACGTGGACGGGCTCCAGGACGACGACGTTGGACGGGCTCCAGGTGCTCGTCGACGGC
GAGTGGCGGCCCGTGGCGCCCAAGCCGGGAGCCATCGTCGTCAACATCGGCG

D

LPWKETLSFGHRDVVEYFTSTLGSDFKPLG*T*TVEIASFATFFFVTRDRSSESFYND*CT
DRAMHGRREVFRDYCQSMKEVSLAIMEVLGASLGVGRRYCRDFFADGCSIMRCNYYPCCPEP
DRTLGTGPHCDPAAHTLLLQDDVDGLQVLVDGEWRPVRPKPGAIVVNIG

E

CGATTGCTGCCGTGGAAGGAGACGCTCTCCTTCCGGGCCAGCCCAACGTCGCCGGCCTTGGTGGAGGA
CTACCTGGTGGGCCGCCTTGGCGACGAGTACAGGCGGCACGGCGAGGTGTACGGGCGCTACTGCTCGG
AGATGAGCCGGCTGTCGCTGGAGATCATGGAGGTGCTGGGCGAGAGCCTGGGCGTGGGCCGGCGCTGC
TTCCGCGACTTCTTCCAGGACAACGACTCCATCATGCGGCTCAACTACTACCCGCCGTGCCAGCGGCC
CAYGGAGACGCTGGGCACGGGCCCGCATTGCGACCCACCTCCCTCACCATCCTGCACCAGGACCACG
TCGCCGGCCTCCAGGTCTTCGCCGGCGGCCGGTGGCTCTCCATYCGCCCGCACGCCGCCGCCTTCGTC
GTCAACATCGGCGA

F

RLLPWKETLSFRASPTSPALVEDYLVGRLGDEYRRHGEVYGRYCSEMSRLSLEIMEVLGESLGVGRRC
FRDFFQDNDSIMRLNYYPCQRPETLGTGPHCDPTSLTILHQDHVAGLQVFAGGRWLS?RPHAAAFVV
NIG

Figure A.2 Homologous sequences of *E. tef* *GA20ox1a* and *GA20ox2*. (C) represents a *E. tef* *GA20ox2* partial coding nucleotide region, (D) deduced amino acid residues of *E. tef* *GA20ox2* sequence with 152 aa (excluding the sequence in grey shade) with conserved domains indicated (bold and underlined) and stop codons (*); (E) *E. tef* *GA20 ox1b* partial coding nucleotide region and (F) deduced amino acid residues of *E. tef* *GA20ox1b* sequence with 140 aa with conserved domains indicated (bold and underlined). Sequence in box is in “C” and “D” is an intron between the concerned region in *tef GA20ox2* sequence.

Table A.1 Primers used for PCR amplification of gene fragments of Rht, Eui and BR using *E. tef* genomic DNA

Target gene	Primers	Degenerate/specific primers
Rht	F1	GTGG(TCA)GGACACGCAGGAGGC
	F2	TTCTACGAGTCCTGCCCCTACCT
	R1	T(TCG)GCGGTGAAGTGGGCGAAC
	R2	TCGGGCTCGTCATCCGTGTCAT
Eui	F1	A(GA)(CG)(CG)(TC)C(CA)ACGGCGA(CG)(AG)AT
	R1	ACAGCCGCAGCGTCTCGTT(GCT)
BR	F1	ACAGCCGCAGCGTCTCGTT(GCT)
	R1	A(GA)(CG)(CG)(TC)C(CA)ACGGCGA(CGA)(GC)(CG)(AT)GTT

Table A.2 *Rht* primers used in RACE- PCR

Target gene	Primers	Degenerate/specific primers
Rht	Rht SPR3	ATCCCGGCCTCCTGCGTGTCCA
	Rht SPR2	CGGTGGCGGGCGGAAGCGATACA
	Rht SPR1	GGGCGAACTTGAGGTAGGGGCAG
	Rht SPF1	TGTATCGCTTCCGCCCGCCACCG
	Rht SPF2	CTGCCCTACCTCAAGTTCGCCC

