Larvae feed on birds and molt to become nymphs, remaining on the same avian host up to 26 days, a period that usually lasts until the trans-Saharan migrating birds have reached Europe (*1*). Thus, the half-fed nymph probably was attached to the whinchat when migration started. Nymphs drop off the bird only after completion of the blood meal and molt on the ground before attaching to their second, final hosts, which are usually large mammals, including humans.

Although detection of virus genome does not necessarily imply the presence of live virus that is able to spread locally, our findings, consistent with the recent autochthonous cases in Spain, underscore the need to monitor any introduction and circulation of CCHFV in southwestern Europe. Such monitoring should focus on sites where migrants rest or nest and where a local population of competent ticks and their hosts interact. Raising awareness of possible outbreaks should also include specific surveillance and contingency plans focused on categories of persons and animals at elevated risk for CCHFV infection.

Acknowledgments

We gratefully acknowledge the support of Sara Riello and all volunteers operating the ringing station of Ventotene. We warmly thank the Natural Reserve of Ventotene and S. Stefano islands for logistic and financial support. All the ticks were collected during the ringing activities in the framework of the Small Island research project (ISPRA).

This work has been supported by Italy's Ministry of Health (research grant no. MSRCTE 03/14).

About the Author

Ms. Mancuso holds an MSc in biology and serves as a junior research assistant in the National Reference of Foreign Animals Diseases at the Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale" in Teramo, Italy. Her research interests include bird migration ecology and the diagnosis of vectorborne pathogens.

References

1. Hoogstraal H. The epidemiology of tick-borne Crimean-Congo hemorrhagic fever in Asia, Europe, and Africa. J Med Entomol. 1979;15:307–417. http://dx.doi.org/10.1093/jmedent/15.4.307
2. Hoogstraal H. Changing patterns of tickborne diseases in modern society. Annu Rev Entomol. 1981;26:75–99. http://dx.doi.org/10.1146/annurev.en.26.010181.000451
3. Negredo A, de la Calle-Prieto F, Palencia-Herrejón E, Mora-Rillo M, Astray-Mochales J, Sánchez-Seco MP, et al.; Crimean Congo Hemorrhagic Fever@Madrid Working Group. Autochthonous Crimean-Congo hemorrhagic fever in Spain. N Engl J Med. 2017;377:154–61. http://dx.doi.org/10.1056/NEJMoa1615162
4. Ramírez de Arellano E, Hernández L, Goyanes MJ, Arsuaga M, Cruz AF, Negredo A, et al. Phylogenetic characterization of Crimean-Congo hemorrhagic fever virus, Spain. Emerg Infect Dis. 2017;23:2078–80. http://dx.doi.org/10.3201/eid2312.171002
5. Lindeborg M, Barboutis C, Ehrenborg C, Fransson T, Jaenson TG, Lindgren PE, et al. Migratory birds, ticks, and Crimean-Congo hemorrhagic fever virus. Emerg Infect Dis. 2012;18:2095–7. http://dx.doi.org/10.3201/eid1812.120718
6. Palomar AM, Portillo A, Santibanez P, Mazuelas D, Crespo A, Gutierrez O, et al. CCHFV from migratory birds, Morocco. Emerg Infect Dis. 2013;19:260–3. http://dx.doi.org/10.3201/eid1902.121193
7. Manilla G. Acari Ixodida. In: Fauna d'Italia. Volume 36. Bologna (Italy): Calderini; 1998. p. 280.
8. Toma L, Mancini F, Di Luca M, Cecere JG, Bianchi R, Khoury C, et al. Detection of microbial agents in ticks collected from migratory birds in central Italy. Vector Borne Zoonotic Dis. 2014;14:199–205. http://dx.doi.org/10.1089/vbz.2013.1458
9. Chitimia-Dobler L, Nava S, Bestehorn M, Dobler G, Wölfel S. First detection of *Hyalomma rufipes* in Germany. Ticks Tick Borne Dis. 2016;7:1135–8. http://dx.doi.org/10.1016/j.ttbdis.2016.08.008
10. Hornok S, Horváth G. First report of adult *Hyalomma marginatum rufipes* (vector of Crimean-Congo haemorrhagic fever virus) on cattle under a continental climate in Hungary. Parasit Vectors. 2012;5:170. http://dx.doi.org/10.1186/1756-3305-5-170

