

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

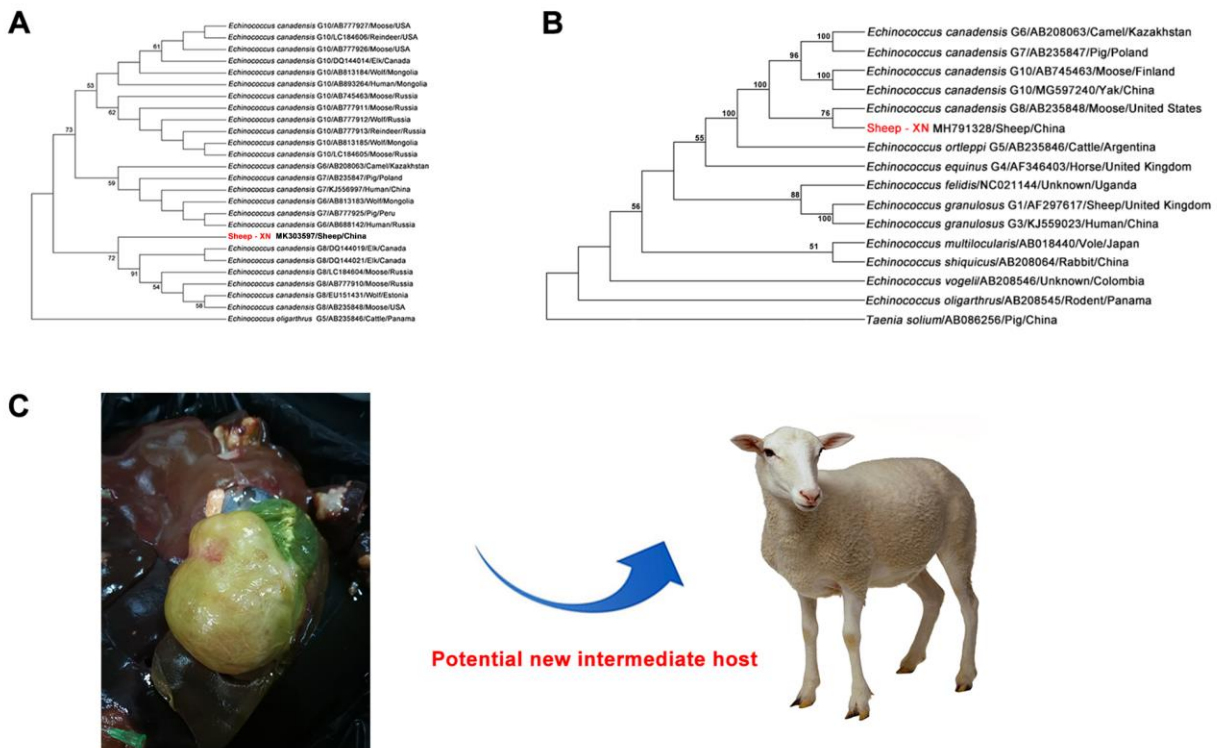
Genotype	Definitive hosts		Geographic distribution	References
	Definitive hosts	Intermediate hosts		
<i>E. canadensis</i> G6/7	Dog, wolf	Camel, pig, cattle, goat, sheep, reindeer	Mexico, Peru, Brazil, Chile, Argentina, Tunisia, Algeria, Libya, Namibia, Mauritania, Ghana, Egypt, Sudan, Ethiopia, Somalia, 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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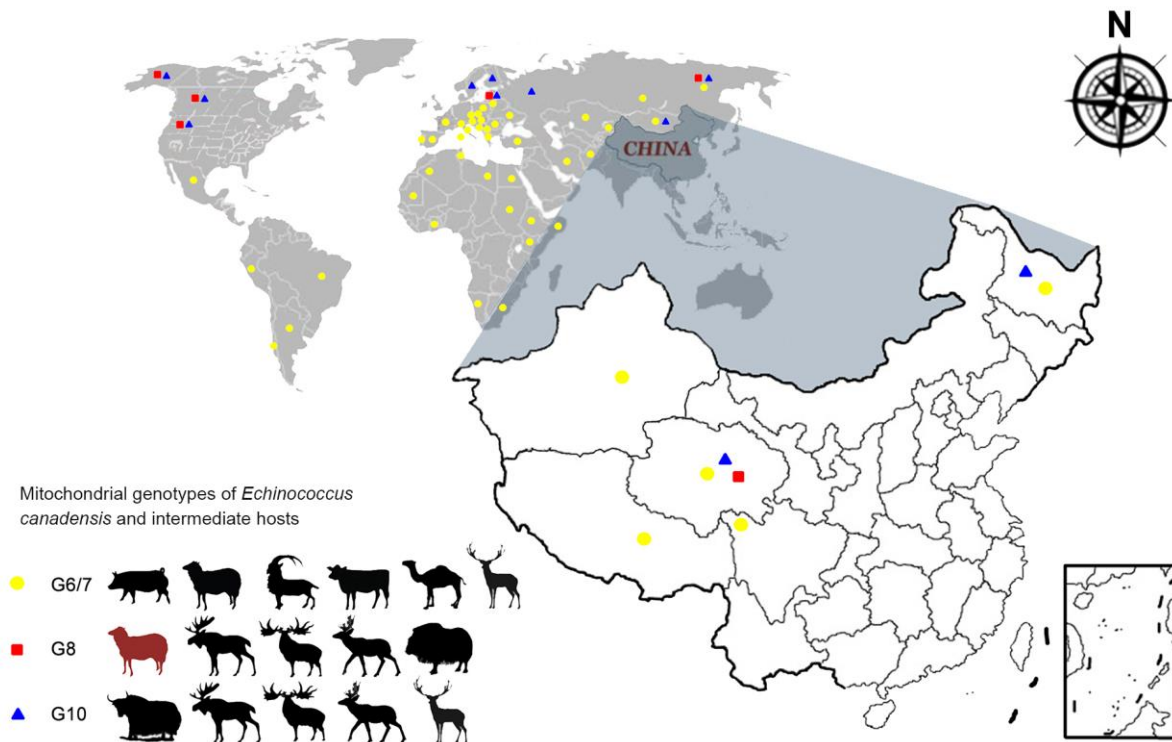
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Appendix Figure 1. Molecular identification of *Echinococcus canadensis* G8 tapeworm from sheep in China, 2018. A) The phylogenetic tree was constructed by using the Kimura 2-parameter model based on maximum-likelihood analysis by using the partial 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.