

## Supplementary materials

### Molecular characteristics of the malate dehydrogenase (MDH) gene family in *Spirometra mansonii* (Cestoda: Diphylobothriidea)

**Table S1** Summary of malate dehydrogenase for medical tapeworm and trematode.

**Table S2.** The putative motifs of *SmMDH*.

**Table S3.** Primers sequences designed for qRT-PCR.

**Figure S1.** *SmMDH1* structural and functional prediction results. (a) hydrophobicity prediction; (b) transmembrane prediction; (c) functional structure domain prediction; (d) phosphorylation site prediction; (e) signal peptide prediction; (f) secondary structure prediction, the yellow indicates strand, the purple represents helix; (g) 3D structure prediction.

Table S1. Summary of malate dehydrogenase for medical tapeworm and trematode.

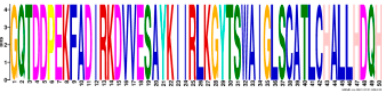






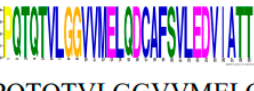


| Class   | Family            | Genus                    | SPECIES                  | Sequence summary | SEQUENCE ID   |
|---------|-------------------|--------------------------|--------------------------|------------------|---|
| Cestoda | Diphyllbothriidae | <i>Dibothriocephalus</i> | <i>D. latus</i>          | 3                | DILT_0001486601, DILT_0001648601, DILT_0000453201   |
|         |                   | <i>Spirometra</i>        | <i>S. mansoni</i>        | 8                | SmMDH1_SERJ2_LOCUS4602, SmMDH2_SPER_0002854401, SmMDH3_SPER_0003366401, SmMDH4_SERJ2_LOCUS18211, SmMDH5_TRINITY_DN32812_c0_g1_i1, SmMDH6_TRINITY_DN32812_c0_g1_i9, SmMDH7_TRINITY_DN32812_c0_g1_i10, SmMDH8_TRINITY_DN32812_c0_g1_i11 |
|         |                   | <i>Schistocephalus</i>   | <i>S. solidus</i>        | 5                | SSLN_0000919501, SSLN_0001553101, SSLN_0001884001, SSLN_0001588801, SSLN_0001017101   |
|         | Taeniidae         | <i>Echinococcus</i>      | <i>E. canadensis</i>     | 3                | EcG7_04628, EcG7_08839, EcG7_08021  |
|         |                   |                          | <i>E. granulosus</i>     | 8                | EgrG_00578, EgrG_000893100, EgrG_000517200, EgrG_07281, EgrG_001185000, EgrG_000417100, EgrG_07010, EgrG_08628  |
|         |                   |                          | <i>E. oligarthrus</i>    | 1                | Eoli_000517200  |
|         |                   |                          | <i>E. multilocularis</i> | 4                | EmuJ_000893100, EmuJ_001185000, EmuJ_000417100, EmuJ_001185100  |
|         |                   | <i>Taenia</i>            | <i>T. asiatica</i>       | 9                | TASK_TASs00004g01136, TASK_0000488101, TASK_0000266701, TASK_TASs00143g08337, TASK_0000036701, TASK_TASs00010g02429, TASK_0000299001, TASK_TASs00010g02428, TASK_0000644501   |
|         |                   |                          | <i>T. multiceps</i>      | 3                | Tm1G001281, Tm1G001282, Tm1G001697  |
|         |                   |                          | <i>T. saginata</i>       | 4                | TsAs00003g01040, TsAs00063g07180, TsAs00026g04349, TsAs00026g04348  |

|           |                  |                      |                         |    |   |
|-----------|------------------|----------------------|-------------------------|----|---|
|           |                  |                      | <i>T. solium</i>        | 4  | TsM_000048200, TsM_000657300, TsM_000267800, TsM_000460300  |
|           |                  | <i>Hydatigera</i>    | <i>H. taeniaeformis</i> | 5  | TTAC_0000405101, TTAC_0000780101, TTAC_0000298901, TTAC_0000412301, TTAC_0001013001   |
|           | Hymenolepididae  | <i>Hymenolepis</i>   | <i>H. diminuta</i>      | 11 | HDID_0000660801, HDID_LOCUS6753, HDID_0000060201, HDID_0000060301, HDID_LOCUS8449, HDID_0000561501, HDID_LOCUS6544.1, HDID_LOCUS6544.2, HDID_LOCUS2678, HDID_LOCUS8540, HDID_0001029401   |
|           |                  |                      | <i>H. nana</i>          | 5  | HNAJ_0000045201, HNAJ_0000045301, HNAJ_0000388801, HNAJ_0000594201, HNAJ_0001192401   |
|           |                  |                      | <i>H. microstoma</i>    | 3  | HmN_000258300, HmN_000063000, HmN_000063100   |
|           | Mesocestoididae  | <i>Mesocestoides</i> | <i>M. corti</i>         | 11 | MCU_0001007601, MCU_008646, MCU_003955_RA, MCU_003955_RB, MCU_006567_RA, MCU_006567_RB, MCU_006567_RC, MCU_009062, MCU_0000749901, MCU_014229, MCU_0000835901   |
| Trematoda | Schistosomatidae | <i>Schistosoma</i>   | <i>S. japonicum</i>     | 13 | Sjp_0041910, Sjp_0024400, Sjp_008117.1, Sjp_008117.2, Sjp_008117.3, Sjp_010981.1, Sjp_010981.2, Sjp_000090.1, Sjp_000090.2, Sjp_000090.3, Sjp_000090.4, Sjp_000090.5, Sjp_000090.6  |
|           |                  |                      | <i>S. haematobium</i>   | 15 | SHAE1_78140, SHAE2_80780, SHAE_MS3_00007547.1, SHAE_MS3_00007547.2, SHAE2_30640, SHAE_MS3_00005651.1, SHAE_MS3_00005651.2, SHAE_MS3_00005651.3, SHAE1_29410, SHAE2_57410.1, SHAE2_57410.2, SHAE2_57410.3, SHAE2_57410.4, SHAE1_55450, SHAE_MS3_00010820 |
|           |                  |                      | <i>S. mansoni</i>       | 4  | Smp_035270, Smp_047370, Smp_070860.1, Smp_070860.2  |
|           |                  |                      | <i>S. margrebowiei</i>  | 5  | SMRG1_76940, SMRG1_28460.1, SMRG1_28460.2, SMRG1_28460.3, SMRG1_54720   |