Address for correspondence: Federica Monaco, Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale" Campo Boario, Teramo 64100, Italy; email: f.monaco@izs.it

Echinococcus canadensis G8 Tapeworm Infection in a Sheep, China, 2018

Ruiqi Hua,[1] Yue Xie,[1] Hongyu Song, Yuan Shi, Jiafei Zhan, Maodi Wu, Xiaobin Gu, Xuerong Peng, Guangyou Yang

Author affiliation: Sichuan Agricultural University, Chengdu, China

DOI: https://doi.org/10.3201/eid2507.181585

We report a sheep infected with *Echinococcus canadensis* G8 tapeworm in China in 2018. This pathogen was previously detected in moose, elk, muskox, and mule deer in Europe and North America; our findings suggest a wider host range and geographic distribution. Surveillance for the G8 tapeworm should be conducted in China.

[1]These authors contributed equally to this article.

Cystic echinococcosis (CE) is a zoonotic disease of worldwide distribution that causes disease, death, and economic loss in many domestic and wildlife ungulates and carnivore species, as well as in humans. Animals and humans can become infected through the accidental ingestion of *Echinococcus* tapeworm eggs (*1*,*2*). *Echinococcus granulosus* sensu stricto (G1, G3) tapeworms are considered the major cause of CE globally; however, cases attributable to *E. canadensis* genotypes within the *E. granulosus* tapeworm complex are increasingly being recognized (*3*). Overall, *E. canadensis* tapeworms comprise 4 genotypes (G6, G7, G8, G10), although the taxonomy is still being debated (*4*). *E. canadensis* G8 tapeworms were initially identified in 1994 in a moose (*Alces alces*) in Minnesota, USA (Appendix Table, https://wwwnc.cdc.gov/EID/article/25/7/18-1585-App1.pdf). Then, in 2002, two infections were reported in humans in Alaska. G8 tapeworms have also been found in elk (*Cervus canadensis*, 2006) and muskox (*Ovibos moschatus*, 2013) in Canada. Updated epidemiologic data show infections have also occurred in Estonia moose (2008), Russia moose (2013), and a US mule deer (*Odocoileus hemionus*, 2018). As of April 2019, at least 4 species (moose, elk, muskox, and mule deer) have been proven to serve as intermediate hosts of G8 tapeworms in Europe and North America. We report a potential new public health threat regarding sheep (*Ovis aries*) infected with *E. canadensis* G8 tapeworms in China and highlight the potential wider host range and geographic distribution of this species.

During 2017, we conducted a molecular epidemiologic survey of CE in northwestern China and collected 277 hydatid cysts from sheep (78 from Qinghai-Tibet Plateau, 60 from Xinjiang Autonomous Region) and yaks (*Bos mutus*; 139 from Qinghai-Tibet Plateau) at local slaughterhouses. During sampling, we handled all animals in strict accordance with the animal welfare laws of China. We genotyped the hydatid cysts using the partial mitochondrial *cox1* gene sequence, as described previously (*5*), and found that most cyst specimens were represented by *E. granulosus* G1 and G3 tapeworms (data not shown), and 1 sheep cyst was diagnosed as an *E. canadensis* G8–like tapeworm infection (herein designated sheep-XN) (Appendix Figure 1, panel A). To further investigate the genotype of tapeworm sheep-XN, we amplified the full-length *cox1* gene (1,608 bp) and the mitochondrial *nad1* gene (894 bp), a method proven effective for *Echinococcus* tapeworm genotyping (*4*). This analysis verified that sheep-XN clustered with *E. canadensis* G8 tapeworms (Appendix Figure 1, panel B). However, given that partial mitochondrial DNA (mtDNA) sequences are insufficient to identify genotype (because of limited loci information) (*6*), we amplified the complete mtDNA of sheep-XN and compared it with *Echinococcus* mtDNA sequences from GenBank. The resulting phylogenetic tree showed the same topologic structure as that acquired when using the *cox1* and *nad1* genes, suggesting that sheep-XN was an *E. canadensis* G8 tapeworm (Figure).

