

Supplementary Information

Table S1. Primers used for fragment cloning, rapid amplification of cDNA ends, and quantitative real-time polymerase chain reaction analyses of *M. nipponense* catalase (*cat*), glutathione *S*-transferase (*gst*), Cu/Zn-superoxide dismutase (*sod*), and glutathione peroxidase (*gpx*).

Primer Name	Primer Sequence (5' to 3')	Remark	Reference
<i>cat</i> -F	CGCAGGTGCCCTTTGGATAC	<i>cat</i> fragment	
<i>cat</i> -R	GCCTTCTCCGCACTCAAAT	cloning	
<i>cat</i> -5gsp1	GTCTCGGATAAAGAACACGGGT	<i>cat</i> 5'-RACE	
<i>cat</i> -5gsp2	AGCAATAGGTGTCTTCTTCCCAA		
<i>cat</i> -3gsp1	CGTGTCTTTATCCGAGACCCT	<i>cat</i> 3'-RACE	
<i>cat</i> -3gsp2	ACCAGGTCACCATCCTTTTCTC		
<i>gst</i> -F	CTTCCCCAACCTTCCCTACTA	<i>gst</i> fragment	
<i>gst</i> -R	CGACGCCATGTACTTCTTGAT	cloning	
<i>gst</i> -5gsp1	CACCAGCATACCAGGGTTGTT	<i>gst</i> 5'-RACE	
<i>gst</i> -5gsp2	TTCTCAGATTCAGTCTTGCCACA		
<i>gst</i> -3gsp1	TGAATCTGAGAAAGTCCGTGTTG	<i>gst</i> 3'-RACE	
<i>gst</i> -3gsp2	AGCAATAGGTGTCTTCTTCCCAA		
5'-RACE Outer Prime	CATGGCTACATGCTGACAGCCTA	<i>cat</i> gene	
5'-RACE Inner Primer	CGCGGATCCACAGCCTACTGATGATCAGTCGATG	walking	
3'-RACE Outer Primer	TACCGTCGTTCCACTAGTGATTT	<i>gst</i> gene	
3'-RACE Inner Primer	CGCGGATCCTCCACTAGTGATTTCACTATAGG	walking	
<i>cat</i> -qRT-F	GAAGTGGGATTTGGTTGGCA	<i>cat</i> qRT-PCR	This study
<i>cat</i> -qRT-R	GGTCCGAGAAAAGGATGGTG		
<i>gst</i> -qRTF	GAAGTGGGATTTGGTTGGCA	<i>gst</i> qRT-PCR	This study
<i>gst</i> -qRTR	GGTCCGAGAAAAGGATGGTG		
Cu/Zn- <i>sod</i> -qRT-F	AGTTTCAGCCGTCTGTTCG	Cu/Zn- <i>sod</i>	Accession number:
Cu/Zn- <i>sod</i> -qRT-R	CACAGTGCTTACATCACCCCTTA	qRT-PCR	JX045662
<i>gpx</i> -qRT-F	CCTGGCTTTCCCCTGTAACC	<i>gpx</i> qRT-PCR	Accession number:
<i>gpx</i> -qRT-R	ACCGAGTCATCCGAAGGCA		HQ651155
β -actin-qRTF	AATGTGTGACGACGAAGTAG	β -actin	Sun <i>et al.</i> 2015 [26]
β -actin-qRTR	GCCTCATCACCGACATAA	qRT-PCR	

