



Molecular identification of *Echinococcus granulosus* on the Tibetan Plateau using mitochondrial DNA markers

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ABSTRACT. Cystic echinococcosis (CE) is an important worldwide zoonotic disease that causes large economic losses and human suffering. *Echinococcus granulosus*, the causative agent of CE, exhibits different genotypes in different locations. In order to identify its genotypes and analyze its genetic structure on the Tibetan Plateau, we collected 72 hydatid cysts from different intermediate hosts and amplified and sequenced their mitochondrial cytochrome c oxidase subunit 2 (*cox2*) genes. Seventy isolates were identified as the *E. granulosus* G1 genotype, while two isolates belonged to the G6 genotype. There were 18 haplotypes among the 70 *E. granulosus* isolates, which exhibited a star-like network pattern and shared a common haplotype (H₁). There was little difference between geographical sub-populations. Our results suggest that a recent *E. granulosus* population expansion occurred

on the Tibetan Plateau, suggesting that *E. granulosus* was introduced into China. This study increases the basic molecular data needed for the molecular diagnosis, epidemiology, prevention, and control of *Echinococcus* diseases.

Key words: *Echinococcus granulosus*; Mitochondrial DNA; Tibetan Plateau; Molecular identification