

Table S1 Sequences and relevant information used for phylogenetic analysis of the trehalase genes

Genes name	GenBank No.	Species	Phylogenetic group
<i>AaTre2</i>	XP_021705796.1	<i>Aedes aegypti</i>	Diptera
<i>AgTre2</i>	XP_320471.4	<i>Anopheles gambiae</i>	Diptera
<i>AglTre1</i>	AFJ00065.1	<i>Aphis glycines</i>	Hemiptera
<i>AmTre1</i>	XP_393963.3	<i>Apis mellifera</i>	Hymenoptera
<i>AmTre2</i>	NP_001106141.1	<i>Apis mellifera</i>	Hymenoptera
<i>DmTre2</i>	ABH06695.1	<i>Drosophila melanogaste</i>	Diptera
<i>BmTre1</i>	BAA13042.1	<i>Bombyx mori</i>	Lepidoptera
<i>BmTre2</i>	BAE45249.1	<i>Bombyx mori</i>	Lepidoptera
<i>LmTre1</i>	ACP28173.1	<i>Locusta migratoria manilensis</i>	Orthoptera
<i>NlTre1</i>	ACN85420.1	<i>Nilaparvata lugens</i>	Hemiptera
<i>NlTre2</i>	ACV20872.1	<i>Nilaparvata lugens</i>	Hemiptera
<i>OmfTre1</i>	ABO20846.1	<i>Omphisa fuscidentalis</i>	Lepidoptera
<i>OmfTre2</i>	ABO20845.1	<i>Omphisa fuscidentalis</i>	Lepidoptera
<i>SeTre1</i>	ABY86218.1	<i>Spodoptera exigua</i>	Lepidoptera
<i>SeTre2</i>	ABU95354.1	<i>Spodoptera exigua</i>	Lepidoptera
<i>SfTre1</i>	AQS60672.1	<i>Sogatella furcifera</i>	Homoptera
<i>SfTre2</i>	AFO54713.1	<i>Sogatella furcifera</i>	Homoptera
<i>TcTre1</i>	XP_973919.1	<i>Tribolium castaneum</i>	Coleoptera
<i>TcTre2</i>	XP_972610.2	<i>Tribolium castaneum</i>	Coleoptera
<i>HaTre1</i>	AJK29979.1	<i>Helicoverpa armigera</i>	Lepidoptera
<i>HaTre2</i>	AJK29980.1	<i>Helicoverpa armigera</i>	Lepidoptera
<i>HvTre1</i>	AZM68711.1	<i>Heortia vitessoides</i>	Lepidoptera
<i>HvTre2</i>	AYO46921.1	<i>Heortia vitessoides</i>	Lepidoptera
<i>SlTre1</i>	ADA63846.1	<i>Spodoptera litura</i>	Lepidoptera
<i>SlTre2</i>	ADA63845.1	<i>Spodoptera litura</i>	Lepidoptera
<i>CmTre1</i>	ALF03966.1	<i>Cnaphalocrocis medinalis</i>	Lepidoptera
<i>CmTre2</i>	ANC68249.1	<i>Cnaphalocrocis medinalis</i>	Lepidoptera
<i>GpTre1</i>	MN915101	<i>Glyphodes pyloalis</i>	Lepidoptera
<i>GpTre2</i>	MN915102	<i>Glyphodes pyloalis</i>	Lepidoptera
<i>OfTre1</i>	ANY30160.1	<i>Ostrinia furnacalis</i>	Lepidoptera
<i>OfTre2</i>	ANY30159.1	<i>Ostrinia furnacalis</i>	Lepidoptera

