

Supplemental information

**Mitogenomic exploration supports the historical
hypothesis of anthropogenic diffusion
of a zoonotic parasite *Echinococcus multilocularis***

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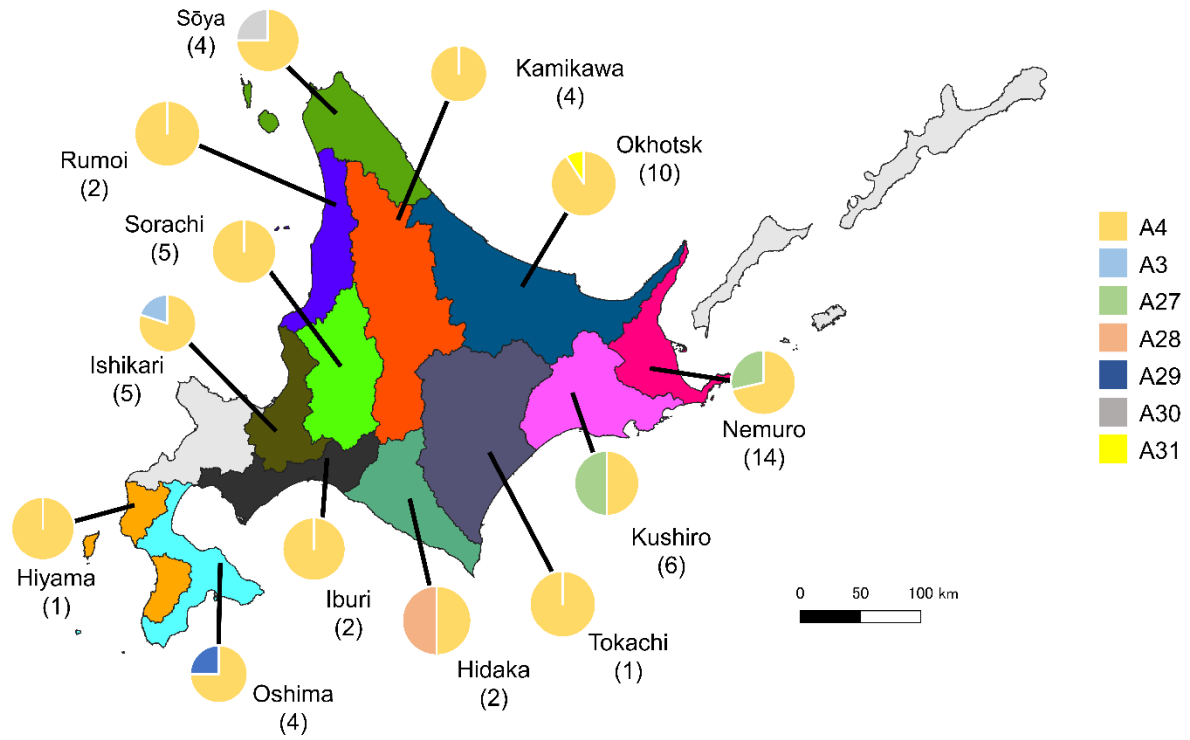


Figure S1. Geographical mapping of detected haplotypes based on three mitochondrial protein coding sequences (CYTB/ND2/COI) of *Echinococcus multilocularis*, related to Table 1. The numbers of parasites, distribution, and frequency of each haplotype on 13 subprefectures in Hokkaido are shown. The color of each pie chart corresponds to the haplotypes listed on the right.