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1 gaaaagtctgggagtgagtgaggtacgtgacacagacaacacagcagtcagtcacacagacggtagcttagtgtccggagtgaaagtaca
M P R D R A A E Q L N E F K K
91 ctttttaaaagtctcaagtgatctatccacggctcctatatccacgATGCTCGCGACAGAGCTGCCGAGCAACTGAACGAGTTCAAGAAG
K Q T T P E V L T T S Q G C P L A D K L N S P T V G P R G P
181 AAGCAGACGACTCCTGAAGTCTTAACAACCTCGCAAGGATGTCCCCTGGCAGACAAGCTCAATCCCCGACAGTGGGTCCCAGAGGTCTT
I L L Q D I Q L L D E M A H F D R E R I P E R V V H A K G A
271 ATCCTCTGCAGGATATCCAACCTCTGGACGAGATGGCCCACTTCGACAGGGAGCGCATCCCGGAGAGAGTAGTGCACGCTAAGGGCGCT
G A F G H F E V T H D I T K Y C R A N I F S E I G K K T P I
361 GGTGCCCTTTGGACACTTCGAAGTACCCATGACATTACGAAGTATTGCAGAGCCAACATATTAGTGCAGATTGGGAAGAAGACACCTATT
A V R F S T V G G E S G S A D T A R D P R G F A V K F Y T E
451 GCTGTAAGATTCTACTGTAGGAGGTGAAAGTGGTTCTGCAGACACGGCTAGGGATCCTCGTGGCTTCGCTGTCAAGTTCTACACCGAA
E G N W D L V G N N T P V F F I R D P I L F P S L I H T Q K
541 GAAGGGAACCTGGGATTGGTTGGCAACAACACACCCGTGTTCTTTATCCGAGACCCTATTCTTTCCCTTCACTCATCCACACTCAAGAAG
R N P A T H L K D P D M F W D F I T L R P E T T H Q V T I L
631 AGGAATCCAGCAACACACCTGAAGGACCCGACATGTTCTGGGACTTCATAACCTGAGACCTGAGACCACGACACAGGTCAACCATCCTT
F S D R G G T P D G Y R H M N G Y G S H T F K L V N T E G K A
721 TTCTCGGACCGAGTCTCTGATGGCTACAGGCATATGAATGGTATTGGTTCTCACACTTCAAGCTGGTGAATACTGACATGAAAGGAAAAGCC
V Y C K F H Y K T D Q G I R N L S A E K A D D L A G T D P D
811 GTTTACTGTAAATCCACTACAAGACTGACCAAGGAATCAGAAATTTGAGCGCGAGAAGGCCGACGACTTAGCTGGAAGTACCCCTGAC
Y A I R D L Y N A I E G G D Y P S Y T M Y I Q V M T Y E E A
901 TATGCTATTCGTATTGTACAACGCTATTGAAGCGGAGACTACCCATCATATACTATGTACATCCAGGTATTGACATGATGAAGAGGCT
E K H R F N P F D L T K V W P H K D F P L I P V G R L T F D
991 GAGAAGCACCGGTTCAATCCTTTGACTTGACCAAGTGTGGCCACACAAGGATTTCCCTCTCATCCCTGTGGGACGCCTCACTTTTGAC
R N P R N Y F A E V E Q I A F S P A N M V P G I E A S P D K
1081 AGAAATCCTAGGAACACTTTGCAGAGGTGGAACAGATTGCCTTTCTCCAGCAAATATGGTCCCTGGCATCGAAGCATCACCCGACAAG
M L Q G R L F S Y N D T H R H R L G A N Y T Q I P V N C P Y
1171 ATGTTGCAAGGACGCCTTTTCTCTACATGACCCATCGCCATAGGCTGGGCGCAAACACTACACTCAGATACCTGTCAATTGTCTCTAT
R S R A R A N Y Q R D G P M T V D Y N Q E S A P N Y F P N S F
1261 CGCTCTCGTGTAGGAACACTACGCGAGATGGGCCAATGACCTTCGATTACAAACAGGAAAGTGTCCCAACTAGTCCCAACAGCTTC
S G P M D C K R H S E S T F T C S T D V N R Y N S G D E D N
1351 TCTGGACCTATGGATTGTAAAGGCATTGAGAGTCCACTTTCCTGCTGACCGACGTTAATCGGTACAACAGCGCGATGAAGATAAC
F T Q A G N L F R H V M N E E E R Q R L V S N I A G H L V N
1441 TTTACTCAAGCTGGTAAGTGTGTAGACATGTCATGAACGAGAGGAACGCCAGCGGCTAGTCAGCAACATTGCTGTCACCTCGTGAAC
A Q K F L Q D R A I N N F S Q A D P E Y G A G I R G T A E K
1531 GCACAGAAGTTCCTGCAAGATCGTCCATCAACAACCTTCAGCAAGCTGATCCTGAGTACGGTGTGGAATTCGACGGGCTCTTGAAAAA
L Q K A A A S H P V N L V A A P A S N A K L
1621 CTACAGAAGGCAGCGCTCACCTGTGAACCTTGTAGCTGCTCCTGCTTCAATGCCAAGCTATTAaaaaaaaaa