Table S2 Primers used to synthesize dsRNA

Primer Names	Sequence(5'-3')
GpTre1-1-Olig-1	GATCACTAATACGACTCACTATAGGGGCAAGGACTTGAACGGTATTT
GpTre1-1-Olig-2	AA ATACCGTTCAAGTCCTTGCCCCCTATAGTGAGTCGTATTAGTGATC
GpTre1-1-Olig-3	AAGCAAGGACTTGAACGGTATCCCTATAGTGAGTCGTATTAGTGATC
GpTre1-1-Olig-4	GATCACTAATACGACTCACTATAGGG ATACCGTTCAAGTCCTTGCTT
GpTre1-2-Olig-1	GATCACTAATACGACTCACTATAGGGGCTCGTGTCTTGGAATATTTT
GpTre1-2-Olig-2	AAAATATTCCAAGACACGAGCCCCCTATAGTGAGTCGTATTAGTGATC
GpTre1-2-Olig-3	AAGCTCGTGTCTTGGAATATTCCCTATAGTGAGTCGTATTAGTGATC
GpTre1-2-Olig-4	GATCACTAATACGACTCACTATAGGGAATATTCCAAGACACGAGCTT
GpTre2-1-Olig-1	GATCACTAATACGACTCACTATAGGGGCAGCATGTCAAGGAGAATTT
GpTre2-1-Olig-2	AAATTCTCCTTGACATGCTGCCCCCTATAGTGAGTCGTATTAGTGATC
GpTre2-1-Olig-3	AAGCAGCATGTCAAGGAGAATCCCTATAGTGAGTCGTATTAGTGATC
GpTre2-1-Olig-4	GATCACTAATACGACTCACTATAGGGATTCTCCTTGACATGCTGCTT
GpTre2-2-Olig-1	GATCACTAATACGACTCACTATAGGGGCGTCTGGTTAGACTTCAATT
GpTre2-2-Olig-2	AATTGAAGTCTAACCAGACGCCCCCTATAGTGAGTCGTATTAGTGATC
GpTre2-2-Olig-3	AAGCGTCTGGTTAGACTTCAACCCTATAGTGAGTCGTATTAGTGATC
GpTre2-2-Olig-4	GATCACTAATACGACTCACTATAGGGTTGAAGTCTAACCAGACGCTT

Table S3 Primers used in RT-qPCR

Gene Names	Forward Primer (5'-3')	Reverse Primer (5'-3')
<i>GpTre1</i>	GAGCCTCGGAAAACATCGCA	CAAGACACGAGCGGAATGCT
<i>GpTre2</i>	ACGGAAACACGATTTTCGGCA	CCATCACGACGAGTAACGCC
<i>GpCHSA</i>	TACGCTTTCCACATCACCGC	ACGGGCCTTCTCTTCCTTGT
<i>GpCHSB</i>	ACTTGGCTTTGGGCAGCTTT	GGTCCCTCGTCAACGCATTT
<i>GpCDA1</i>	TTCAAGCCATTCGCTGTCCC	CCAGGAAGCCATCTTGGCAG
<i>GpCDA5</i>	GTGCTTCCCTCCTAACACGC	CCCTTTCGATGGCAGGGTTC
<i>GpCDA2</i>	TTGGTGTGCGTGCTCCTTAC	TATGGGCGTTACCGTTGCAC
<i>GpCHT-h</i>	GCGACCCCTACAGAGGCAAC	TTTTCGCTTCACCGCATCGT
<i>GpCHT3a</i>	TTCAACGACTACAGCCCCGA	GAGAAGTAGCCGTTCAAGGCG
<i>GpCHT3b</i>	TCGGGGAGAAGGTCGAGAGA	ATTCCAGGGCCAGTCGCAT
<i>GpUAP</i>	ACAACGTCGGTTTACCCTCC	CAGTTGGAGCCATTGTGTGC
<i>GpPAGM</i>	ATCAAGCAGGTGAACGCAGA	CGTGGTGACGATACCGAACT
<i>GpCDA4</i>	GCCCTATACCAACAACGCCC	AGAAAGTCCCGCGTATGGGA
<i>GpCHT7</i>	GGAGGAGTCTGTGGTGGGAA	ACGCTACTGAGGCCCAATCT
<i>GpRpl32</i>	CGATCACCTTCCGCTTCT	TGCTACCCAATGGCTTCC

