



Molecular Sequencing Analysis of *Fasciola* Spp. in Sheep

ISRAA M. ESSA*, GHAZI Y. AZZAL, ALAA TARIQ ABDULWAHID

Department of Parasitology, College of Veterinary Medicine, University of Basrah, Basra, Iraq.

Abstract | This study aims to investigate the prevalence rate of *Fasciola* in livers of 361 slaughtered sheep at Basra province (Iraq) with molecular testing and phylogenetic analysis of obtained flukes in the National Center For Biotechnology Information (NCBI). The findings showed that 8.03% of livers were infected with *Fasciola* spp., in which, juvenile flukes were observed significantly (79.31%) when compared to adults (20.69%). Based on morphology, all adult flukes were diagnosed as *Fasciola*. Accordingly, positive rate, risk and Odd ratio of fasciolosis were reported significantly in sheep of larger than 3 years than those of larger than 2-3 years, 1-2 years and sheep of less than 1 year. Concerning sex, no variation was detected between female (9.02%) and male (5.26%) sheep; however, females were appeared at higher risk of infection males. Molecular examination using the PCR assay demonstrated that 93.1% of samples were *Fasciola*; whereas, phylogenetic analysis of five isolates indicated its identity to Saudi Arabian (MN559388.1) *F. hepatica* isolate. In conclusion, Molecular and phylogenetic analysis of ovine liver flukes indicated worthily that *F. hepatica* was the more prevalent *Fasciola* species in sheep of Basra province. In addition, our results provided an initial basic data for monitoring this potentially important parasite in field. However, the main limitations of the present study include the low number of examined animals, short period of study, and disapproving of some owners to examine their slaughtered animals. Therefore, it is necessary to develop the suitable parasite control measures (e.g. controlling the snails, judicious annual using of flukeicide, frequent examination of fecal samples of field animals, and destroying of infected livers) and evaluation the local epidemiology of fasciolosis. Also, wider surveys including different areas and animals with using the advanced diagnostic assay in combination with morphology should be conducted.

Keywords | Fasciolosis, Ovine liver fluke, Conventional PCR, Phylogeny, *Fasciola hepatica*, Iraq

Received | June 14, 2024; **Accepted** | July 26, 2024; **Published** | August 22, 2024

***Correspondence** | Israa M. Essa, Department of Parasitology, College of Veterinary Medicine, University of Basrah, Basra, Iraq; **Email:** israa.essa@uobasrah.edu.iq

Citation | Essa IM, Azzal GY, Abdulwahid AT (2024). Molecular sequencing analysis of *fasciola* spp. in sheep. Adv. Anim. Vet. Sci. 12(10): 1846-1852.

DOI | <https://dx.doi.org/10.17582/journal.aavs/2024/12.10.1846.1852>

ISSN (Online) | 2307-8316; **ISSN (Print)** | 2309-3331



Copyright: 2024 by the authors. Licensee ResearchersLinks Ltd, England, UK.

This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

INTRODUCTION

Fasciola, commonly known as liver fluke, is a parasitic flatworm which classify under the Plagiorchiida Order of the Trematoda Class in the Platyhelminthes Phylum. The genus of *Fasciola* includes mainly *F. hepatica* Linnaeus, 1758, and *F. gigantica* Cobbold, 1855 in addition to a number of invalid species such as *F. indica*, *F. californica*,

F. halli and *F. nyanzae* (Itagaki *et al.*, 2022; Madsen *et al.*, 2022). Wide range of animal species and humans can infect with *Fasciola* resulting in a public health concern and severe economic losses in livestock industry (Beesley *et al.*, 2018; Regasa *et al.*, 2021; Zerna *et al.*, 2021). Lifecycle of *Fasciola* comprises five phases; egg (pass through feces of mammalian host), miracidia (free-swimming and infect the intermediate host), cercariae (erupt from snail host and attached