

Table S1. Result of the BLAST analyses for the nucleotide sequence obtained in this study MicroBac 01. (QC: query cover; Idt: identity).

Microsporidia	Acc. Number	Host	Taxonomy	QC	Idt
<i>Cucumispora</i> sp. KKB15	MG063425.1	<i>Brandtia latissima</i>	Crustacea	99%	94.89%
<i>Cucumispora</i> sp. KK1B16	MG063426.1	<i>Brandtia latissima</i>	Crustacea	99%	94.81%
<i>Microsporidium</i> sp. MSCLHCY01	HM800853.2	<i>Lepeophtheirus hospitalis</i>	Crustacea	99%	94.86%
<i>Hyperspora aquatica</i>	KX364284.1	<i>Marteilia cochillia</i>	Paramyxida	99%	94.72%
<i>Microsporidium</i> sp. Dhae17W	KP699690.1	<i>Dikerogammarus haemobaphes</i>	Crustacea	99%	94.01%
<i>Microsporidium</i> sp. 1049	FN434092.1	<i>Gammarus duebeniduebeni</i>	Crustacea	99%	93.93%
<i>Microsporidium</i> sp. JES2002G	AJ438962.1	<i>Gammarus chevreuxi</i>	Crustacea	99%	93.49%
<i>Cucumispora ornata</i>	KR190602.1	<i>Dikerogammarus haemobaphes</i>	Crustacea	94%	93.58%
<i>Cucumispora dikerogammari</i>	GQ426188.1	<i>Dikerogammarus villosus</i>	Crustacea	99%	91.86%
<i>Cucumispora dikerogammari</i>	GQ258752.1	<i>Dikerogammarus villosus</i>	Crustacea	99%	91.85%
<i>Cucumispora dikerogammari</i> (in GenBank: <i>Microsporidium</i> sp. RW-2009a)	KR871370.1	<i>Dikerogammarus haemobaphes</i> <i>Dikerogammarus villosus</i>	Crustacea	76%	91.97%
<i>Microsporidium</i> sp. CRANPA	AJ966718.1	<i>Crangonyx pseudogracilis</i>	Crustacea	65%	94.89%
<i>Microsporidium</i> sp. EC-3	KT956054.1	<i>Eulimnogammarus cyaneus</i>	Crustacea	69%	94.60%
<i>Microsporidium</i> sp. EC-1	KR080135.1	<i>Eulimnogammarus cyaneus</i>	Crustacea	69%	94.50%
<i>Microsporidium</i> sp. EC-2	KT956053.1	<i>Eulimnogammarus cyaneus</i>	Crustacea	68%	94.94%
<i>Microsporidium</i> sp. G	KR871369.1	<i>Dikerogammarus haemobaphes</i> <i>Gammarus pulex</i> <i>Gammarus roeseli</i>	Crustacea	76%	94.37%

Table S2. Comparison of small subunit gene (SSU rDNA) sequences among microsporidia parasites. Pairwise distance (bottom diagonal) obtained by p-distance.

Species (GenBank Acc. Number)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1. <i>Microsporidia</i> sp. EC-1 (KR080135.1)	-															
2. <i>Microsporidia</i> sp. EC-2 (KT956053.1)	0.006	-														
3. <i>Microsporidium</i> sp. (FN434092.1)	0.040	0.035	-													
4. <i>Microsporidium</i> sp. CRANPA (AJ966718.1)	0.053	0.047	0.043	-												
5. <i>Microsporidium</i> sp. Dhae17W (KP699690.1)	0.023	0.017	0.049	0.049	-											
6. <i>Thelohania butleri</i> (DQ417114.1)	0.134	0.128	0.118	0.116	0.137	-										
7. <i>Potasporea morhaphis</i> (EU534408.1)	0.274	0.266	0.268	0.274	0.263	0.238	-									
8. <i>Toguebayera baccigeri</i> (MZ413057)	0.043	0.037	0.043	0.039	0.049	0.114	0.268	-								
9. <i>Cucumispora</i> sp. KKBIS (MG063425.1)	0.009	0.004	0.035	0.052	0.021	0.125	0.266	0.041	-							
10. <i>Cucumispora</i> sp. KK1BI6 (MG063426.1)	0.009	0.004	0.035	0.051	0.021	0.125	0.266	0.041	0.000	-						
11. <i>Microsporidium</i> sp. MSCLHCY01 (HM800853.2)	0.057	0.051	0.053	0.047	0.063	0.120	0.277	0.051	0.049	0.049	-					
12. <i>Hyperspora aquatica</i> (KX364284.1)	0.055	0.049	0.055	0.049	0.065	0.123	0.274	0.053	0.047	0.047	0.002	-				
13. <i>Unikaryon legeri</i> (KX364285.1)	0.263	0.255	0.267	0.246	0.258	0.230	0.250	0.252	0.255	0.255	0.239	0.239	-			
14. <i>Unikaryon panopei</i> (MW377751.1)	0.260	0.253	0.259	0.242	0.255	0.233	0.251	0.242	0.253	0.253	0.234	0.234	0.051	-		
15. <i>Cucumispora ornata</i> (KR190602.1)	0.023	0.017	0.049	0.049	0.000	0.137	0.263	0.049	0.021	0.021	0.063	0.065	0.258	0.255	-	
16. <i>Cucumispora dikerogammari</i> (GQ258752.1)	0.067	0.061	0.078	0.055	0.070	0.146	0.277	0.067	0.065	0.065	0.078	0.076	0.266	0.267	0.070	-