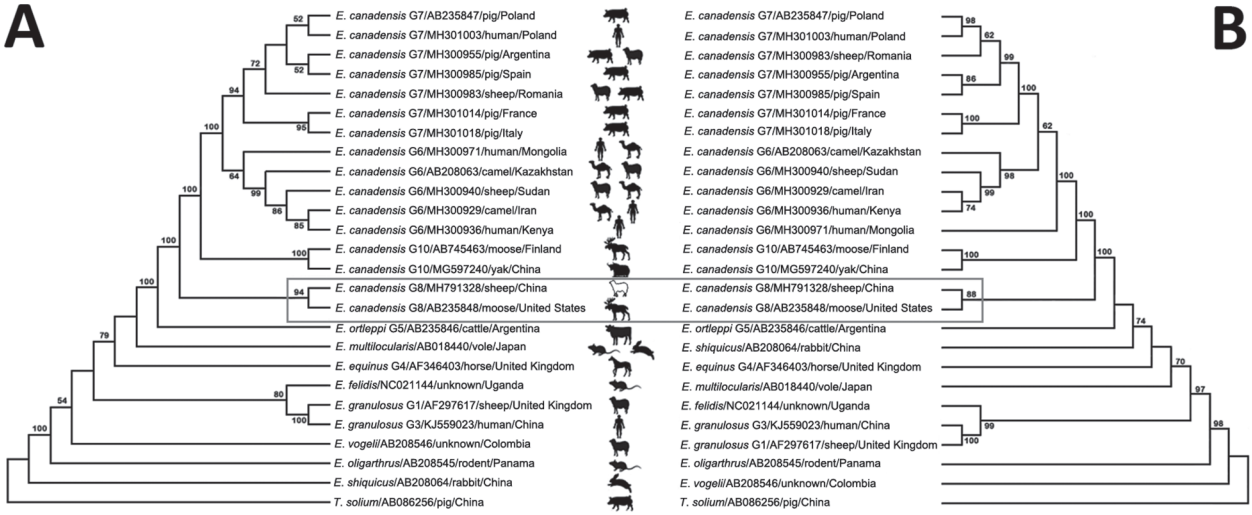


Figure. Phylogenetic analysis of *Echinococcus* species of different genotypes, strains, and host origins, including the *E. canadensis* G8 tapeworm identified in a sheep in China, 2018. Phylogenetic trees were inferred by maximum-likelihood analysis on the basis of concatenated amino acid data of 12 protein-coding genes by using the Jones-Taylor-Thornton model (A) and concatenated nucleotide data of 12 protein-coding genes by using the Tamura-Nei model (B) in MEGA7.0 (https://www.megasoftware.net). The reference species *Taenia solium* was used as the outgroup. We performed bootstrapping with 1,000 replicates to calculate the percentage reliability for each node in both data sets; only values of ≥50% are shown. Tree branch lengths are proportional to the evolutionary distance. The box contains the *E. canadensis* G8 tapeworm identified in this study (GenBank accession no. MH791328) and its closest relative from a moose in the United States (GenBank accession no. AB235848). Sheep shown in white represents a potential new intermediate host of *E. canadensis* G8.

