

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.

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

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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.

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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 $\geq 50\%$ 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 herds 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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Appendix

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

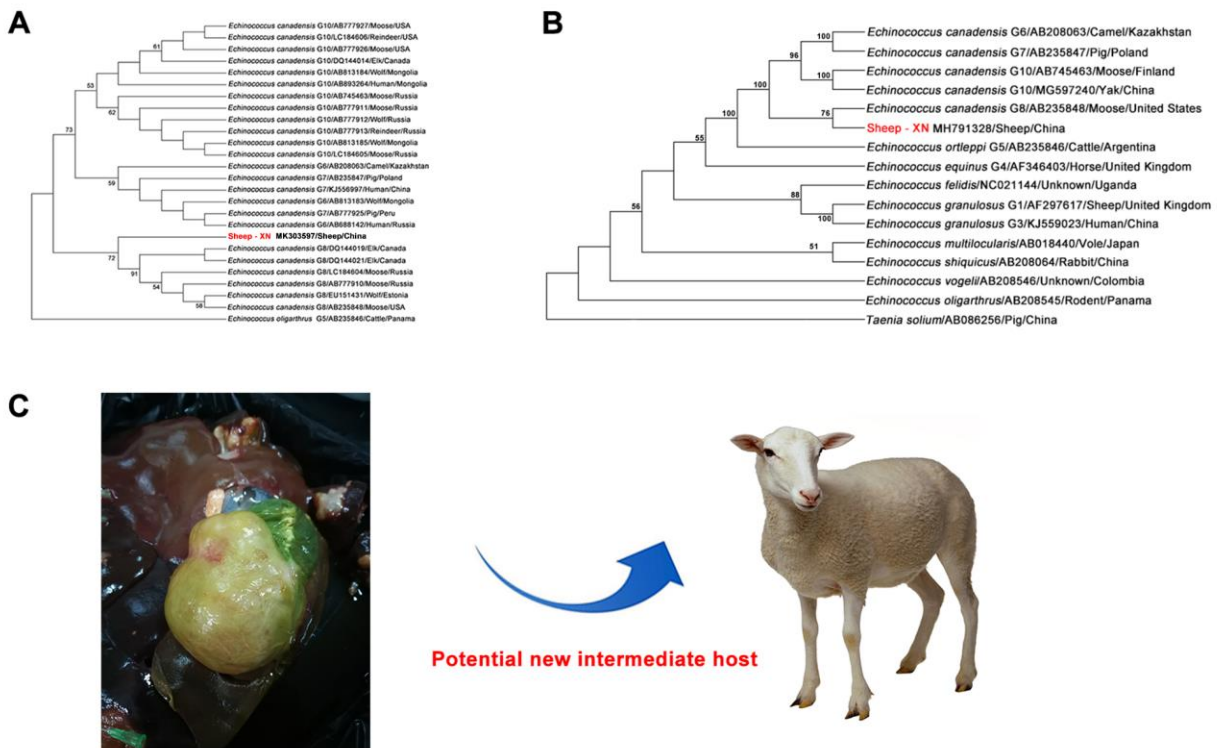
Genotype	Definitive hosts		Geographic distribution	References
	Definitive hosts	Intermediate hosts		
<i>E. canadensis</i> G6/7	Dog, wolf	Camel, pig, cattle, goat, sheep, reindeer	Mexico, Peru, Brazil, Chile, Argentina, Tunisia, Algeria, Libya, Namibia, Mauritania, Ghana, Egypt, Sudan, Ethiopia, Somalia, 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)
<i>E. canadensis</i> G8	Wolf	Moose, elk, muskox, mule deer, sheep	America, Canada, Estonia, Latvia, Russia, China	
<i>E. canadensis</i> G10	Dog, wolf	Moose, elk, reindeer, mule deer, yak	Finland, Mongolia, America, Canada, Estonia, Latvia, Sweden, Russia, China	

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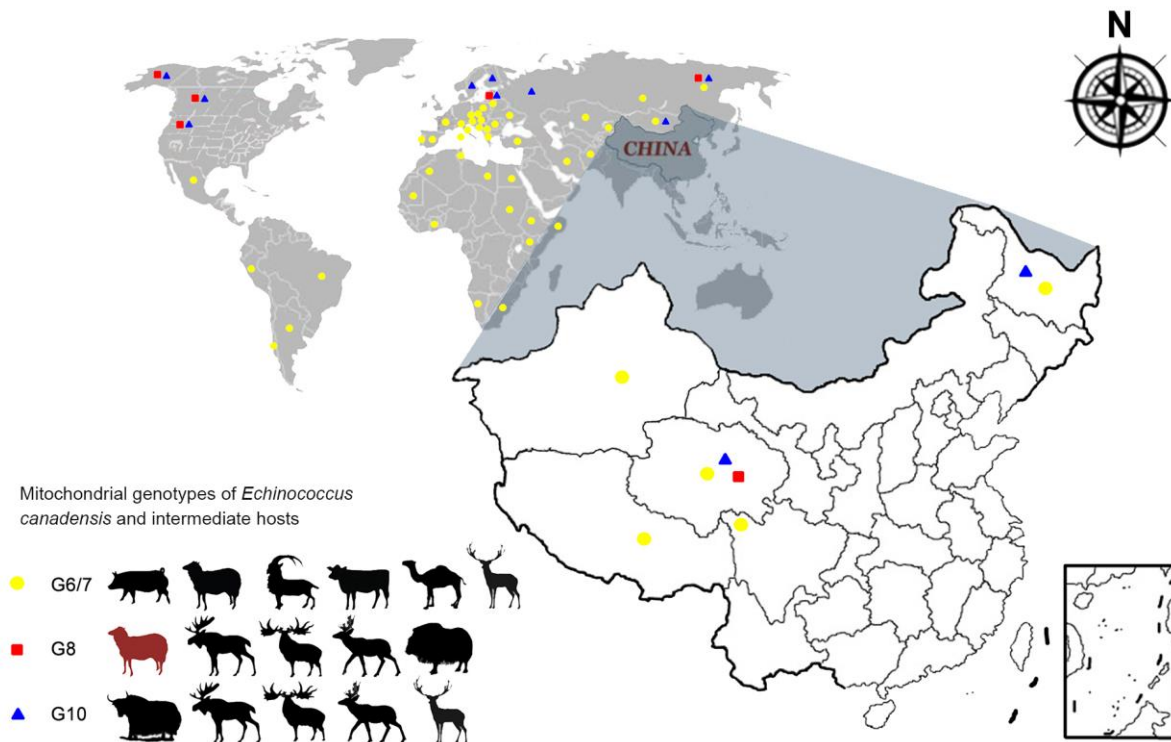
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Appendix Figure 1. Molecular identification of *Echinococcus canadensis* G8 tapeworm from sheep in China, 2018. A) The phylogenetic tree was constructed by using the Kimura 2-parameter model based on maximum-likelihood analysis by using the partial 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 $\geq 50\%$ 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 $\geq 50\%$ 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.