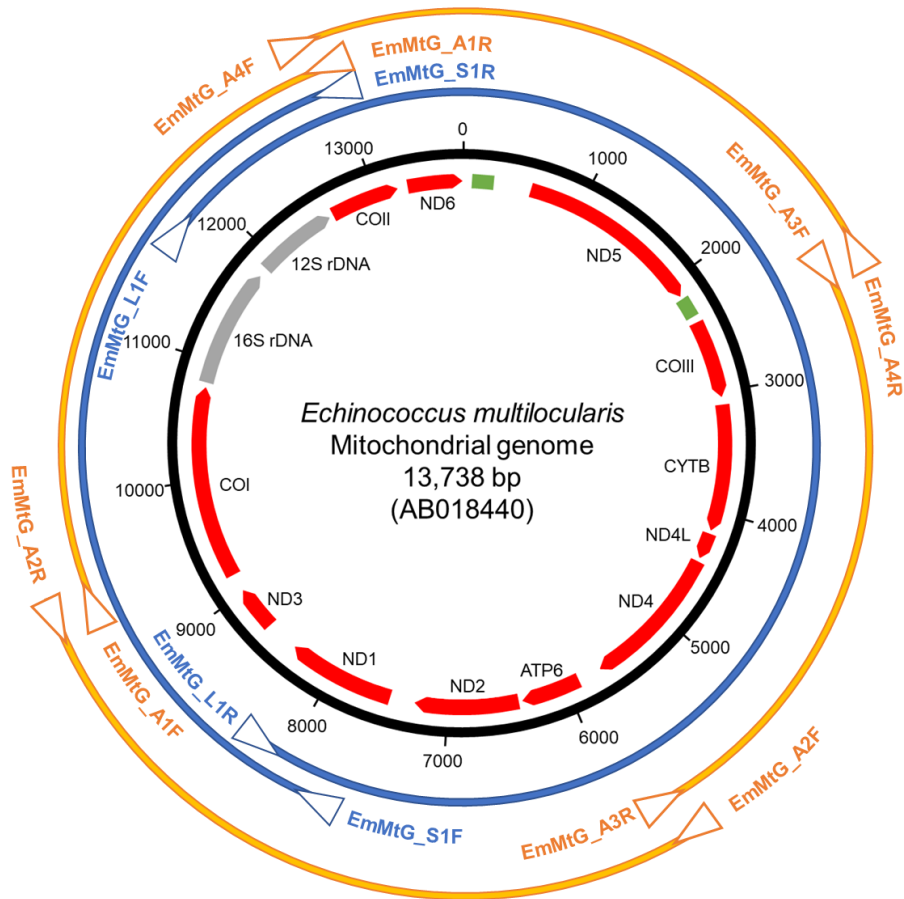


Figure S2. PCR strategies for mitochondrial genome construction, related to STAR Methods. The diagram of the mitochondrial genome of *E. multilocularis* (Accession no. AB014880) is illustrated with protein-coding sequences (red), ribosomal RNA (gray), and two major noncoding regions (green). Blue lines are two overlapping PCR fragments. Orange lines are four alternative PCR fragments. Arrowheads show each primer position.

Table S2. Bayes factors (BFs) between two locations, related to Figure 4.

To From	Austria	Belgium	Canada	Sichuan, China	Estonia	France	Germany	Hokkaido	Inner Mongolia	Kazakhstan	Kyrgyzstan	Poland	Slovakia	St. Lawrence Island	Indiana, USA	Missouri, USA	South Dakota, USA
Austria		0.903	0.842	0.838	0.903	0.884	1.92	0.760	0.866	0.813	0.832	0.887	0.862	0.831	0.800	0.881	0.801
Belgium	1.42		2.35	1.13	2.05	1.97	1.12	1.05	1.00	1.01	1.04	1.31	0.982	1.13	1.05	3.33	0.983
Canada	1.32	2.98		0.942	2.58	2.45	1.02	1.02	1.10	1.02	0.944	1.12	0.969	1.14	0.957	3.00	0.990
Sichuan, China	0.854	0.738	0.770		0.827	0.860	0.696	731	1.45	0.792	1.35	2.97	0.646	1.62	0.930	0.797	0.890
Estonia	1.30	2.63	2.93	0.942		3.40	0.977	1.01	1.18	0.917	0.989	1.26	0.910	1.02	0.992	2.84	0.961
France	13.5	11.8	8.76	0.710	8.30		172	0.715	0.659	0.657	0.659	1.14	0.700	0.676	0.676	13.3	0.644
Germany	3.59	1.39	1.22	1.29	1.16	1.34		1.23	1.31	1.21	1.21	1.36	1.19	1.33	1.22	1.16	1.11
Hokkaido	1.74	1.17	1.28	1.34	1.21	1.42	1.29		1.70	1.38	1.57	1.50	1.32	2.61	1.35	1.33	1.48
Inner Mongolia	1.35	1.05	1.09	1.43	1.05	1.14	1.03	1.01		1.13	1.06	3.91	1.02	6.03	1.31	1.20	1.27
Kazakhstan	1.71	1.39	1.43	1.38	1.37	1.59	1.24	1.37	1.43		1.26	1.68	1.28	1.52	1.32	1.33	1.25
Kyrgyzstan	0.952	0.867	0.841	1.00	0.780	1.01	0.759	0.920	0.949	71.3		0.922	0.702	1.77	0.804	0.764	0.922
Poland	14.0	4.20	10.2	11.4	10.5	22.5	0.965	0.751	4.23	0.819	2.54		14500	8.39	2.05	4.43	2.58
Slovakia	1.60	1.37	1.33	1.41	1.35	1.61	1.30	1.35	1.48	1.36	1.39	1.31		1.43	1.54	1.35	1.39
St. Lawrence Island	0.858	1.24	1.43	16.8	1.79	2.56	0.670	216	9.43	3.95	68.5	19.1	0.657		10.5	1.13	9.22
Indiana, USA	1.31	1.08	1.07	1.12	1.05	1.02	1.02	1.04	1.37	1.08	1.00	1.42	1.02	1.53		1.05	16.6
Missouri, USA	1.62	4.74	2.30	1.18	2.29	2.21	1.17	1.19	1.18	1.21	1.19	1.38	1.23	1.19	1.26		1.22
South Dakota, USA	1.48	1.01	1.07	0.970	1.06	1.05	1.08	1.03	1.28	1.00	1.12	1.38	1.06	1.51	16.4	1.07	

