

Table S1. Primers designed for sequencing of cytosolic malate dehydrogenase (cMDH)

cDNAs

Primer ID	Description	Sequences (5'–3')
GSP-Ma-1	3'-RACE	CAGCGACCAGCCAATCAT
GSP-Ma-2	3'-RACE	ATCCCTACCTGTGACGAGAAA
MaRa-F1	5'-ORF primer	CGTCAACCCATCTTCTGCT
MaRa-F2	5'-ORF primer	GCAGCGACCAGCCAATC
MaRa-R1	3'-ORF primer	CTTTATGCGTATGACACCGTTA
MaRa-R2	3'-ORF primer	CAAACCCACGCAACTGTCTA

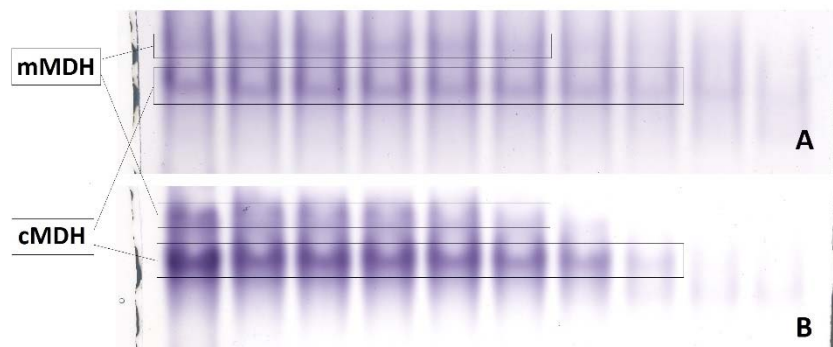
Table S2. The accuracies of the molecular modeling for *EmcMDH* and *ErcMDH* and the template structure 5MDH-A

Program	Overall quality factor (%)		
	<i>EmcMDH</i>	<i>ErcMDH</i>	5MDH-A
PROCHECK	99.7	99.7	99.3
Verify3D	90.9	90.0	88.3
ERRAT	81.7	81.7	92.9

PROCHECK: the percent of residues in most favored regions, additional allowed regions and generously allowed regions; Verify3D: pass, at least 80% of the amino acids have scored ≥ 0.2 in the 3D/1D profile; ERRAT: for low resolutions (2.5 to 3 Å), the average overall quality factor is around 91%.

EmcMDH, the cytosolic malate dehydrogenase from *Echinolittorina malaccana*; *ErcMDH*, the cMDH from *E. radiata*; 5MDH-A, a template structure file in PDB format of porcine (*Sus scrofa*) cMDH (Chain-A).

Fig. S1. Native-polyacrylamide gel electrophoresis (PAGE) of two isoforms of malate dehydrogenase (MDH) from *Echinolittorina malaccana* (A) and *E. radiata* (B).



cMDH, cytosolic isoform of MDH; mMDH, mitochondrial isoform of MDH.

Fig. S2. Nucleotide sequence alignments of the 999bp coding regions of *cmdh* (cytosolic malate dehydrogenase) cDNAs from *Echinolittorina malaccana* and *E. radiata*.

<i>E. malaccana</i>	ATGAGTGAACCAGTGAAAAGTATGCGTAACTGGTGTGCTGGCCAGATTGCTTACTCCCTGCTGTACTCCATCGCCAAGGGAGATGTCTTTGGCAGCGACCAG	102
<i>E. radiata</i>	-----t-----c-----a-----	102
<i>E. malaccana</i>	CCAATCATCCTGACCCCTGCTGGACATTGCCCCATGGAGGGTGTCTCAATGGAGTGGTCATGGAGCTCATGGACTGTGCCATGCCCTCCTCAAAGAGGTG	204
<i>E. radiata</i>	-----t-----a-----g----c--c-----	204
<i>E. malaccana</i>	ATCCCTACCTGTGACGAGAAAGTGGCCTTCAAGGATATTGATGCGGCCTTCTGGTGGGCGCCATGCCGCGTCGTGAGGGCATGGAGCGCAAGGACCTGCTG	306
<i>E. radiata</i>	-----c-----a-----a-----t-----	306
<i>E. malaccana</i>	GCAGCCAACATCAAGATCTTCAAGTCCCAGGGCGGGCGCCCTTGACACTGTGGCCAAGAAGACCGTCAAGGTGGTTGTGGTGGGCAACCCTGCCAACACCAAC	408
<i>E. radiata</i>	-----tct--t-----c--t-----a-----t-----	408
<i>E. malaccana</i>	GCTCTGATCTGCAGCAAGTACGCCCTTCCATTCTAAGGAGAACTTCTCCTGTCTCACCAGACTGGACCAGAACCGTGCCCAGGCACAGATTGCGGCTCGC	510
<i>E. radiata</i>	-----a-----t-----t-----a-----a-----a---	510
<i>E. malaccana</i>	TTGGGCATTCCCAACAGTGTCTGTTAGTAACGTCATCATCTGGGGCAATCACTCATCCACACAGTTCCTGACGTTTCGTACGCCAAGGCCATCGTCAACGGC	612
<i>E. radiata</i>	----t----t-----c-----a-----g--a----c--t-----t-----t-----	612
<i>E. malaccana</i>	AAAAACAGTGCCTGTCCCTGAGGCTGTCAAGGATGACAACACTTGAAGAATGAATTTTGGACAACAGTGCAGAAGCGTGGTGGGGAAGTGATCAAGGCCCGT	714
<i>E. radiata</i>	-----c--a-----g-----t-----	714
<i>E. malaccana</i>	AAGCTGTCCAGTGCAATGTCAGCTGCCAAGGCTACAGCCGATCACATGCGTGACTGGTGGTTTGGAACTCAGGGGACAACCTGGGTGTCCATGGGCGTGTTT	816
<i>E. radiata</i>	-----c-----c-----t-----	816
<i>E. malaccana</i>	TCCACGGGAGCCTACGGCATCCCAGAAGGATCATGTACAGTACCCAGTGCGCATTGCCAACAAACAGTGAAGATCGTGGAGGGACTGGAGATCAACGAT	918
<i>E. radiata</i>	-----t-----	918
<i>E. malaccana</i>	TTTGCTCGTGAGAAGATGGACCTGACGGCCAAAGAGCTGTGTGAGGAGAGGCCATGGCTGAAGAAATCTGCAACCAGTGA	999
<i>E. radiata</i>	-----c-----c-----g-----c-----	999