

Supporting Information

Table S1. Haplotype data in three host crab species (*Cancer irroratus*=native [white shading]; *Carcinus maenas*=historical invader [light grey shading]; *Hemigrapsus sanguineus*=contemporary invader [dark grey shading]) in the Northwest Atlantic with additional sequence data included from Northeast Atlantic populations where *C. maenas* is native. The first column is the haplotype number, followed by the lineage (clade) from Fig. 4. The putative trematode species is listed next (MT=*Microphallus turgidus*; MS=*M. similis*; GA=*Gynaecotyla adunca*; MP=*M. primas*; UNK=unknown). Sites within the sampling region (New England, USA) are listed next; followed by additional sequences from past work (Blakeslee et al. 2020) in Newfoundland, New Brunswick, Nova Scotia, and Europe. OIME=Orr Island, ME; SCME=Camden, ME; RH=Rye Harbor, NH; JEL=Durham, NH; SLMA=Scituate Lighthouse, MA; GMA=Gloucester, MA; CC=Woods Hole, MA; HM=Harbor Main, Newfoundland; HLY=Holyrood, Newfoundland; FT=Foxtrap, Newfoundland; FOX=Fox Harbor, Newfoundland; NH=North Harbor, Newfoundland; FH=Fairhaven, Newfoundland; YRM=Yarmouth, Nova Scotia; CLH=Cole Harbor, Nova Scotia; KJI= Kejimikujik Park, Nova Scotia; STA=St. Andrews, New Brunswick; SW=Tjarno, Sweden; DEN=Esbjerg, Denmark; NIOZ=Texel, Netherlands; BI=Ireland and England.

HAP #	LINE-AGE	PUTA SPP	New England, USA									Newfoundland, Canada									New Brunswick & Nova Scotia, Canada					Europe				Freq								
			CI OI ME	CM SC ME	CM RH	CM JEL	CI SL MA	CM SL MA	HS SL MA	CM GMA	CM CC	CI HM	CI H L Y	CI FT	CI FO X	CM FO X	CI NH	CM NH	CI FH	CM FH	CM GU N	CM YR M	CM CL H	C M K JI	CM ST A	LS SW	CM DE N	CM NIO Z	CM BI									
1	A.1	UNK												1																						0.0050		
2	A.1	UNK	1							1																										0.0151		
3	A.1	UNK																																		0.0101		
4	A	UNK		3		2		1		4																										0.0603		
5	B	MS	3	3	1	2	3	3			5	5	1	5	2	8	2	5	4	1	2	6	1										11	2		29	0.5226	
6	B	MS												2																						0.0101		
7	B	MS																																		0.0503		
8	B	MS													1																					0.0050		
9	B	MS																																		0.1156		
10	B	MS																																		0.0050		
11	A.4	GA													2																					0.0101		
12	A.4	GA																																		0.0101		
13	A.4	GA																																		0.0050		
14	A	UNK																																		0.0050		
15	C	MP																																		0.0201		
16	B	MS																																		0.0101		
17	B	MS																																		0.0050		
18	A	UNK																																		0.0050		
19	C	MP																																		2	0.0101	
20	A	UNK																																		6	0.0302	
21	B	MS																																		2	0.0101	
22	B	MS																																		1	0.0050	
23	C	MP																																			1	0.0050
24	C	MP																																			1	0.0050
25	C	MP																																			1	0.0050
26	A	UNK																																			1	0.0050
27	A	UNK																																			1	0.0050
28	B	MS																																			1	0.0050
29	A.3	UNK								1																											0.0050	
30	A	UNK								5																											0.0251	

31	A.4	GA						1																									0.0050
32	A.3	UNK						1																									0.0050
33	A.2	MT?						1																									0.0050
TOTALS			4	6	1	4	3	4	9	5	5	5	3	5	2	12	6	10	9	2	11	17	8	1	3	15	6	3	40	199			

Table S2. Major clades and subclades identified in phylogenetic analyses of microphallid trematode samples in our study along with top BLAST results (<https://blast.ncbi.nlm.nih.gov/Blast.cgi#>) represented. The putative trematode species for clades, if known, are also listed per Table S1 and Figure 4. The % identity (% Ident) and % cover for each record is also listed along with the reference for the sequences found during BLAST searches on Genbank.