1 ATGATGTTTCAACTCTGGTAGTAGCGGTGGCTGCCGACGCTGTGGTCGGTGATGACCTTCCACCGTCATCGCGTTAA
7 M M F Q G C L L V V A V A A A A V V G T D D L P F S C G K
19 CAGGCTACTGCGACAGCGAGCTGTGCACTTTGTGCAGATGGCAGCGCTACCTGACCTCCAAAGTCCTTCGTCGAC
27 P V Y C D S D L L H F V Q M A R L Y P D S K S F V D
157 ATGCACATCGGTCGAGACCCCGAAGAATTTCTCGAAGACTTCGATCAACTTCTCAACAGCTCGCAAAGGAATCCACC
53 M H C M R R D P E E I L D F D Q L L N S S Q R N P T
235 AGAGAAACAATCCAGGCTCTCGTTAACGAAACCTTTAACGAGGAAGTCGAAATGAAACCTGGTTACCATCTGATTAC
79 R E Q I Q A F V N N E N F E E V E I E N W L P S D Y
313 ACGGAGAACCCCAATCTCCTTTGGGAATTCGGCAGGAAACCTTCGGCAATATGGCAAGGACTGAACGGTATTTGG
405 T E N P K F L L G I R D E K L R Q Y G K D L N G I W
391 CCAAACTCTGGGAGGAAAGTCAAGGCATCCGTTCTAGAGAATCCTGATCGGTACAGTCTCATCCCAATCCCAATGGG
131 P N L G R K V K A C S V L E N C P D R Y S L I P I P N G
469 TTCATAGTCCTCGGAGCGAGTTTAGAGAAATATACTACTGGGACAGCTACTGGATAATCGAAGTTTGTCTACAGT
157 F I V P G G R F R E I Y W D T Y W I I E G L L I S
547 GGAATGCCAGACAGCTAAGGCTAGTTGACAAATTAATCAACTATTAAAAAATTAGCGCATGTGCCAACCGG
183 G M P E T A A K G M I D N L I Q L L K K L G H V P N N G
625 AGCAGATACTATTACCGAGGACGAAGCGCCGCTTTGCTAACCGCTATGGTATCCCTTTATATCCGCGAACTGGC
209 S R Y Y Y Q E R S Q P P L L T A M V S L Y I R E T G
703 GATACTAAGTTTTTGAAGATAACATCGAGGCGCTGGAAGACAGTTACGTTACTGGCTTGACACTCAAATTGTTACT
235 D T K T K L D N I E A L E D E L R Y W L D T Q I V T
781 TTCGATAAAGGTGAGGAACTACACCCCTTTTAAGTACTACTTCCAAGTAAGACCTCGTCCGAGCTCTTACTAC
261 F D K E G E T H T L T L R Y V S P S K G P R P E S Y V
559 GAAGACTACAGTGGCGCAAAATTTCCAATTATAGCAGACAGACGGGAATATTACATTGACTTAAAAAGTGGCGCT
287 E D Y S S G A Q N F Q S N D R Q T E Y Y I D L K S A A
937 GAGATGGATGGGACTTTTCCAGCGCTTGGTTCATGAGCGCTGATGGAAATAACTCCGGTAACCTTTCCAGGATTAC
313 E S G W D F S T R W F M D A D G N N S G N L S T I H
1015 ACTAAGACATAGTGCGCTGTGGATTGAATGCTATTTTGGCAATGCTCTTCAAACAGTGGCCATTTCGAGAGGCCCT
339 T K D I V P V D L N A I F A N A L Q N M A Y F E G L
1093 TTGAAAAACCGCGTAGGCGCTCTCACTGGGCGCTATCTCGCTAAACAATGGAGACCATATCCCAAGAGGTTATTTGG
365 L K N T R R A S H W A Y L A K Q W R S T I Q E V F W
1171 GACGAGACGACGGCATATGGTACAGTATAGCTGAGCGCTCGGAAACACTCGCAAACTACTTCTACCAAGCAATGTG
391 D E D D G I W Y D Y S L S L G K H R K Y F Y P S N V
1249 GCTCCTCTTTGGATGGGAGCGGTGCAGAACAGATTAGTGAAGAAGCATTCGCTCGTCTTGGAAATTTGGCGAA
417 A P L W M G A V D K R L V K K H S A R V L E Y Y L A K
1327 TCGCAGCGGACTGGACTTCTTGGTGGTGTTCGCGTGTCTTTGATCAACGAGGGGAGCAATGGGACTTCGGTATGCA
443 S H L D F P G G G V P V S L I N S G E Q W D F P Y A
1405 TGGCCACCTCTAGTAAGTGTGTTGTGAATGCATTGGAGGCTTTAGATACTGAAGAGGGGAAGAAAGTGGCCTTCAGG
469 W P P L V S V V N A L E A L D T E G K K A V A F R
1483 GTTCTGAGACATGGGTGAGGGCATGCACAAGGTTTCCCTTGAAGATAGCAGATGTTTGAAGAAATGATGATGTCGAA
495 V A E T T W R A C H K G F L E S K Q M F E K Y D V E
1561 GTCCAGGCGAATTGGCGGTGTGGCGCAATTACTGTATACAGACGGCTTCGGTGGGCAACGGAGTGGTCTTGAA
521 V P G R G F G G G G G E Y Y V Q T G F G W A N G V V L E
1639 TTCTTAACAAGTACGGTAGGACGCTAACGGCAGAAGTATCACGAGGATGAGGGGCTCTTCATTA
547 F L T K Y G R T L T A A E D S P S D E G S S *