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Figure S1. Nucleotide and amino acid sequences of the full length cDNA of the *M. nipponense* catalase (*cat*) gene. The translated amino acid sequence is shown in standard one-letter code below the nucleotide sequence. The initiation codon and stop codon are indicated in the box.

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1 gaaaagagtggttgaaattggctaaccggtaacaagtcagttgagagcgggctttttgtaaacaccggatcgagaactctttcggttggt
M S P
91 ttatctgtgcatttggcttttaattaggtcttctcagcacaattgtttggtgtattaccaataccagtttaattcttgcgaagATGTCGC
T L A Y W N I R G L A Q P I R L L L E Y T G T E F E D K M Y
181 CAACTCTTGCTACTGGAACATTGAGGTCTTGCCCGCCTATTAGACTGCTGCTGGAATATACTGGAAGTGTGAAGACAAGATGT
E C G P A P K F D K S C W F D I K Y S L G L D F P N L P Y Y
271 ATGAATGTGGACCGCCCAAGTTTGACAAGTCTTGCTGGTTTGATATTAAGTACTCCTTAGGCCTCGACTTCCTCAACCTCCCTTACT
I D G D V K V T Q S N I M R Y I A R K H D L C G K T E S E
361 ACATTGATGGAGATGTGAAAGTAACCCAGAGCAATGCCATTATGCGGTACATTGCAAGAAAGCATGATCTATGTGGCAAGACTGAATCTG
K V R V D I M E N Q S M D F R N G F V R L C Y V D F D T Q K
451 AGAAGTCCGTGTTGATATTATGGAACCAATCAATGAGCTTCAGGAATGGTTTGTTCGACTGTGCTATGTAGATTTTGATACCCAGA
Q T Y L E A L P T T L K L F S T F L G E Q P W Y A G D N I T
541 AGCAGACCTACTTAGAGGCTTTACCCACTACATTGAAGCTGTTCTCAACATTCTTGGTGAACAACCCTGGTATGCTGGTGATAATATCA
F V D F I M Y E L I D Q H L Q L D P N L L K D F K N L E D F
631 CTTTGTGGATTTCATTATGTATGAACCTATTGATCAGCATCTGCAATTAGACCCAAACCTACTTAAGGATTTCAAGAACCTTGAAGACT
Q K R F E E L E P I K K Y M A S S R F M K S P L N N K M A K
721 TCCAGAAGCGTTTGAAGAATTAGAACCATCAAGAAGTACATGGCCTCCTCAGATTATGAAGTCTCCACTTAATAACAAAATGGCAA
F G N
811 AGTTTGGAAACCTTcttgggttggaagaccataaatgttttaacttttttcttacaatacaaatgtgcagcattataagtataaaag
901 ttcttaatttagtgagtacatatatgctaaagaaaatagtaatttccagtttgacgtctgttatattatactaggtaaaccaaataatg
991 ataaatattgtttctcgaatagtgtaattttgttttgagaaattgtgcaaaatttattgaaggtcttatttgaagacactgtttgat
1081 ataaacagctttgaaataaaagggtttaagtaaaaaaaaaa

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Figure S2. Nucleotide and amino acid sequences of the full length cDNA for glutathione *S*-transferase (*gst*) in *M. nipponense*. The translated amino acid sequence is shown in standard one-letter code below the nucleotide sequence. The initiation codon and stop codon are indicated in the box. The polyadenylation signal is shaded light gray.

