

Occurrence and molecular phylogeny of *Fasciola* species in camels of southwestern Iraq

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Abstract

Background and Aim: *Fasciola* spp. are important trematodes of public health concern in various animals, including camels. This study aimed to determine the occurrence of liver flukes in camels, to determine the molecular confirmation of *Fasciola*, and to perform phylogenetic analysis of study isolates to identify the species of *Fasciola*.

Materials and Methods: In total, 107 slaughtered camels were inspected to collect liver flukes that were examined molecularly using polymerase chain reaction (PCR) to confirm *Fasciola* species. Then, the study isolates were sequenced, submitted to the National Center for Biotechnology Information (NCBI) database, and analyzed phylogenetically to identify the species of each study isolate.

Results: Liver flukes were detected in 17.67% of the camels. Regarding the migratory stages of the collected worms, juvenile worms (73.91%) were significantly more prevalent than adult worms (26.09%). Regarding the risk factors, a significantly greater occurrence rate and risk of infection was detected in Al-Najaf compared with Al-Muthanna, as well as in younger camels (1–4 years) compared with older camels. Although the occurrence rate of liver flukes was insignificantly different between females (9.38%) and males (6.98%), females appeared to be at a significantly higher risk of infection than males. Molecularly, 33.33% of the worm samples were positive for species in the *Fasciola* genus. Phylogenetic analysis of all positive PCR products (total no = 19) confirmed that 63.16% of the local *Fasciola* spp. isolates were related to the NCBI-Basic Local Alignment Search Tool (NCBI-BLAST) Saudi Arabian *Fasciola hepatica* isolate at an identity range of 95.94%–99%; while 36.84% of the local *Fasciola* spp. isolates were related to the NCBI-BLAST Iranian *F. gigantica* isolate at an identity range of 97.73%–99%.

Conclusion: This study found a 17.67% occurrence of *Fasciola* spp. in camels, with juvenile worms being more common than adult worms. Molecular analysis revealed that 63.16% of the isolates were related to *F. hepatica* from Saudi Arabia, while 36.84% matched *F. gigantica* from Iran. Younger camels and those from Al-Najaf were at higher risk, highlighting the need for targeted control measures.

Keywords: camel trematode, conventional polymerase chain reaction, fascioliasis, one-humped camel, phylogenetic analysis.

Introduction

Fasciola, which is commonly known as liver fluke, is a genus of trematode parasites that have been described as dorsoventrally flattened, bilaterally unsegmented, and soft-bodied invertebrates that cause a disease known as fasciolosis or fascioliasis [1]. Taxonomically, although various species are found within the genus *Fasciola*, *F. hepatica* and *F. gigantica* alone are well known [2]. These parasites have economic and welfare importance in the livestock sector, particularly in cattle, camels, sheep, and goats, because of changes in climate and farming practices [3]. *Fasciola* has a complete life cycle, including free-living stages and an intermediate host

(snails). Adult parasites reside in the large bile ducts of the host, where they shed eggs into the gall bladder. Eggs are transported along the intestine to be excreted in the host's feces [4, 5]. In the environment, once eggs are freed from fecal matter, free-swimming miracidia hatch and penetrate a suitable snail intermediate host, then migrate to the digestive duct of snail where they transform into sporocysts. After many asexual reproduction rounds, large numbers of cercariae are produced and released from the snail host, followed by migration to vegetation and the formation of resistant cysts or metacercaria, which are ingested by mammalian hosts. Finally, metacercaria excyst in duodenum, migrate to the liver as immature flukes, and then develop into adult individuals in the bile ducts [6, 7].

The dromedary camel (*Camelus dromedaries*) is an even-toed, ungulate animal that has adapted physiologically and anatomically to survive the harsh conditions of desert and semi-desert areas in numerous countries located in Asia, Africa, and South America [8]. In Iraq, the number of camels was estimated at 330,000 in the 1970s and had decreased

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