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Short communication

Phylogenetic analysis of *Sarcocystis nesbitti* (Coccidia: Sarcocystidae) suggests a snake as its probable definitive host

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ABSTRACT

Sarcocystis nesbitti was first described by Mandour in 1969 from rhesus monkey muscle. Its definitive host remains unknown. 18S rRNA gene of *S. nesbitti* was amplified, sequenced, and subjected to phylogenetic analysis. Among those congeners available for comparison, it shares closest affinity with those species of *Sarcocystis* which use snakes as definitive hosts. We therefore hypothesize that a snake may serve as the definitive host for *S. nesbitti*.

1. Introduction

A number of cases of *Sarcocystis* infection in humans, monkeys, and other nonhuman primates have been reported from South-East Asia, for example from Malaysia (Prathap, 1973; Kannan and Dissanaike, 1975; Kannan et al., 1975; Pamphlett et al., 1978; Wong and Pathmanathan, 1992, 1994; Ravi et al., 1996) and other parts of the world (Beaver et al., 1979; Abdel, 1990; Pamphlett and O'Donoghue, 1990). The prevalence of infection with this parasite in humans is believed to be higher in South Asia than in Europe (Wong et al., 1993). However, in the Chinese mainland, there are only five reported cases of *Sarcocystis* infection in humans (Feng, 1932; Mao, 1963; Li and Jiau, 1981) and only one case infection in monkeys (Yang et al., 2005). Preventing human infections from such potentially zoonotic parasites requires better understanding of their natural epidemiology, including the identity of their definitive hosts.

Sarcocystis nesbitti was first described by Mandour in 1969 from rhesus monkey muscle (Dahlgren et al., 2008), but its definitive host remains unknown. We previously reported the first case of *S. nesbitti* Mandour, 1969 on the Chinese mainland, based on the morphology of the sarcocyst detected in a monkey (*Macaca fascicularis*) raised on a farm in Yunnan Province (Yang et al., 2005). Morphological affinities give reason to suspect that one parasite species, *S. nesbitti*, may utilize *Macaca mulatta*, *M. fascicularis*, *Cercocebus atys*, and *Papio papionis*, as well as human intermediate hosts. As such, *S. nesbitti* may be a zoonotic species whose

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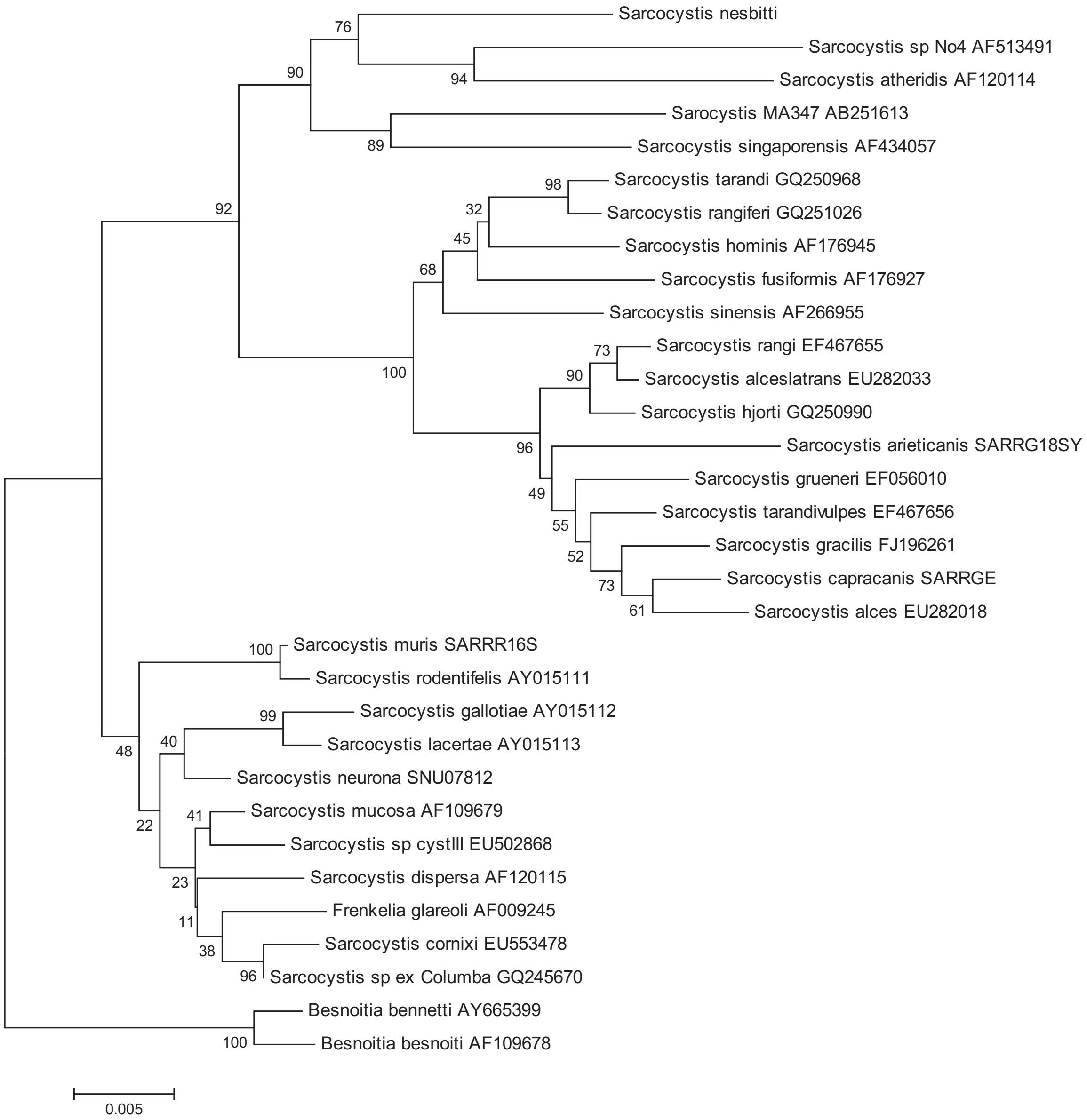

Fig. 1. Evolutionary relationship of *S. nesbitti* to other species. Phylogenetic relationships among sequences most similar to *S. nesbitti* were reconstructed under the criterion of Mininum Evolution from an alignment of 1111 ungapped positions of 18S rDNA using the Maximum Component Likelihood method (Tamura et al., 2004). Nodal support is represented as a proportion of 1000 bootstrap replicates, and branch lengths are proportional to genetic distances and are in the units of the number of base substitutions per site. *S. nesbitti* shares greatest affinity with other species sampled from East Asia that complete their lifecycle in snakes.

reservoir hosts are South Asian monkeys (Yang et al., 2005). Genetic characterization would assist in future efforts to establish the identity and epidemiology of such parasites, and a phylogenetic context could assist future efforts to establish the complete life cycle of zoonotic and enzootic parasites. Accordingly, we here analyzed the 18S rRNA gene of an isolate of *S. nesbitti* and assessed its likely definitive host type based on phylogenetic affinity.

2. Materials and methods

2.1. *S. nesbitti* sarcocysts isolation

S. nesbitti sarcocysts were isolated from muscle samples of one naturally infected *M. fascicularis*, and prepared for genetic characterization, using previously reported methods (Yang et al., 2001). The muscle samples were examined