G

TCGATTGACTTCGTGGTGGAGGACTGCAAGAACATCTACTTCGCGGGGTACGAGACCACCGC
GGTGACCGCGGCCTGGTGCCTGATGCTCCTGGCGCCGCACCCGGAGTGGCAGGACCAGGTGC
GCGACGAGGCGTGCCAGGCGTGCGCAGGTGGCGCCGCGGCCAGACTTCACCTCTCTCCAG
AGGATGAAGAAGGTACTGCAGGTCAAATGAATCACACAGTTCATGCATGCACGTTTCAGTAC
ACACGCGCGCGCTGATCTGACCAACCTTGTGCATCCAAATATTTGTTTTTTCGGCAGCTG
ACGATGGTGATCCAGGAAACGCTGCGGCTGTACA

H

SIDFVVEDCKNIYFAGYETTAVTAAWCLMLLAPHEWQDQVRDEACQACAGGAAAPDFTSLQ
RMKKVLQVK*ITQFHACTFSTHARALI*PTLCIQIFVFS AADDGDPGNAAAV

Figure A.3 Partial coding region of the Elongated Uppermost Intenode (EUI) gene in *tef*. (G) represents a *E. tef* EUI partial coding nucleotide region (344bp), (H) deduced amino acid residues of *E. tef* EUI sequence with 115 aa. The underlined region (109 bp) is a predicted intron.

Figure A.4. Derived nucleotide sequence alignment of the putative tef *Uppermost Elongated Internode (EUI)* to orthologous monocot sequences from sorghum (*S. bicolor*; Acc No. XM_002439928.1), maize (*Z. Mays*; Acc No. BT043273.1), rice (*O. sativa* Acc No. AY987040.1), wheat (*T. aestivum* Acc No. AL816398) and brachypodium (*T. sylvaticum*). Identical regions (>80%) are shown by dark shaded areas and dots whereas number indicates the position of the nucleotide within the sequence.

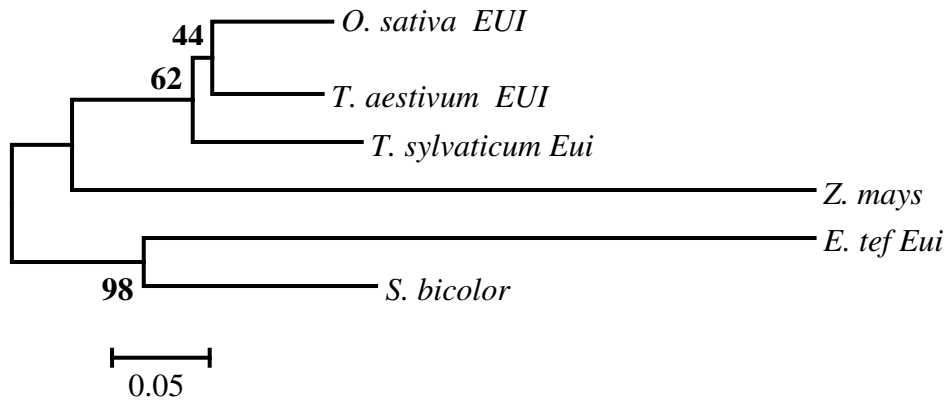


Figure A.5 Molecular phylogenetic analysis of the rice *EUI* ortholog gene in *tef*. The tree was inferred by Maximum Likelihood method using partial gene sequence. Initial alignment was done by mafft (<http://mafft.cbrc.jp/alignment>) software. The phylogeny was inferred by using the Maximum Likelihood method based on the Tamura-Nei model (1993). The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. There were a total of 368 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 (Tamura *et al.*, 2011).