We confirmed that the sheep-origin hydatid cyst was *E. canadensis* G8 tapeworm (Appendix Figure 1, panel C) and suggest that this pathogen potentially poses a new public health threat on the Qinghai-Tibet Plateau of China, where human echinococcosis is prevalent. Previous research has shown that sterile cysts usually result when *Echinococcus* spp. infect species not commonly infected (*7*). However, for the sheep-origin cyst, we found numerous protoscoleces in the hydatid fluid, indicating the cyst was fertile. Thus, sheep might serve as another intermediate host of the *E. canadensis* G8 tapeworm in nature and spread protoscoleces to definitive hosts, posing a threat to local herdsmen and livestock.

G6 and G7 tapeworms can circulate through the domestic cycle (in animals such as camels, pigs, and dogs) or the sylvatic cycle (in animals such as reindeer and wolves), and G8 and G10 tapeworms are generally believed to be restricted to the sylvatic cycle in circumpolar regions (Appendix Table) (*2*,*8*). Our finding of an *E. canadensis* G8 tapeworm in a sheep in China should not only alert the local population to be aware of this pathogen but also contributes to the discussion concerning *E. canadensis* tapeworm taxonomy. Further research is required to determine the transmission dynamics of this pathogen and determine whether the domestic life cycle of *E. canadensis* G8 tapeworm (circulation through sheep and dogs) has been or is present.

Since 2017, a mandatory vaccination campaign of sheep and goats with the CE vaccine EG95 has been sponsored in high-prevalence areas of China because of China's policy, the National Medium- and Long-Term Plan for Animal Disease Control (2012–2020) (*9*). However, EG95 was developed against the *E. granulosus* G1 tapeworm (*10*) and might not provide effective protection against the *E. canadensis* G8 tapeworm. Our findings indicate the G8 tapeworm might be prevalent in sheep in China, suggesting a wider host range and geographic distribution (Appendix Table; Appendix Figure 2). Thus, we propose the need for increased surveillance of the *E. canadensis* G8 tapeworm in China and that integration of this pathogen into ongoing echinococcosis programs is essential for tapeworm prevention and control.

This work was supported by grants from the Key Technology Research and Development Program of Sichuan Province in China (grant no. 2015NZ0041) and the National Natural Science Foundation of China (grant no. 31672547).

About the Author

Mr. Hua is a graduate student studying at the Department of Parasitology, College of Veterinary Medicine, Sichuan Agricultural University, Chengdu, Sichuan, China. His primary research interest is parasite genomics.

References

1. Cardona GA, Carmena D. A review of the global prevalence, molecular epidemiology and economics of cystic echinococcosis in production animals. Vet Parasitol. 2013;192:10–32. http://dx.doi.org/10.1016/j.vetpar.2012.09.027
2. Cerda JR, Buttke DE, Ballweber LR. *Echinococcus* spp. tapeworms in North America. Emerg Infect Dis. 2018;24:230–5. http://dx.doi.org/10.3201/eid2402.161126
3. Alvarez Rojas CA, Romig T, Lightowlers MW. *Echinococcus granulosus* sensu lato genotypes infecting humans—review of current knowledge. Int J Parasitol. 2014;44:9–18. http://dx.doi.org/10.1016/j.ijpara.2013.08.008
4. Davidson RK, Lavikainen A, Konyaev S, Schurer J, Miller AL, Oksanen A, et al. *Echinococcus* across the north: current knowledge, future challenges. Food Waterborn Parasitol. 2016;4:39–53. http://dx.doi.org/10.1016/j.fawpar.2016.08.001
5. Bowles J, Blair D, McManus DP. Genetic variants within the genus *Echinococcus* identified by mitochondrial DNA sequencing. Mol Biochem Parasitol. 1992;54:165–73. http://dx.doi.org/10.1016/0166-6851(92)90109-W
6. Laurimäe T, Kinkar L, Romig T, Omer RA, Casulli A, Umhang G, et al. The benefits of analysing complete mitochondrial genomes: deep insights into the phylogeny and population structure of *Echinococcus granulosus* sensu lato genotypes G6 and G7. Infect Genet Evol. 2018;64:85–94. http://dx.doi.org/10.1016/j.meegid.2018.06.016
7. Bružinskaitė R, Šarkūnas M, Torgerson PR, Mathis A, Deplazes P. Echinococcosis in pigs and intestinal infection with *Echinococcus* spp. in dogs in southwestern Lithuania. Vet Parasitol. 2009;160:237–41. http://dx.doi.org/10.1016/j.vetpar.2008.11.011
8. Oksanen A, Lavikainen A. *Echinococcus canadensis* transmission in the North. Vet Parasitol. 2015;213:182–6. http://dx.doi.org/10.1016/j.vetpar.2015.07.033
9. Zhong Z. The national medium- and long-term plan for animal disease control (2012–2020). 2014 Nov 4 [cited 2018 Nov 11]. http://ap.fftc.agnet.org/ap_db.php?id=308
10. Alvarez Rojas CA, Gauci CG, Lightowlers MW. Antigenic differences between the EG95-related proteins from *Echinococcus granulosus* G1 and G6 genotypes: implications for vaccination. Parasite Immunol. 2013;35:99–102. http://dx.doi.org/10.1111/pim.12009