|  |                 |                        |                         |    |   |
|--|-----------------|------------------------|-------------------------|----|---|
|  |                 |                        | <i>S. mattheei</i>      | 5  | SMTH1_31430.1, SMTH1_31430.2, SMTH1_84930.1, SMTH1_84930.2, SMTH1_60330   |
|  |                 |                        | <i>S. rodhaini</i>      | 11 | SRDH2_28760, SRDH1_74570, SRDH1_39570, SRDH1_48420.1, SRDH1_48420.2, SRDH1_48420.3, SRDH2_55100, SRDH2_78190.1, SRDH2_78190.2, SRDH2_78190.3, SRDH2_78190.4 |
|  |                 |                        | <i>S. bovis</i>         | 10 | SBOV2_75390.1, SBOV2_75390.2, SBOV1_39370, SBOV2_39230, SBOV_DC041_0008291, SBOV1_51080, SBOV2_51440, SBOV_DC041_0012974, SBOV1_74870, SBOV_DC041_0002698   |
|  |                 |                        | <i>S. curassoni</i>     | 8  | SCUR1_28450, SCUR1_75730.1, SCUR1_75730.2, SCUD_0000539301, SCUD_0001337701, SCUD_0001603901, SCUD_0002203501, SCUR1_54230                                  |
|  |                 |                        | <i>S. intercalatum</i>  | 6  | SINT1_75170, SINT2_74490, SINT2_52660, SINT1_54060, SINT2_27250, SINT1_28460  |
|  |                 |                        | <i>S. guineensis</i>    | 4  | SGUI1_76760, SGUI1_28050.1, SGUI1_28050.2, SGUI1_54400  |
|  |                 |                        | <i>S. spindale</i>      | 3  | SSPN1_73470.1, SSPN1_73470.2, SSPN1_27270   |
|  |                 |                        | <i>S. turkestanicum</i> | 3  | STRK1_73010, STRK1_51400, STRK1_27030,  |
|  |                 | <i>Trichobilharzia</i> | <i>T. regenti</i>       | 4  | TREG1_105430, TREG1_70880, TREG1_48600.1, TREG1_48600.2   |
|  |                 |                        | <i>T. szidati</i>       | 5  | TSZD1_103560, TSZD1_71860, TSZD1_103540, TSZD1_103580, TSZD1_103500   |
|  |                 | <i>Heterobilharzia</i> | <i>H. americana</i>     | 5  | HAMR1_95450, HAMR2_84560, HAMR2_48220, HAMR2_58740, HAMR1_66780   |
|  | Opisthorchiidae | <i>Clonorchis</i>      | <i>C. sinensis</i>      | 6  | CSKR_110103, CSKR_103326, CSKR_csin102558, CSKR_csin101489, CSKR_csin112591, CSKR_111940  |