I

GAGGAGGTGGACGAGCTGCTGGCCGCGCTCGGGTACAAGGTGCGCTCGTCGGACATGGCGGA
CGTGGCGCAGAAGCTGGAGCAGCTCGAGATGGCCATGGGGATGGGCGGCGTCCCCGCCGCGG
ACGACGGGTTCGTGTGCGACCTGGCCACGGACACCGTGCACACTACAACCCCTCCGACCTGTGCG
TCCTGGGTGGAGAGCATGCTGTCCGAGCTCAACGCCCGCCGCGCCGCTCCCGCCCGCGCC
CGCGCCGCGGCCCGCCGAGCTGGTTTCCACCTCGTCCACCGTACAGGGCGGCGGCTCCGGCG
CCGGGTACTTCGATCCCCCGCCGCGTCTGACTCCTCCAGCAGCACGTACGCGCTGAAGCCG
ATCCCTCGCCGGTGGCGGCGCCGGCCGACCCGTCCGCGGACTCCGCGGGGAGCCGAAGAG
GATGCGCACTGGCGGCGGCAGCACGTCGTCTTCCCTCGTCTTCGTCTTCGTCCATGGGCGGCG
GCGGCGCCAGGAGCTCCGTGGTTGAGGCTGCCCGCCCGCATCCGCGGCGGCGAACGCGCCC
GCGGTGCCTGTGGTGGTGGTGGACACGCAGGAGGCCGGGATCCGGCTCGTGCACGCGCTGCT
GGCGTGC GCGGAGGCCGTGCAGCAGGAGA ACTTCTCCGCCGCGGAGGCGCTGGTGAAGCAGA
TCCCCATGCTGGCCTCGTCGCAGGGCGGCCATGCGCAAGGTGGCCGCCTACTTCGGCGAG
GCTCTCGCTCGCCGCGTGTATCGTCCCCCCCCCGCCCCGACAGTCCCTCCTCGACGCC
GCCTTCGCCGACCTCCTCCACGCCCACTTCTACGAGTCTGCCCCTACCTCAAGTTCGCC
ACTTCACCGCGAACCCAGGCCTTCCCTCGAGGGGTTTCGCCGGCTGCCGTGCGGTCCACGTCGTC
GACTTCGGCATCGAGCAGGGGATGCAGTGGCCGGCGCTCCTCCAGGCCCTCGCCCTCCGCC
CGGCGGCCCCCGTCCCTCCGCCTCACCGGCGTCGGCCCACCGCAGCCTGACGAGACCGACG
CCTTGACAGAGGTGGGTGGAGCTCGCCCAGTTCGCTCACACCATCCGCGTCTGACTTCCAG
TACCGCGCCTCGTGC GCGCCACGCTCGCAGACCTGGAGCCGTTTCATGCTGCAACCGGAGGG
CGAGGAGAATGACGAGGAGCCCGAGGTGATCGCCGTCAACTCGGTGTTGAGATGCACCGGC
TGCTGGCGCAGCCCGGCGCCCTGGAGAAGGTCCTGGGCACGGTGC GCGCGGTGCGGCCCAAG
ATCGTGACCGTGGTGGAGCAGGAGGCCAACCAACTCCGGCTCGTTCCTGGACCGCTTCAC
GCAGTCTCTGCACTACTACTCCACCATGTTCGA

J

EEV**DELLA**ALGYKVRSSDMADVAQKLEQLEMAMGMGGVPAADDGFVSHLATDT**VHYNP**SDLS
SWVESMLSELNAPPPPLPPAPAPPAPQLVSTSSSTVTGGGSGAGYFDPPPAVDSSSSTYALKP
IPSPVAAPADPSADSAREPKRMRTGGGSTSSSSSSSSSMGGGARSSVVEAAPPASAAANAP
AVPVVVVDTQEAGIRLVHALLACAEAVQQENFSAAEALVKQIPMLASSQGGAMRKVAAYFGE
ALARRVYRSPPPPPTAPSSTPPSPTSSTPHFYESCPLYLKFHFTANQAFLEAFAGCRR**VHV**
DFGIEQGMQWPALLQALALRPGGPPSFRLTGVGPPQPDETDALQQVGWKLQFAHTIRVDFQ
YRGLVAATLADLEPFMLQPEGEENDEEPEVI AVNSVFEMHRLLAQPGALEKVLGTVRAVRPK
IVTVVEQEANHNSGSFLDRFTQSLHYSTMF