Address for correspondence: Guangyou Yang, Department of Parasitology, College of Veterinary Medicine, Sichuan Agricultural University, 211 Huimin Rd, Chengdu, Sichuan, 611130, China; email: guangyouyang@hotmail.com

Article DOI: https://doi.org/10.3201/eid2507.181585

Echinococcus canadensis G8 Tapeworm Infection in a Sheep, China, 2018

Appendix

Appendix Table. The host range and geographic distribution of *Echinococcus canadensis* tapeworm, 1992–2018

Genotype	Definitive hosts	Intermediate hosts	Geographic distribution	References
E. canadensis G6/7	Dog, wolf	Camel, pig, cattle, goat, sheep, reindeer	Mexico, Peru, Brazil, Chile, Argentina, Tunisia, Algeria, Libya, Namibia, Mauritania, Ghana, Egypt, Sudan, Ethiopia, Somalia, Kenya, South Africa, Spain, Portugal, Poland, Ukraine, Czechia, Austria, Hungary, Romania, Serbia, Russia, Vatican City State, Bosnia and Herzegovina, Slovakia, France, Lithuania, Italy, Turkey, Iran, Afghanistan, India, Nepal, Kazakhstan, Kyrgyzstan, China, Mongolia	(*1–15*)
E. canadensis G8	Wolf	Moose, elk, muskox, mule deer, sheep	America, Canada, Estonia, Latvia, Russia, China	
E. canadensis G10	Dog, wolf	Moose, elk, reindeer, mule deer, yak	Finland, Mongolia, America, Canada, Estonia, Latvia, Sweden, Russia, China	

References

1. Moks E, Jõgisalu I, Valdmann H, Saarma U. First report of *Echinococcus granulosus* G8 in Eurasia and a reappraisal of the phylogenetic relationships of 'genotypes' G5-G10. Parasitology. 2008;135:647–54. PubMed http://dx.doi.org/10.1017/S0031182008004198

2. Nakao M, Lavikainen A, Yanagida T, Ito A. Phylogenetic systematics of the genus *Echinococcus* (Cestoda: Taeniidae). Int J Parasitol. 2013;43:1017–29. PubMed http://dx.doi.org/10.1016/j.ijpara.2013.06.002

3. Thompson RCA. Biology and systematics of *Echinococcus*. In: Thompson RCA, Deplazes P, Lymbery AJ, editors. Advanced parasitology. Vol. 95. San Diego: Elsevier Academic Press Inc.; 2017. p. 65–110.

