

Morphological, molecular and pathological appraisal of *Hymenolepis nana* (Hymenolepididae) infecting laboratory mice *Mus musculus*

Ebtsam Al-Olayan

King Saud University College of Science

Rewaida Abdel-Gaber (✉ rewaida@sci.cu.edu.eg)

King Saud University <https://orcid.org/0000-0001-9263-6871>

Abeer Aloufi

King Saud University College of Science

Zainab Alanazi

King Saud University College of Science

Research article

Keywords: Laboratory animals; Rodents; *Hymenolepis* species; Morphological characterisation; Molecular analyses

Posted Date: October 1st, 2019

DOI: <https://doi.org/10.21203/rs.2.14737/v1>

License:   This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Version of Record: A version of this preprint was published at Microscopy and Microanalysis on March 5th, 2020. See the published version at <https://doi.org/10.1017/S1431927620000161>.

Abstract

Background: *Hymenolepis nana*, commonly found parasite in mice colonies maintained under conventional conditions, has zoonotic potential and is characterised by autoinfection and direct life cycle. Results: This study intended to determine parasitic infection rate in laboratory mice. Of the 50 mice, 40.0% were found to be infected with hymenolepidid cestode. Infection rate was higher in males (52.0%) than in females (28.0%). Light and scanning electron microscopic studies of cestode parasite revealed that the worms were medium-sized; had globular scolex with four suckers, a retractable rostellum equipped with 20-30 hooks, and a short unsegmented neck; remaining strobila consisted of immature, mature, and gravid proglottids; irregularly alternating genital pores; lobulated ovary; post-ovarian vitelline gland; and uterus containing ~200 small eggs in gravid proglottids. Molecular characterisation based on mitochondrial COX1 gene sequence analysis used to confirm taxonomy of the parasite. The parasite showed identity ~80.0% with other species available in GenBank. High blast scores and low divergence were noted between isolated parasite and previously described *H. nana* (gb| AP017666.1). Phylogenetic analysis using COX1 sequence place this hymenolepidid species within Cyclophyllidea. Conclusions: The present species was found to be deeply embedded in the genus *Hymenolepis* with close relationships to other *H. nana* as a putative sister taxon.

Text

The authors have retracted the text of this preprint.