1 ATGATCTGGGAATATTATTAGGTTTCTCTTGCTGGTGCTGCGCTGCGGCAGACGGGAGCTATCTACCTCCCTACTGTTT

79 M M W N I L L G F L L V V A V A A D R S Y L E P T C F

27 AGTGAGATCTACTGCCATGGCCCATTTGCTGGACACCGTGCARAATTGGCGGGCCCTCTACAACGACTCCAAGACCTTCGTC

157 S E I Y C H G P L L D L T V Q M A G L Y N D S K T F V

53 GACATGAAGCTGAGGAATCTTCCTCCGTGACCATGGACCACTTCATCGAAATGATGACAGAGATGGCTCCGACGC

235 D M K L R N L P S V T M D D H F I E M M N R T R S Q P

79 TCGAAACGGGAGATCTTGCACTTTGCTCGAGAATTTTGAAGCAGAGGCGCTGAGTTTGAAACTGGGTGCCTGAA

313 S K A E I L Q F V L E N F E A G E A F E N W V P E

105 GACTGGGAAGCTGACCTCAATCTCCTTAAAGGAATAAAGGACCCCTTGCTGTCATGAGTGGGCTCCCGCTTGAAACA

391 D W K S D P Q F L L K G I K D P L L H E W A S R L N K

131 CTGGCTGTGCTCGGCGGAAGATGAAGCAGCATGTCAAGGAGAATCTTCGACCTCTACTCATCTCATCTGAGTGGAC

469 L W L V L I G G R K M K Q H V K E N F D L Y S I Y V D

157 AACCTTCATCATGCTTCAGGTGGCGGTTTCAGAGATTTCTACTACTGGGACTCATACTGGATCATCAAGGGCTCTCTA

547 N P I I V P G G R F R E F E Y Y W D S Y W I I K G L L

183 CTGTGGAGATGCGGCAGACTGCGAGGGGGATGGTCTCCAACTTATGGACGTGTGAAAGGATGGGCTTCATCCCC

625 L S E M R Q T A R G M V S N L M D V V E R M G F I P

209 AACGGTGGGAAGATATACGCCATAGAGTCCCAACCCCACTACTGATTCCTCATGAGTCAAGTCACTGATGGAGGAT

703 N G G R I Y Y A M R S Q P P L L I P M M K L L M D D

235 GGTGATCGGAGAGTTCCTCAAGTCACGGATGCACACCTGGACAGAGGATTCGACCTTCTGGGTCAACACCAACC

781 G E S E E F L L K S R I D T L K E F D F W V N N H T

261 ATAGACGTGGAGACTGAGGCGAAGATATACAAATTGGCTCGGTTTATTGACCAATCGCGGGGCGCGGGCGGAGAGC

859 I D V E H E G K I Y A K L R A F I D Q S R G R P E S

287 TATAAAGAGGATGTAGACATCGCCAAAACCTTTGACACGCAAGACAAGAAGGAGGAATTTGACCTGAGCTGAAGTCC

937 Y K E D V D I A K N F D T Q D K K E E L V I A E L K S

313 GCGGCTGAGTCAGGATGGGACTTTTCTCTAGATGGTTTATCATACCGGAAGCAATTAAGACAAATCTTATCTACAA

1015 A A E S G A W D F S S R W F I L N G T N K D N P Y L Q

339 TTGACACTTAAAGTAGCTGTCTACAAATTGACTGGGCGAGGAACCAATCGTGGTAATTTGACCAACCTCAAGACCCGT

1093 L A L K D K L L O M T G Q E P I I G N L T N L K T R