4. Ito A, Nakao M, Lavikainen A, Hoberg E. Cystic echinococcosis: Future perspectives of molecular epidemiology. Acta Trop. 2017;165:3–9. PubMed http://dx.doi.org/10.1016/j.actatropica.2016.05.013

5. Addy F, Wassermann M, Kagendo D, Ebi D, Zeyhle E, Elmahdi IE, et al. Genetic differentiation of the G6/7 cluster of *Echinococcus canadensis* based on mitochondrial marker genes. Int J Parasitol. 2017;47:923–931. PubMed http://dx.doi.org/10.1016/j.ijpara.2017.06.003

6. Yanagida T, Lavikainen A, Hoberg EP, Konyaev S, Ito A, Sato MO, et al. Specific status of *Echinococcus canadensis* (Cestoda: Taeniidae) inferred from nuclear and mitochondrial gene sequences. Int J Parasitol. 2017;47:971–979. PubMed http://dx.doi.org/10.1016/j.ijpara.2017.07.001

7. Wu Y, Li L, Zhu G, Li W, Zhang N, Li S, et al. Mitochondrial genome data confirm that yaks can serve as the intermediate host of *Echinococcus canadensis* (G10) on the Tibetan Plateau. Parasit Vectors. 2018;11:166. PubMed http://dx.doi.org/10.1186/s13071-018-2684-0

8. Laurimäe T, Kinkar L, Romig T, Omer RA, Casulli A, Umhang G, et al. The benefits of analysing complete mitochondrial genomes: Deep insights into the phylogeny and population structure of *Echinococcus granulosus* sensu lato genotypes G6 and G7. Infect Genet Evol. 2018;64:85–94. PubMed http://dx.doi.org/10.1016/j.meegid.2018.06.016

9. Cerda JR, Ballweber LR. Confirmation of *Echinococcus canadensis* G8 and G10 in Idaho Gray Wolves (*Canis lupus*) and Cervids. J Wildl Dis. 2018;54:403–405. PubMed http://dx.doi.org/10.7589/2017-05-119

10. Bowles J, Blair D, McManus DP. Molecular genetic characterization of the cervid strain ('northern form') of *Echinococcus granulosus.* Parasitology. 1994;109:215–21. PubMed http://dx.doi.org/10.1017/S0031182000076332

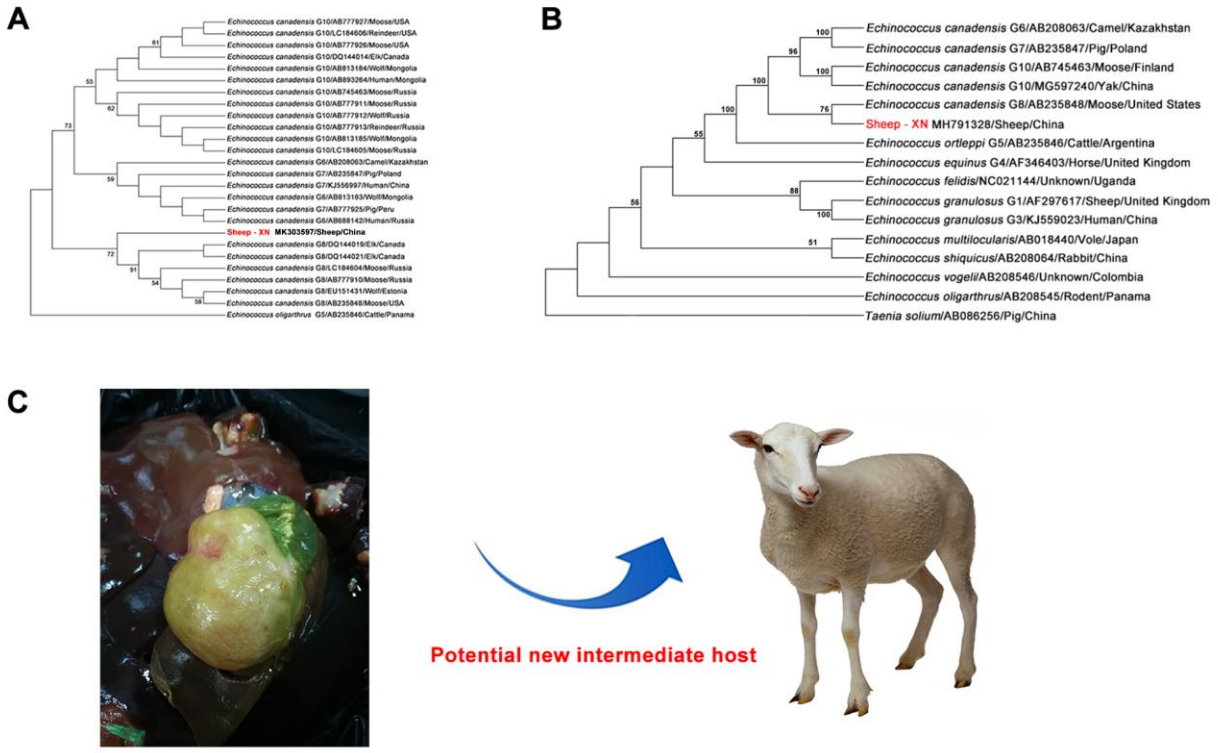
11. Schurer J, Shury T, Leighton F, Jenkins E. Surveillance for *Echinococcus canadensis* genotypes in Canadian ungulates. Int J Parasitol Parasites Wildl. 2013;2:97–101. PubMed http://dx.doi.org/10.1016/j.ijppaw.2013.02.004