Figure A.6 Full coding region of the *E. tef* RHT gene. (I) represents a *E. tef Rht* near full coding nucleotide sequence (1397 bp), (J) deduced amino acid residues of *E. tef Rht* sequence (465 aa) with characteristic domains (bold and underlined): the DELLA motif, VHYNP and VHVVD of the GRAS domain.

K

TAAGGCCACGGCGAGGAGTGGGCGCGCCGCCGAAGATCCTCACCCCGCCTTCCACACCGAGAACC
TCAAGCTGCTGGTGCCGTTTCGTCGGCGAGACGGTGCAGCGGATGCTGGAGGAGCGCGTGCTCTCGCCG
TCGGCGTCGGCGGCGAACGGCGGCGAGGTGGAGGTGGACGTCGCGGAGTGGTACCCGCGGCTGCCGCA
GGAGGCCATCACGCTCGCCACGTTTCGGCCGGAACACTACGCCGAGGGCAGCGTCGTGTTCCGGCTGCAGG
GCGAGCACGCCAGCCACGCCACGGTGGCGCACAGCAAGGTCTTCATCCCGGGGTACAGGTTTCATCCCG
ACAAGGCGGAACCGGCGCGTGTGGCAGCTGGACAGGGAGATCAAGAGCACCCCTGGCCAAGTTCGTCTGT
CGCCCTGCAGAGCCGCGGGCGGCGGGTGACCACCACCACCGCCGGGACGAGGGGCGAGCGGACGACG
GCTTGAGGGACTTCATGAGCTTCATGGCGCCGGCCATGACGGCGGACGAGATCATAGAGGAGTGCAAG
AACTTCTTCTTCGCCGGCAAGGAGACCCTGACCAGCCTCCTCACCTGGGCCACCGTTCGCGCTCGCCAT
GCACCCGGAGTGGCAGGACCGCGCGCGCCGGGAGGTCTGCTCCGTCTGCGGCCACCGCGGCCTCCCGA
CGAGAGACCACCTTCCAAGCTCAAGACCCTGGGGATGATCGTGAACGAGACGCTGCGGCTGTAATCG
A

L

KAHGEWARRRKILTPAFHTENLKLVPFVGETVQRMLEERVLSPSASAANGGEVEVDVAEWYPRLPQ
EAITLATFGRNYAEGSVVFRLOGEHASHATVAHVKVFIPIGYRFIPTRRNRRVWQLDREIKSTLAKFVV
ALQSRGGGDHHRDEGRADDGLRDFMSFMAPAMTADEIEECKNFFFAGKETLTSLLTWATVALAM
HPEWQDRARREVSVCGHRGLPTRDHLPLKLTGMIVNETLRL

Figure A.7 Putative *E. tef* brassinosteroid deactivation related Cytochrome P450 monooxygenase gene partial sequence. (K) represents brassinosteroid deactivation gene partial coding region (749 bp), (L) deduced amino acid residues of the sequence (247 aa).