BFs with a value >10 are highlighted in bold font (values >100 are highlighted in bold red font).

Table S3. Primer sequences and PCR product sizes, related to STAR Methods.

Primer name	Primer sequence (5'→3')	Product size (bp)
EmMtG_S1F	CGTAAGGGTCCTAAYAAGGTTGG	5,469
EmMtG_S1R	GATTAAGACGACCMGGRAYAGCATCC	
EmMtG_L1F	CCAGGTCGGTTCTTATCTATTGTRGAAG	10,436
EmMtG_L1R	CCATTTCTTGAAGTTAACAGCATCACG	
EmMtG_A1F	TGCCACGTTTGAATGCTTTGAGTGCGTG	3,614
EmMtG_A1R	GATTAAGACGACCCGGAATAGCATCC	
EmMtG_A2F	GGGATAACTTATGTTAGGGAGACTGG	3,864
EmMtG_A2R	CTCTAGAAACACCTGCTAAATGCAAAG	
EmMtG_A3F	GGCGATATAGATATGTCTGTGGTTCC	3,531
EmMtG_A3R	CATAAACCCGACCTATTAAGAACC	
EmMtG_A4F	GGCGGTTGAGTTGATATGAACTATAGTTCC	3,447
EmMtG_A4R	AATAACCCAACCAAACCTAAGCCAAC	

Table S4. Accession numbers and references of sequences used in this study, related to STAR Methods.