365 TCGATCGTGCCACTGACTTGAATGCAATGATGTGCGGCAACCGGAGGCTGATGAGGCAATTTTCATGCGGAAGTGAAC

1171 S I V P V D L A N A M M C G N A K L M S E F H A K A L N

391 AACCACTTGAAGCGGATTACTATAGGAAAATGCACGCAGACTATAAGGAGGCTGTGGAGAAGGTATTATGSCACGAG

1249 N Q L K A D Y Y R K M H A D Y K E A V E A V L W H E

417 GAGCTCGCGCTTGTGTAGACTTCAACCTGGAGTCAGGCGGGCGGAGACTACTTCTACCGCTCGAACATCAACCCCT

1327 D V G V G L D F N L E S G R R R D Y F Y P S N I N P

443 CTCTGGACTAACTCTAGCATAGTCCAGGAAGAAGTACTACGTCAACAGGTCATCAATTACTTGGATAGGTCAAG

1405 L W T N C Y D Q S R K E Y Y V N K V I N Y L D K V K

469 GTGGACATCTTTGAAGGTGGCGTCCCAACACCGTTTGAACATCGGCGGAACAGTGGGACTCCCCAACCGCTGGCOA

1483 V D I F E G G V P N T F E H T G E Q W D Y P N A W P

495 CCAACCATGCATATTATCATGAGGCTCGCCGACATGGGCTCGCGAGGCTGAAGATACGCCAAGAATATAGCC

1561 P T M H I F I M S L A D T G V P E A E R Y A K E I A

521 ACGAAGTGGGTCCGGTCCAACCTTCGAGGTCGGAAGCAGAAGGACGCTATGTTGGAAGAAAGTATGATGCTACTAGATT

1639 T K W V R S N F E V W K Q K D A M L E K Y D A T R F

547 GCGGGTTCGCGGGTGGCGGAGAGTACGTGCTGCAAACTGGTTTCGGTTGGACGAACTGGGTTATATTGGCCCTTTTG

1717 G G F G G G G E Y V V Q T G F G W T N G V I M A C G L

573 GACAATAACGGAACAGATTTCGGCAGCGGACGCTTCGCTACTGCGCTGCTGACTCTGGTGGGTTGACGGAGCC

1795 D K Y Y N C T I S A A D A F G T A P A D S G A V Y G A

599 CAGTGGGCGCTGGAGGGGTGGCCACGGCGTTACTGTCGTGATGGCTTCGGTTCAGCTGGAGCGTATAGGCTGA

609 H V G A G G V A T A L L V M A S V A A G A L G *

Figure S1. Characteristic analysis of GpTre1 and GpTre2 sequence. (A) and (B) are GpTre1 and GpTre2 nucleotide and deduced amino acid sequences, respectively.

Underlines are potential N-glycosylation sites predicted by PROSCAN. The gray background is the amino acid sequence of the putative catalytic domain. The red letters are signature sequences that might be involved in catalytic function. Double-underlines are signal peptide. The boxes are highly conserved glycine-rich regions. The blue letters are the putative transmembrane region predicted by TMHMM Server v. 2.0.