KAHGEWARRRKILTPAFHTENLKLKLVFVGETVQRMLEERVLSPSASAANG-GEVEVDVAEWYPRLPQEAITLATFGR-NYAEGSVVFRLOGEHASHAT 98
 NL..D.....NA.....A..AD.....L..S...G.S.....V...Q...K...V.....-SD...A.....A...Y.. 99
 NL..R.....RV.....HRMIA..AG..T...D.--LAERAR.G.A.A.....FQ.V.....F.A...R..DD.AA.....D.L.GY.. 97
 NL..R.....RV.....FQ.V.....F.A...R..DD.AA.....D.L.GY.. 65
 SL..DK..LH.RV.V...YPD..NR...H..RS.AALA.R----WR.M.CASG.....FQAVAE...R.....-S..S.R...M..RLMAF.S 95
 SL.DDK..LH.RV...YPD..NR.A.H.ARS.VALA.R----WR.M.SAAG.....QAVAE...R...S-S.DS.R...M..ARLMAF.S 95
 SLR.DK..H...V...M.....L...R..VDVVDK---WHDM..AAS...I..S..FQVVTE...RTA...-S.ED.KA..K..TQLMAF.S 95
 SLR.DK..H...V...M.....L...R..VDVVDK---WHDM..AAS...I..S..FQVVTE...RTA...-S.ED.KA..K..TQLMAF.S 95
 SLK..K..HH...I..T.YI..R.MI.MM.KSMKE..DK---W.KMSN-AS.K..IE.S.MFST.AEDV..RIV..N-S.ED.KAI.E..AQQMIY.. 94
 SLK..K..HH.R.IS.T.M.....I.VMATS.VE...N---W.EMS--HK...IE.S.CFQT.TEDV...KTA...S-S.QD.KAI...AQQMVL.A 93

VAHSKVFIPGYRFIPTRRNRRVWQLDREIKSTLAKFVVALQSRGGGGDHHRRDEG-RADDGLRDFMSFMA-----PAMTADIEIEECKNFF 185
 E.....L.....RRL..L.AG...--D..R..GRDP..G..M.N.....S... 182
 E...Y.....L...K.....R.H.....TG...--CSSS.GDDA.D.GDGGG.M.E.....G.....S... 183
 E...Y.....L...K.....R.H.....TG...--CSSS.GDDA.D.GDGGG.M.E.....G.....S... 151
 E.FR..LV.....L..KK..MS.G...RRG.VQLIGRRSD--AAEEREAEIKDKG---F..LLGL.INARDKK----SQP.PVE.MV...T... 184
 E.FR..V.....L..KK..LQ.S...RRG.VTLIGHRND--AAQDDSEPNDKSSN.F..LLGL.INASDKKKQEEAR..PVEDML...T... 193
 E.FR.....L..KK.TTS.K..K..RKN..TLIGRR.EA--AD.EKLSG-----CAK.LLGLL.INAGSNG---GKVSP.I.VND.V...T... 182
 E.FR.....L..KK.TTS.K..K..RKN..TLIGRR.EA--AD.EKLSG-----CAK.LLGLL.INAGSNG---GKVSP.I.VND.V...T... 182
 E.YQ.....L.SKK..IC.R..KQVRKS.M.LIEERRKK--EE-VLSEE-----CPN.LLEV.IKAGSDD---EYRNTI.VND.V...TI... 180
 D.FQ.....F...IKS..K..KQ..KS.V.LIERREN--SN-ERIEK-----PK.LLGL.IQASN-----KTNV.V.D.VG...S... 175

Sequence	Identity (%)	Protein Name	
AGKETLTSLLTWATVALAMHPEWQDRARREVVSVCGRHGLPTRDHLPKLKTLLGMIVNETLRL	247	100	<i>E. tef</i> P450 monooxygenase
..L..N.....	244	50	<i>S. bicolor</i>
..S.N.....T.....E.....A...RGD..K.....L.....	245	52	<i>O. sativa</i> CYP734A1/BAS1
..S.N.....T.....E.....A...RGD..K.....L.....	213	50	<i>O. sativa</i> P450 monooxygenase
..Q.T.N.....L.....D.A..Q..LA...PGE..KE..H.....L.....	246	52	<i>H. vulgare</i>
..Q.T.N.....L.....D.E..Q..LA...ADE..SKE.....L.....	255	50	<i>Z. mays</i> P450 monooxygenase CYP734A7
..Q.TSN.....T..L.....EL..Q..LQ...A.DI..S.EQ.T.....L...---	241	51	<i>Z. mays</i>
..Q.TSN.....T..L.....EL..Q..LQ...A.DI..S.EQ.T.....L.....	244	42	<i>Z. mays</i> P450 monooxygenase CYP734A8
..H.TSN.....T..IL.....K..EL..D..LT...A.DP.SKQQIS.....I..SV--	240	42	<i>S. lycopersicum</i> P450 monooxygenase
..Q.TSN.....T..IL.....Q...VQ...D...LKM...S.DV..K..VV...N.....S---	234	48	<i>P. sativum</i> P450 monooxygenase