Clade	Representative Sequence	Putative Trem Species	BLAST Results	Accession Numbers	% Ident	% Cover	Reference
A.1	TCCTTTAACGAGGAACAACACTGGAGGGCAAGTCTGG TGCCAGCAGCCGCGGTAACCTCCAGCTCCAGAAGCG TATATTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTG GATCTGGGTCGCATGGCTACGTGCCGTAGCTTGTA TTCTCGGCTTGGCTACGGTTGGGTCGGGTTTGTGA GTCGGTTTCGTGGCTGTGTAGCCTTTCTGCCGTGT CTGTTTCGACAGGTGCTGATGGTTCTTCCGTTGGCA TGCTTCCGAATGCCTTTAACCAGGTTGTCGGGGGCG GACGGCACGTTTACTTTGAACAAATTTGAGTGCTCA AAGCAGGCCTATGCCTGAAAATTTCTGCATGGAATA ATGGAATAGGACTTCGGTTCTATTTTGGTTTTTC GGATCCGAAGTAATGGTTAAGAGGGACAGACGGGG GCATTTGTATGGCGGTGTTAGAGGTGAA	UNK	<i>Microphallus</i> sp. HAP1- HAP4 haplotype MICROPHALLIDSP_ HAP1 - MICROPHALLIDSP_ HAP4 small subunit ribosomal RNA gene, partial sequence	MT025341.1 - MT025344.1	99.56% - 100.00%	100%	Blakeslee et al. (2020a)
			<i>Microphallus</i> sp. HAP20- HAP 21 haplotype MICROPHALLIDSP_ HAP20 - MICROPHALLIDSP_ HAP21 small subunit ribosomal RNA gene, partial sequence	MT025350.1 - MT025351.1	98.02% - 98.24%	100%	Blakeslee et al. (2020a)
A.2	TCCTTTAACGAGGAACAACACTGGAGGGCAAGTCTGG TGCCAGCAGCCGCGGTAACCTCCAGCTCCAGAAGCG TATATTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTG GATCTGGGTCGCATGGCTACGTGCCGTAGCTTGTA TTCCCGTCTTGGCTACGGTTGGGTCGGGTTTGTGA GTCGGTTTCGTGGCTGTGTAGCCTTTCTGCCGTGT CTGTTTCGACAGGTGCTGATGGTTATTCCGTTGGCA TGCTTCCGGATGCCTTTAACCAGGTTGTCGGGGGCG GACGGCACGTTTACTTTGAACAAATTTGAGTGCTCA AAGCAGGCCTATGCCTGAAAATTTCTGCATGGAATA ATGGAATAGGACTTCGGTTCTATTTTGGTTTTTC GGATCCGAAGTAATGGTTAAGAGGGACAGACGGGG GCATTTGTATGGCGGTGTTAGAGGTGAA	MT?	<i>Microphallus</i> sp. HAP4 haplotype MICROPHALLIDSP_HAP4 small subunit ribosomal RNA gene, partial sequence	MT025344.1	99.56%	100%	Blakeslee et al. (2020a)
			23 records from Blakeslee et al. (2020a) - including <i>Microphallus</i> sp., <i>Microphallus primas</i> , <i>Microphallus similis</i>	MT025331.1 - MT025338.1, MT025342.1 - MT025344.1, MT025349.1 - MT025355.1	97.14% - 99.56%	100%	Blakeslee et al. (2020a)
			Microphallidae sp. KK2014 gene for 18S ribosomal RNA, partial sequence	AB974359.1	97.14%	100%	Kakui & Kajihara (2014)
			<i>Collyriclum faba</i> 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S	JQ231122.1	96.70%	100%	Heneberg & Literak (2013)

			ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence				
			<i>Microphallus turgidus</i> 18S ribosomal RNA gene, partial sequence	EU825773.1	96.09%	100%	Cho et al. (2008)
A.3	TCCTTTAACGAGGAACAACACTGGAGGGCAAGTCTGG TGCCAGCAGCCGCGGTAATTCCAGCTCCAGAAGCG TATATTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTG GATCTGGGTGCGATGGCTACGTGCCGTGCTTGTA TCCTCGGTTTGGCTACGGTCGGACCGGGTTTGTGA GTCGGCTTCGTGGCTGTGCAGCCTTTCTGCCGTGT CTGTTACGACAGGTGCCGATGGTTAATCCGTTGGC ATGCTCCAGATGCCTTTGACCGGGTGTGGGGGC GGACGGCACGTTTACTTTGAACAAATTTGAGTGCTC AAAGCAGGCCTATGCCTGAAAAATCTTGCATGGAAT AATGGAATAGGACTTCGGTTCTATTTGTTGGTTTTC GGATCCGAAGTAATGGTTAAGAGGGACAGACGGGG GCATTTGTATGGCGGTGTTAGAGGTGAA	UNK	Microphallus sp. HAP14 haplotype MICROPHALLIDSP_HAP14 small subunit ribosomal RNA gene, partial sequence	MT025348.1	96.70%	100%	Blakeslee et al. (2020a)
			Microphallus sp. HAP1 - 4, HAP 21 haplotype MICROPHALLIDSP_HAP1 - MICROPHALLIDSP_HAP4, MICROPHALLIDSP_HAP21 small subunit ribosomal RNA gene, partial sequence	MT025341.1 - MT025344.1, MT025351.1	95.59% - 96.48%	100%	Blakeslee et al. (2020a)
A.4	TCCTTTAACGAGGATCAACTGGAGGGCAAGTCTGG TGCCAGCAGCCGCGGTAATTCCAGCTCCAGAAGCG TATATTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTG GATCTGGGTGCGATGGCTTCGTGCCGTGCTTGCA TTCTCGTTCTGAGCATTGCTTGTGGGTTTGTAAAT CGGCTTCGTAGCTGTGCAGCCTTTCTGCCGTGTCT GTTTCGACAGGTGCTGATGGTCAATCCGTTGGCAT GTTCCAGATGCCTTTAACCGGGTGTGGGGGGCGG ACGGCACGTTTACTTTGAACAAATTTGAGTGCTCAA AGCAGGCCTATGCCTGAAAAATCTTGCATGGAATAA TGGAATAGGACTTCGGTTCTATTTGTTGGTTTTCG GATCCGAAGTAATGGTTAAGAGGGACAGACGGGG CATTTGTATGGCGGTGTTAGAGGGAA	GA	<i>Gynaecotyla adunca</i> haplotype GA_HAP11 small subunit ribosomal RNA gene, partial sequence	MT025345.1	100%	100%	Blakeslee et al. (2020a); unpublished sequences of cercariae from first-intermediate host, <i>Ilyanassa obsoleta</i> (Blakeslee, unpublished)
			<i>Gynaecotyla adunca</i> haplotype GA_HAP12 small subunit ribosomal RNA gene, partial sequence	MT025346.1	99.78%	100%	Blakeslee et al. (2020a)
			<i>Gynaecotyla adunca</i> haplotype GA_HAP13 small subunit ribosomal RNA gene, partial sequence	MT025347.1	98.45%	100%	Blakeslee et al. (2020a)
B	TCCTTTAACGAGGAACAACACTGGAGGGCAAGTCTGG TGCCAGCAGCCGCGGTAATTCCAGCTCCAGAAGCG TATATTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTG GATCTGGGTGCGATGGCTACGTGCCGTAGCTTGTA	MS	<i>Microphallus similis</i> haplotype MS_HAP5 - MS_HAP10, MS_HAP16 - MS_HAP17 small subunit	MT025331.1 - MT025338.1	99.56% - 100%	100%	Blakeslee et al. (2020a); unpublished sequences of

	<p>TTCTGGCTCGGCTACGGTTGGGTCGGGTTTTTGA GTCGGTTTCGTGGCTGTGTAGCCTTCTGCCGTGT CTGTTTCGACAGGTGCCGATAGTTCTACTGTTGGCA TGCTTCCAGATGCCTTTAACCGGGTGTGCGGGGCG GACGGCACGTTTACTTTGAACAAATTTGAGTGCTCA AAGCAGGCTTATGCCTGAAAATTCTTGCATGGAATA ATGGAATAGGACTTCGGTTCTATTTTGTGGTTTTTC GGATCCGAAGTAATGGTTAAGAGGGACAGACGGGG GCATTTGTATGGCGGTGTTAGAGGTGAA</p>		<p>ribosomal RNA gene, partial sequence</p>				<p>cercariae from first- intermediate host, <i>Littorina saxatilis</i> (Blakeslee, unpublished)</p>
			<p><i>Microphallus</i> sp. HAP20 - HAP22 haplotype MICROPHALLIDSP_HAP20 - MICROPHALLIDSP_HAP22 small subunit ribosomal RNA gene, partial sequence</p>	<p>MT025350.1 - MT025352.1</p>	<p>99.34% - 99.56%</p>	<p>100%</p>	<p>Blakeslee et al. (2020a)</p>
C	<p>TCCTTTAACGAGGAACAACACTGGAGGGCAAGTCTGG TGCCAGCAGCCGCGGTAACCTCCAGCTCCAGAAGCG TATATTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTG GATCTGGGTGCATGGCTACGAACCGTAGCTTATAT TCCTGGCTTGGCTACCGTTGGGTCGGGTTTGTGAG TCGGTTTGTGGCTTTGTAGCCTTCTGCTGTGTCTG TTTTCGACAGGTGCCGATGGTTTTACTGTTGGCATGC TTCCAGATGCCTTTAACCGGGTGTGCGGAGGCGGAC GGCATGTTTACTTTGAACAAATTTGAGTGCTCAAAG CAGGCTTATGCCTGAAAATTCTTGCATGGAATAATG GAATAGGACTTCGGTTCTATTTTGTGGTTTTTCGGA TCCGAAGTAATGGTTAAGAGGGACAGACGGGGGCA TTTGTATGGCGGTGTTAGAGGTGAA</p>	<p>MP</p>	<p><i>Microphallus primas</i> haplotype MP_HAP15 small subunit ribosomal RNA gene, partial sequence</p>	<p>MT025339.1</p>	<p>100%</p>	<p>100%</p>	<p>Blakeslee et al. (2020a)</p>
			<p><i>Microphallus primas</i> 18S rRNA gene</p>	<p>AJ287541.1</p>	<p>99.56%</p>	<p>100%</p>	<p>Littlewood & Olson (2001)</p>
			<p><i>Microphallus primas</i> haplotype MP_HAP19, MP_HAP23 - MP_HAP25 small subunit ribosomal RNA gene, partial sequence</p>	<p>MT025349.1, MT025353.1 - MT025355.1</p>	<p>98.24%</p>	<p>100%</p>	<p>Blakeslee et al. (2020a)</p>