12. Nakao M, Yanagida T, Konyaev S, Lavikainen A, Odnokurtsev VA, Zaikov VA, et al. Mitochondrial phylogeny of the genus *Echinococcus* (Cestoda: Taeniidae) with emphasis on relationships among *Echinococcus canadensis* genotypes. Parasitology. 2013;140:1625–36. PubMed http://dx.doi.org/10.1017/S0031182013000565

13. Konyaev SV, Yanagida T, Nakao M, Ingovatova GM, Shoykhet YN, Bondarev AY, et al. Genetic diversity of *Echinococcus* spp. in Russia. Parasitology. 2013;140:1637–47. PubMed http://dx.doi.org/10.1017/S0031182013001340

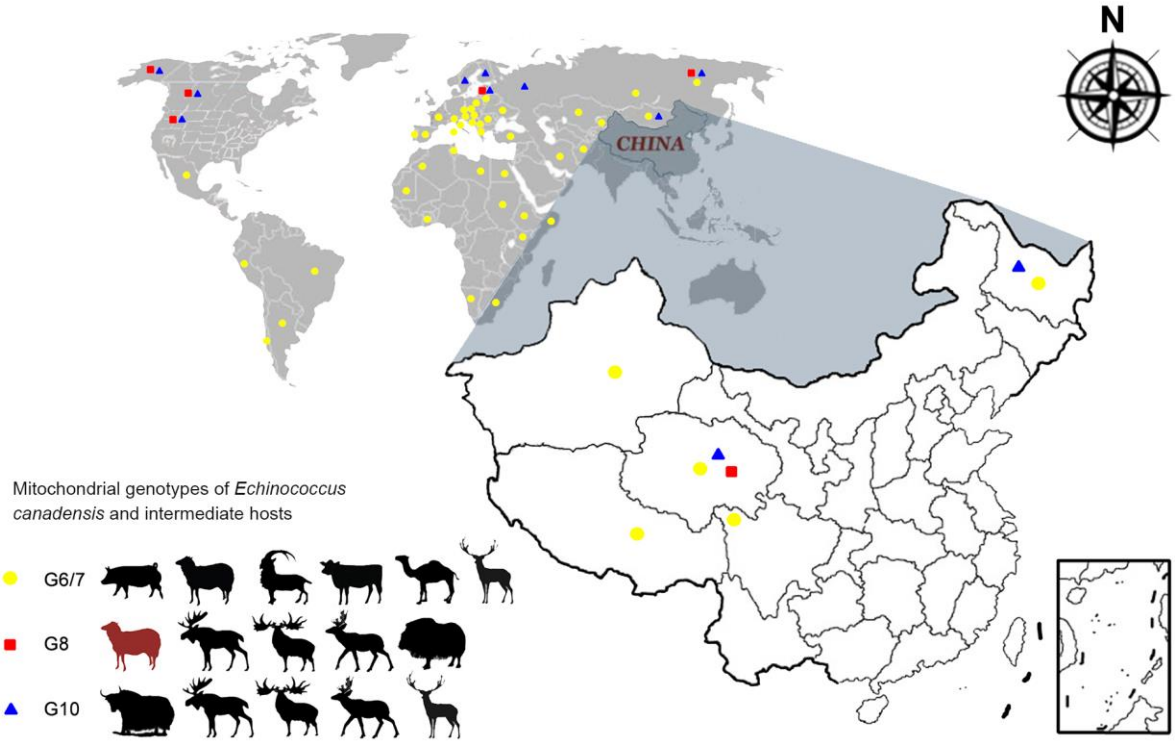
14. McManus DP, Zhang L, Castrodale LJ, Le TH, Pearson M, Blair D. Short report: molecular genetic characterization of an unusually severe case of hydatid disease in Alaska caused by the cervid strain of *Echinococcus granulosus.* Am J Trop Med Hyg. 2002;67:296–8. PubMed http://dx.doi.org/10.4269/ajtmh.2002.67.296

15. Thompson RCA, Boxell AC, Ralston BJ, Constantine CC, Hobbs RP, Shury T, et al. Molecular and morphological characterization of *Echinococcus* in cervids from North America. Parasitology. 2006;132:439–47. PubMed http://dx.doi.org/10.1017/S0031182005009170



Appendix Figure 1. Molecular identification of *Echinococcus canadensis* G8 tapeworm from sheep in China, 2018. A) The phylogenetic tree was constructed by using the Kimura 2-parameter model based on maximum-likelihood analysis by using the partial sequences of mitochondrial *cox1* gene inferred from isolates of *Echinococcus* spp. *Echinococcus oligarthrus* was used as an outgroup. The maximum-likelihood tree