Figure A.8 Amino acid sequence alignment of the putative brassinosteroid deactivating gene sequences from *E. tef* with amino acid sequences from other species. sorghum rice (*O. Sativa*; Acc No. EAY84935.1), barley (*H. vulgare*; Acc. No. BAK00002.1), sorghum (*S. bicolor*; Acc No. XP_002453514.1), maize (*Z. mays*; Acc No. ACG29333.1), pea (*P. sativum*; Acc No. BAF56240.1), and tomato (*S. Lycopersicum*; Acc. No. BAF02550.1). Identical and similar regions are shown by dark (100%) and light shaded areas and dots whereas number indicates the position of the amino acid within the predicted peptide.

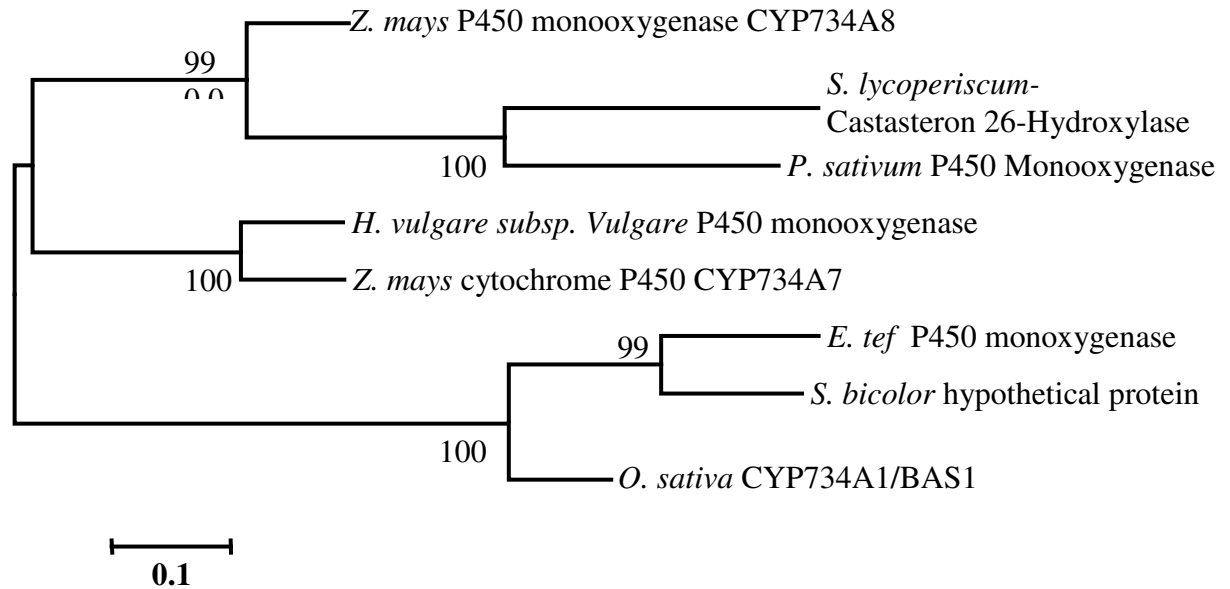


Figure A.9 Molecular Phylogenetic analysis of putative *E. tef* brassinosteroid deactivation gene sequence. The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based (Jones *et al.*, 1992). Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. There were a total of 269 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 (Tamura *et al.*, 2011).