|  |                  |                          |                        |   |   |
|--|------------------|--------------------------|------------------------|---|---|
|  |                  |                          | <i>C. felineus</i>     | 5 | CRM22_008362, CRM22_002201.1, CRM22_002201.2, CRM22_008422.1, CRM22_008422.2                |
|  |                  |                          | <i>C. viverrini</i>    | 3 | T265_16243, T265_04260, T265_05466  |
|  | Fasciolidae      | <i>Fasciolopsis</i>      | <i>F. buski</i>        | 3 | FBUS_11060, FBUS_08099, FBUS_02962  |
|  |                  | <i>Fasciola</i>          | <i>F. gigantica</i>    | 7 | FGIG_07754, FGIG_06624, FGIG_06623, FGIG_07755, FGIG_00665, FGIG_08365, FGIG_05200          |
|  |                  |                          | <i>F. hepatica</i>     | 6 | Fhe_859_0.47, Fhe_377_0.75, Fhe_D915_009078, Fhe_120_0.22, Fhe_D915_010544, Fhe_D915_004345 |
|  | Paragonimidae    | <i>Paragonimus</i>       | <i>P. westermani</i>   | 1 | DEA37_0012094   |
|  | Echinostomatidae | <i>Echinostoma</i>       | <i>E. caproni</i>      | 3 | ECPE_0000453101, ECPE_0001285701, ECPE_0001684501   |
|  | Microphallidae   | <i>Atriophallophorus</i> | <i>A. winterbourni</i> | 3 | jcf_7180000222489_0.19, jcf_7180000242691_0.4, jcf_7180000271253_0.4                        |
|  | Dicrocoeliidae   | <i>Dicrocoelium</i>      | <i>D. dendriticum</i>  | 6 | DDND1_112850.1, DDND1_112850.2, DDND1_112850.3, DDND1_112850.4, DDND1_112850.5, DDND1_32360 |
|  | Gyrodactylidae   | <i>Gyrodactylus</i>      | <i>G. salaris</i>      | 1 | scf_7180006950882_0.1   |

**Table S2.** The putative motifs of *SmMDH*.

| Motif | Consensus sequence   | Length | No. of MDH proteins | e-value              |
|-------|--|--------|---------------------|----------------------|
| 1     |  <p>GQTDDPEKFADIRKDVVESAYKIIRLKGYTSWAIGLSCATLCHA<br/>LLHDQH</p> | 50     | 4                   | 4.8e-105             |
| 2     |  <p>MSIVNLELSEKETKRIQSSAE</p>                                   | 21     | 8                   | 1.6e-043<br>1.6e-043 |
| 3     |  <p>SILPVVTNVKGLFGIDYDVFLSMPCVISS</p>                           | 29     | 8                   | 1.1e-052             |
| 4     |  <p>TRPDJPKFNFSVLARLDHARAKYQPEAKJGVVTNPVNNVIP</p>              | 41     | 4                   | 2.5e-020             |
| 5     |  <p>ILNAASSDLVW</p>   | 11     | 4                   | 7.6e-011             |
| 6     |  <p>WGNHGNSQFPDISQA</p>                                       | 15     | 4                   | 8.5e-011             |
| 7     |  <p>MLADVYPK</p>  | 8      | 4                   | 2.7e-008             |
| 8     |  <p>PQTQTVLGGVVMELQDCAFSVLEDVIATT</p>                         | 29     | 2                   | 1.3e-006             |
| 9     |  <p>QGEALDKYAKKTVKVLVVGNPANTNALMM</p>                         | 29     | 2                   | 8.6e-005             |
| 10    |  <p>MTGALKVLITGAAGQIAYNLS</p>                                 | 21     | 2                   | 3.1e-001             |

**Table S3.** Primers sequences designed for qRT-PCR.

| Gene                      | Primer name                | Sequence (5'-3')     | Product size (bp) |
|---------------------------|----------------------------|----------------------|-------------------|
| SERJ2_LOCUS4602           | SERJ2_LOCUS4602-F          | CCAAGAAGACTGTGAAGGT  | 233               |
|                           | SERJ2_LOCUS4602-R          | GTGGGAGATGTCAGGAAAC  |                   |
| SPER_0002854401           | SPER_0002854401-F          | AATCGCCTACAATCTTTCC  | 121               |
|                           | SPER_0002854401-R          | CATTACAACACCACCCAAG  |                   |
| SPER_0003366401           | SPER_0003366401-F          | GTTGCCTCCCTGACTCTT   | 271               |
|                           | SPER_0003366401-R          | TACGCACATCCAAACCCT   |                   |
| SERJ2_LOCUS18211          | SERJ2_LOCUS18211-F         | ATTGCCGCCGAACTGATG   | 230               |
|                           | SERJ2_LOCUS18211-R         | AACTGCTCACGCTCCTCC   |                   |
| TRINITY_DN32812_c0_g1_i1  | TRINITY_DN32812_c0_g1_i1F  | CGATAGCCCAAGAGGTGT   | 174               |
|                           | TRINITY_DN32812_c0_g1_i1R  | GCATTTCAAGTTGCCGTAT  |                   |
| TRINITY_DN32812_c0_g1_i9  | TRINITY_DN32812_c0_g1_i9R  | GCCGATAGCCCAAGAGGT   | 172               |
|                           | TRINITY_DN32812_c0_g1_i9F  | GAGCGTTGCCGTATGGAG   |                   |
| TRINITY_DN32812_c0_g1_i10 | TRINITY_DN32812_c0_g1_i10F | GCCGATAGCCCAAGAGGT   | 172               |
|                           | TRINITY_DN32812_c0_g1_i10R | GAGCGTTGCCGTATGGAG   |                   |
| GAPDH                     | GAPDH-F                    | AGCAACCTCGTTGATGTCGT | 97                |
|                           | GAPDH-R                    | TGAATTGACCGTGGGTGGAG |                   |