Table S3. Hepatosomatic Index (HSI) Statistical Results. Bolded p-values are significant at $p < 0.05$. F=F-statistic; df=degrees of freedom.

Source	F	df1	df2	p
Corrected Model	4.588	7	131	0.000
Host Species	3.619	2	131	0.030
Size	5.975	1	131	0.016
Sex	10.674	1	131	0.001
Cyst Abundance	0.671	1	131	0.414
Host Species * Size	5.465	2	131	0.005

Probability distribution: Normal
Link function: Identity

Table S4. Gonadosomatic Index (GSI) Statistical Results. Bolded p-values are significant at $p < 0.05$. F=F-statistic; df=degrees of freedom.

Source	F	df1	df2	p
Corrected Model	16.378	7	130	0.000
Host Species	3.145	2	130	0.046
Size	0.596	1	130	0.442
Sex	44.103	1	130	0.000
Cyst Abundance	0.559	1	130	0.456
Host Species * Sex	9.640	2	130	0.000

Probability distribution: Gamma
Link function: Log

Table S5. Hepatosomatic Index (HSI) Statistical Results with Infection Status. Bolded p-values are significant at $p < 0.05$. F=F-statistic; df=degrees of freedom.

Source	F	df1	df2	p
Corrected Model	4.491	7	131	0.000
Infection Status	0.338	1	131	0.562
Size	5.344	1	131	0.022
Host Species	2.931	2	131	0.057
Sex	9.528	1	131	0.002
Host Species * Size	4.581	2	131	0.012

Probability distribution: Normal

Link function: Identity

Table S6. Gonadosomatic Index (GSI) Statistical Results with Infection Status. Bolded p-values are significant at $p < 0.05$. F=F-statistic; df=degrees of freedom.

Source	F	df1	df2	p
Corrected Model	11.254	10	127	0.000
Infection Status	0.919	1	127	0.340
Size	0.158	1	127	0.691
Species	0.622	2	127	0.538
Sex	24.429	1	127	0.000
Species * Sex	4.202	2	127	0.017
Sex * Infection Status	4.428	1	127	0.037
Species * Infection Status	0.929	2	127	0.397

Probability distribution: Gamma

Link function: Log

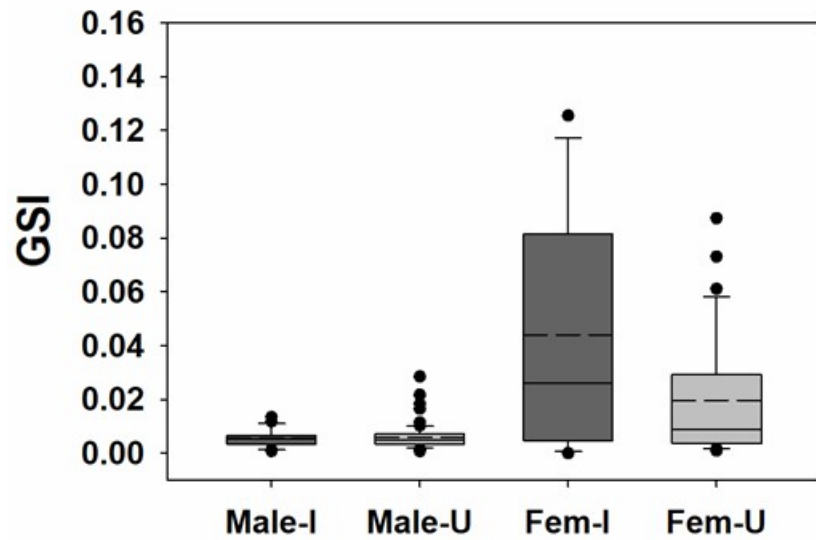


Figure S1. GSI analysis examining infection status pooled across all three host crab species (I=infected, U=uninfected) and sex (Male, Female). Infected females demonstrate the highest GSI of all other combinations (Male-I n=27; Male-U n=67; Fem-I n=12; Fem-U n=33).