

Fallow deer (*Dama dama*) as a new intermediate host for *Sarcocystis cruzi*

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Sarcocystis spp. are cyst-forming protozoan parasites with an obligatory two-host life cycle with carnivores as definitive hosts and herbivores or omnivores as intermediate hosts. Each intermediate and definitive host may harbor more than one *Sarcocystis* species. Wild and domestic ruminants such as red deer, roe deer, fallow deer, cattle, sheep or goats may act as intermediate hosts for many *Sarcocystis* spp. The intermediate hosts become infected with *Sarcocystis* species by ingesting sporocysts excreted in the feces of the definitive host. Some *Sarcocystis* species are important pathogenic organisms which are dangerous to humans and livestock. The harmful pathogenic effects of these parasites mainly occur in intermediate hosts. Monitoring the health of the wildlife population is important for understanding and controlling possible disease transmission between wildlife and humans or livestock; however, few molecular studies examine the *Sarcocystis* spp. which parasitize cervids in Poland.

The present study was undertaken to identify the *Sarcocystis* spp. parasitizing fallow deer (intermediate hosts) farmed at the Breeding Station in Kosewo Górne in the Mazurian Lake District. The hearts of fallow deer were examined for the presence of sarcocysts by light microscope, and DNA was extracted from individual sarcocysts. PCR was used to examine the isolated sarcocysts based on small subunit ribosomal RNA analysis: fragments of 18S rDNA of about 900 b.p. were amplified. Additionally, DNA from the other apicomplexan parasites *Toxoplasma gondii* and *Neospora caninum* were used as positive controls. The PCR products were purified and sequenced.

The Basic Local Alignment Search Tool (BLAST) was used to search for similarities between the newly-obtained sequences and sequences of *Sarcocystis* spp. already published in GenBank. The obtained sequences showed 97% similarity with the *S. cruzi* 18S ribosomal RNA gene. The newly-obtained sequences have been submitted to GenBank.

The present study documents the first molecular identification of *S. cruzi* from a fallow deer in Poland and evaluates the competence of fallow deer as a host for *S. cruzi* – the most pathogenic and specific species for cattle. This is the first study to examine the status of *Sarcocystiosis* in fallow deer in Poland. The findings of the present study are significant as farmed fallow deer have grown in number during last decade and consumer demand for their meat has increased.