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Morphological and molecular differentiation of *Staphylocystis clydesengeri* n. sp. (Cestoda, Hymenolepididae) from the vagrant shrew, *Sorex vagrans* (Soricomorpha, Soricidae), in North America

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Abstract

Staphylocystis clydesengeri n. sp. is described from shrews *Sorex vagrans* in Montana and Washington, United States. It differs from the only previously known North American representative of the genus, *S. schilleri*, in having more numerous (37–42 vs 22–30) and larger (39–44 µm vs 27–30 µm) rostellar hooks. The two species also differ in several other important characters such as relative length of the cirrus pouch, position of gonads and shape of mature proglottides. Morphological differentiation of the new species from all previously known Palearctic species of *Staphylocystis* from *Sorex* is also provided. Differentiation from *Staphylocystis* parasitic in crocidurine shrews is not provided due to the high level of specificity among shrew hymenolepidids to the host genera and much greater levels of sequence divergence between *Staphylocystis* from the two groups of shrews. Molecular differentiation based on 2,800 base pair long sequences of nuclear ribosomal RNA (complete ITS region and partial 28S region), 663 base pair long sequences of mitochondrial nad1 gene and 542 base pair long sequences of mitochondrial ribosomal 16S gene strongly support the status of *Staphylocystis clydesengeri* n. sp. Relative utility of the DNA fragments used in this study for reliable differentiation among closely related species of mammalian hymenolepidids is discussed. Nuclear ribosomal RNA region appears to be too conserved for this purpose. Use of at least one mitochondrial gene in addition to nuclear ribosomal RNA or without it, is recommended. *Vampirolepis novosibirskiensis* Sawada & Kobayashi, 1994 is transferred to *Staphylocystis* as a junior synonym of *S. furcata* (Stieda, 1862). *Rodentolepis gnoskei* Greiman & Tkach, 2012 is transferred to *Pararodentolepis* Makarikov and Gulyaev, 2009 as a new combination *Pararodentolepis gnoskei* (Greiman & Tkach, 2012) n. comb.

Key words: *Staphylocystis clydesengeri* n. sp., *Staphylocystis schilleri*, Hymenolepididae, *Sorex vagrans*, *Sorex palustris*, USA, molecular differentiation, nuclear ribosomal RNA, nad1 mitochondrial gene, 16S mitochondrial gene

Introduction

Staphylocystis Villot, 1877 is a large genus of hymenolepidid cestodes parasitic mainly in shrews, with several species reported from rodents and bats. The vast majority of the members of *Staphylocystis* parasitize crocidurine shrews in Asia, Africa and Europe. Only a few *Staphylocystis* species have been described so far from soricine shrews, all from *Sorex* spp. *Staphylocystis furcata* (Stieda, 1862) parasitizes several *Sorex* Linnaeus species and is broadly distributed throughout the Palearctic region from Western Europe to the Far East of Russia (Vaucher 1971, Genov 1984, Novikov 1995, Karpenko 2004). *Staphylocystis sibirica* (Morozov, 1957) is known from at least three *Sorex* species and is distributed in the eastern Palearctic from Lake Baikal to the Kuril Islands (Morozov 1957, Eltyshev 1975, Novikov 1995, Kornienko *et al.* 2008) and *Staphylocystis amurensis* (Karpenko, 1984) was reported from Laxmann's shrew *Sorex caecutiens* Laxmann and taiga shrew *Sorex isodon* Turov in the Khabarovskiy Krai, in the Russian Far East (Karpenko 1984, 2004).

Only one *Staphylocystis* species, namely *Staphylocystis schilleri* (Rausch & Kuns, 1950), is known from North America. It was originally described from the masked shrew *Sorex cinereus* Kerr in Wisconsin (Rausch & Kuns