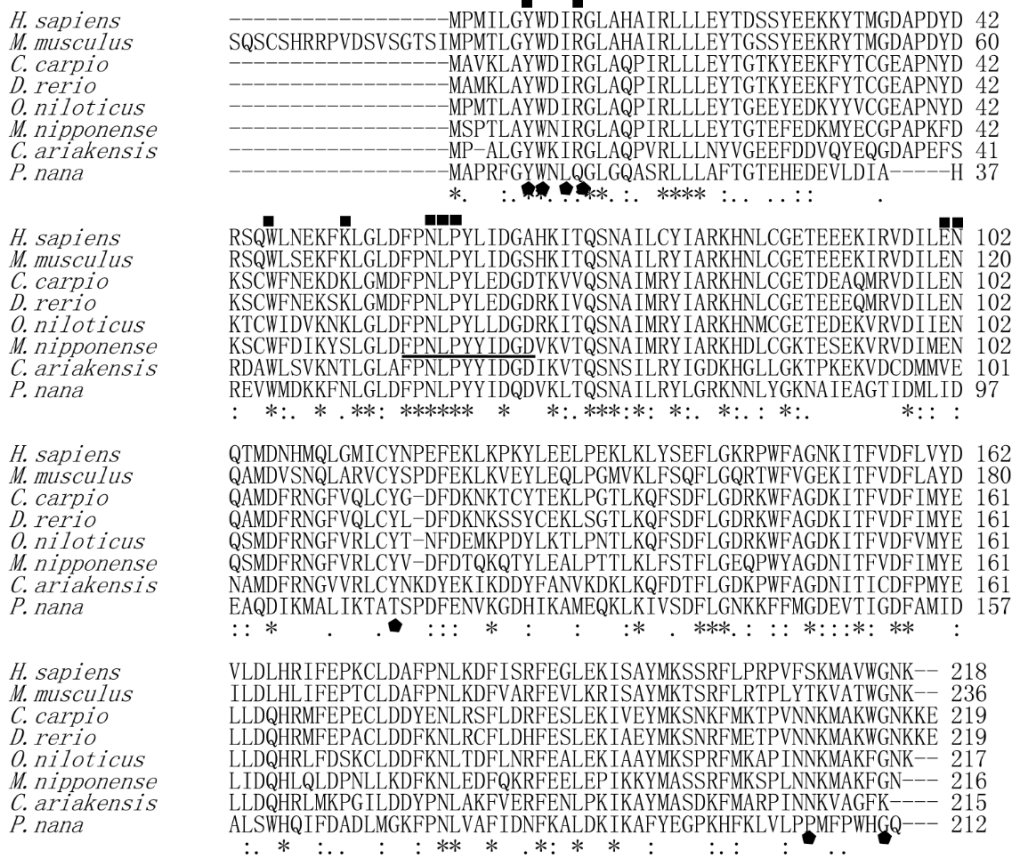


Figure S4. Comparison of *M. nipponense* glutathione S-transferase (GST) amino acid sequences among vertebrates and invertebrates. Accession numbers of the sequences used to compare amino acid residues are as follows: *Homo sapiens*, M63509; *Mus musculus*, X65021; *Cyprinus carpio*, DQ411212; *Oreochromis niloticus*, EU107284; *Crassostrea ariakensis*, EU908270 and *Paracyclops nana*, HQ115574. “■” indicate G-sites and “●” indicate H-sites. Symbols below the amino acid sequences indicate invariant (*), strongly conserved (:) or conserved residues (.).