Haplotype	Location	CYTB	ND2	COI	Reference no.	Remarks
A1	Kazakhstan (1)	AB461398	AB461406	AB461415	[S1]	
A2	St. Lawrence Island (1), Kyrgyzstan (48), Kazakhstan (4)	AB461398	AB461406	AB461416	[S1], [S2], This study	
A3	Hokkaido (2)	AB461399	AB461407	AB461416	[S1], This study	
A4	Hokkaido (49), St Lawrence Island (2)	AB461398	AB461407	AB461416	[S1], This study	
A5	Sichuan (17)	AB461398	AB461408	AB461417	[S1]	
A6	Sichuan (1)	AB461398	AB461408	AB477011	[S1]	
A7	Sichuan (1)	AB461398	AB461408	AB477012	[S1]	
A8	Sichuan (1)	AB477009	AB461408	AB477010	[S1]	
A9	Sichuan (1)	AB461398	AB461408	AB461416	[S1]	
A10	Sichuan (1)	AB461398	AB461406	AB461417	[S1]	
A11	Kyrgyzstan (4)	MN829497	MN829513	MN829529	[S2]	
A12	Kyrgyzstan (3)	MN829498	MN829514	MN829530	[S2]	
A13	Kyrgyzstan (2)	MN829499	MN829515	MN829531	[S2]	
A14	Kyrgyzstan (2)	MN829500	MN829516	MN829532	[S2]	
A15	Kyrgyzstan (2)	MN829501	MN829517	MN829533	[S2]	
A16	Kyrgyzstan (2)	MN829502	MN829518	MN829534	[S2]	
A17	Kyrgyzstan (2)	MN829503	MN829519	MN829535	[S2]	
A18	Kyrgyzstan (1)	MN829504	MN829520	MN829536	[S2]	
A19	Kyrgyzstan (1)	MN829505	MN829521	MN829537	[S2]	
A20	Kyrgyzstan (1)	MN829506	MN829522	MN829538	[S2]	
A21	Kyrgyzstan (1)	MN829507	MN829523	MN829539	[S2]	
A22	Kyrgyzstan (1)	MN829508	MN829524	MN829540	[S2]	
A23	Kyrgyzstan (1)	MN829509	MN829525	MN829541	[S2]	
A24	Kyrgyzstan (1)	MN829510	MN829526	MN829542	[S2]	
A25	Kyrgyzstan (1)	MN829511	MN829527	MN829543	[S2]	
A26	Kyrgyzstan (1)	MN829512	MN829528	MN829544	[S2]	Excluded from analysis due to nucleotide deletion in COI
A27	Hokkaido (7)	LC720729	LC720729	LC720729	This study	
A28	Hokkaido (1)	LC720772	LC720772	LC720772	This study	
A29	Hokkaido (1)	LC720778	LC720778	LC720778	This study	
A30	Hokkaido (1)	LC720763	LC720763	LC720763	This study	
A31	Hokkaido (1)	LC720780	LC720780	LC720780	This study	

E1	Austria (1)	AB461395	AB461403	AB461412	[S1]
E2	France (4), Germany (1)	AB461395	AB461403	AB461414	[S1]
E3	France (1)	AB461396	AB461404	AB461413	[S1]
E4	France (5), Belgium (2), Missouri (1)	AB461395	AB461404	AB461414	[S1], [S4]
E5	Slovakia (10)	AB461397	AB461405	AB461414	[S1]
N1	St. Lawrence Island (9)	AB461400	AB461409	AB461418	[S1], This study
N2	Indiana (5), South Dakota (1)	AB461401	AB461410	AB461419	[S1]
O1	Inner Mongolia (2)	AB461402	AB461411	AB461420	[S1]
EmPL1	Poland (29)	KY205662	KY205692	KY205677	[S3]
EmPL2	Poland (1)	KY205663	KY205693	KY205678	[S3]
EmPL3	Poland (4)	KY205664	KY205694	KY205679	[S3]
EmPL4	Poland (14)	KY205665	KY205695	KY205680	[S3]
EmPL5	Poland (1)	KY205666	KY205696	KY205681	[S3]
EmPL6	Poland (1)	KY205667	KY205697	KY205682	[S3]
EmPL7	Poland (1)	KY205668	KY205698	KY205683	[S3]
EmPL8	Poland (1)	KY205669	KY205699	KY205684	[S3]
EmPL9	Poland (7)	KY205670	KY205700	KY205685	[S3]
EmPL10	Poland (4)	KY205671	KY205701	KY205686	[S3]
EmPL11	Poland (1)	KY205672	KY205702	KY205687	[S3]
EmPL12	Poland (4)	KY205673	KY205703	KY205688	[S3]
EmPL13	Poland (2)	KY205674	KY205704	KY205689	[S3]
EmPL14	Poland (3)	KY205675	KY205705	KY205690	[S3]
EmPL15	Poland (3)	KY205676	KY205706	KY205691	[S3]
EST1	Estonia (1)	KT001421	KT001425	KT001423	[S5]
EST2	Estonia (1)	KT001422	KT001426	KT001424	[S5]
EAB	Canada (4)	MK843307	AB461404	MK843308	[S6]
ECA	Canada (66)	MK843307	AB461404	AB461414	[S6]
ESK	Canada (7)	MK843307	AB461404	MK843309	[S6]

Sequences of EmPL2 are same to those of EmPL4

Numbers enclosed within brackets in the 'Location' column indicate the count of detected haplotypes.

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