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).

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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

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, Yue Xie, Hongyu Song, Yuan Shi, Jiafei Zhan, Maodi Wu, Xiaobin Gu, Xuerong Peng, Guangyou Yang

Author affiliation: Sichuan Agricultural University, Chengdu, China

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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.

1These 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.

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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


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
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Appendix

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

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Definitive hosts</th>
<th>Intermediate hosts</th>
<th>Geographic distribution</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>E. canadensis</em> G6/7</td>
<td>Dog, wolf</td>
<td>Camel, pig, cattle, goat, sheep, reindeer</td>
<td>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</td>
<td>(1–15)</td>
</tr>
<tr>
<td><em>E. canadensis</em> G8</td>
<td>Wolf</td>
<td>Moose, elk, muskox, mule deer, sheep</td>
<td>America, Canada, Estonia, Latvia, Russia, China</td>
<td></td>
</tr>
<tr>
<td><em>E. canadensis</em> G10</td>
<td>Dog, wolf</td>
<td>Moose, elk, reindeer, mule deer, yak</td>
<td>Finland, Mongolia, America, Canada, Estonia, Latvia, Sweden, Russia, China</td>
<td></td>
</tr>
</tbody>
</table>

**References**


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.