
Supplementary Table

Gene	Forward primer (5'→3')	Reverse primer (5'→3')
ShTGA1	AGCTCTCGGATACACAGGGT	CAGAGGAAGAACCTCTCGGC
ShTGA2	AGCACCACATGAACGACCTC	TCTCGTCGTAGTGCAGCATC
ShTGA3	TCCTGACAATCCGACAAGCC	GGCCTAGCAAGCCAAAGAGA
ShTGA4	TGTTGCTGCAAAGGCTGATG	TCAGATGGACGAAAACCCCC
ShTGA5	TCAGGCATGTGGAAGACACC	AAGGATTGCTGAAGGGCCTC
ShTGA7	TGGGAAAACCTTGGCACCCCTT	GCAAGTAGAGCTCGTGCTGA
ShTGA8	TAAGCTCCCTCTGGGCTTCT	CTTTGGGATGGTTGTGCTGC
ShTGA9	AGCGATGCTTCCTCTGGATG	CCTTCGAGGTGGACAGCTT
ShTGA10	AGGCCGACAATCTAAGGCAG	CTCGGTCCCGATGAAGTTGT
ShTGA11	CTCGGTGCTTCCTCTCCATC	GGGAACTGGCTTTGGTGCTA
ShTGA12	GAACTGCACACTGCAAGAGC	CTTGATGCCCACCATCTCGT
ShTGA13	GCAAGAACTCATCAGGGTGC	ACCGCTCGTACTCCAGGT
ShTGA14	AAGACACTGAGGAGGCTTGC	ACATCAGCTTGCTGTGCTCT
ShTGA15	CTTCATTGCGGTTGTCTGGC	TCCATCTGCAGGAGCCAAAG
ShTGA16	ACTGAGGCAGAACTCGGTG	CCCAGGGGAAATGAATGCCT
GAPDH	CACGCCACTGAGCA	TCCAGTTCCATGCC

Supplementary Table S1 The specific nucleotide sequences of primers for qRT-PCR

Query	Top Scoring Sequences	Sequences Logo	Width
motif 1	IVDGIMAHYDELFRKGVAAKADVHL LSGMWKTPAERCFLWLGGFRPSE		50
motif 2	SSRJKLAQLEQELQRRARQQGIFIGGSGD		28
motif 3	FLRQADNLRQQLHQMHRILTTRQAA RALLAISDYFSRLRALSSLWLARP		50
motif 4	QLEPLTEQQLVGICNLQQSSQQAEEALS QGMEALQQSLADT		41
motif 5	FDMEYARWLEEHNKQMAELRAALNA HLSGDGLR		33
motif 6	NVANYMGQMALAMGKLTLEN		21
motif 7	PPPTLNIFPSWPMRSLQTPK		20
motif 8	MADASPRTDTSTDLDTDKNQ		21
motif 9	VIVSVLADPREAGDGDGEGRIPPKPLSRI FVVVLJDGVKYVTYSCVLPFK		50
motif 10	DQKTLRRLAQNREAARKSRLRKKAYV QQLE		30

Supplementary Table S2 The characteristics of conserved motifs in ShTGAs using MEME-suite.

Gene 1	Gene 2	Ks	Ka	Ka/Ks	Mya
ShTGA1	ShTGA14	1.603801041	0.700894485	0.437020844	53.46003471
ShTGA1	ShTGA12	0.907429507	0.661915765	0.729440425	30.24765022
ShTGA1	ShTGA15	2.365839097	1.398357474	0.591061951	78.86130324
ShTGA1	ShTGA10	0.997511923	0.64335157	0.644956271	33.25039744
ShTGA1	ShTGA8	1.877433286	0.562785731	0.299763371	62.58110955
ShTGA1	ShTGA16	2.107938481	1.49997283	0.71158283	70.26461603
ShTGA1	ShTGA11	1.485951274	0.668252021	0.44971328	49.53170913
ShTGA1	ShTGA13	1.284834469	0.755194357	0.587775605	42.82781563
ShTGA2	ShTGA15	2.091926335	1.544157664	0.738151071	69.73087783
ShTGA2	ShTGA16	3.158179388	1.519290527	0.481065304	105.2726463
ShTGA9	ShTGA14	2.199340915	0.585372471	0.266158133	73.31136382
ShTGA9	ShTGA12	1.84781963	0.569800165	0.30836352	61.59398767
ShTGA9	ShTGA10	1.387408902	0.466748599	0.336417475	46.24696339
ShTGA9	ShTGA11	2.405669465	0.516216074	0.214583126	80.18898216
ShTGA9	ShTGA13	2.432109298	0.608494398	0.250192045	81.07030994
ShTGA10	ShTGA14	1.568689162	0.609918033	0.38880745	52.28963872
ShTGA10	ShTGA12	0.757336748	0.669435055	0.883933147	25.24455826
ShTGA10	ShTGA11	1.195858029	0.377644741	0.315793959	39.86193429
ShTGA10	ShTGA13	1.162790397	0.734253718	0.63145836	38.7596799
ShTGA11	ShTGA14	1.973285332	0.590074058	0.29903129	65.77617773
ShTGA11	ShTGA12	1.963295672	0.691831778	0.352382877	65.44318907
ShTGA11	ShTGA13	1.813124015	0.728181137	0.40161684	60.43746716
ShTGA12	ShTGA14	1.197073522	0.454927416	0.380032978	39.90245073
ShTGA12	ShTGA13	0.955799348	0.603285108	0.631183845	31.85997827
ShTGA13	ShTGA14	1.600188613	0.541421089	0.338348295	53.33962043
ShTGA13	ShTGA15	2.762734502	1.498406139	0.542363422	92.09115008
ShTGA13	ShTGA16	2.029334395	1.472166693	0.725443129	67.64447983
ShTGA14	ShTGA15	2.977113303	1.318489129	0.442875025	99.23711009

Supplementary Table S3 The substitution rate ratio Ka/Ks and divergence time between the *TGA* gene family members