was constructed by using MEGA7.0 (https://www.megasoftware.net). The bootstrap values ≥50% are shown for the nodes that appeared along the branches with 1,000 replicates. Most *Echinococcus* isolates used in this study represent the *Echinococcus granulosus* G1 or G3 clusters (data not shown), whereas 1 isolate (XN1, MK303597) from a sheep was identified as *Echinococcus canadensis* G8-like tapeworm and named after its host, Sheep-XN (shown in red). B) To further identify the genotype of Sheep-XN, the full-length *cox1* gene (1,608 bp) together with the complete mitochondrial *nad1* gene (894 bp) were amplified and concatenated to produce a robust maximum-likelihood tree by using the Kimura 2-parameter method. The bootstrap values ≥50% are shown for the nodes that appeared along the branches with 1,000 replicates. *Taenia solium* was used as the outgroup. These

results consistently showed that the genotype of Sheep-XN isolate is *E*. *canadensis* G8 tapeworm. C) Hydatid cyst on the sheep infected with Sheep-XN. XN, Xining.



Appendix Figure 2. Global distribution of *Echinococcus canadensis* tapeworms based on mitochondrial data, with indications of intermediate host affiliation and emphasis on *Echinococcus canadensis* G8 tapeworm from sheep in China, 2018. The size of China is enlarged for easier visualization. The presence of *Echinococcus canadensis* G8 tapeworm in sheep from Xining (shown in red), located on the Qinghai-Tibet Plateau of China, suggests a wider intermediate host range and geographic distribution than previously acknowledged.