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Molecular characterization of fasciola and dicrocoelium species isolated from ruminant livestock in Qazvin, Iran

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Abstract

Introduction: Fascioliasis and dicrocoeliasis are the most frequent zoonotic diseases with increasing human health problems in different parts of Iran. Two species, *Fasciola hepatica* (*F. hepatica*) and *Fasciola gigantica* (*F. gigantica*), are spread in the country. Molecular approaches have a decisive role in identifying both the species. The aim of this study was to detect *Fasciola* spp. and *Dicrocoelium* spp. by amplifying the ITS-2 and 28S rDNA gene sequence. **Methods:** Overall, 30 infected liver samples were collected from the livestock of Qazvin, Iran. The adult flukes were collected from different livestock. DNA extraction and PCR amplification of ribosomal RNA gene region (ITS2) and 28S rDNA gene fragment were conducted and a phylogenetic tree was constructed. **Result:** All the isolates obtained from the cattle (No: 7) and 82.6% (No: 19) of sheep isolates were infected with *F. hepatica* species, whereas 17.4% (No: 4) of sheep isolates were infected with *F. gigantica*. It was also shown that *F. hepatica* was the predominant species of *Fasciola* present in the region. All the specimens were infected with *Dicrocoelium dendriticum* (*D. dendriticum*). **Conclusion:** Both the species of *Fasciola* were found in Qazvin. *D. dendriticum* was the sole infecting species of the *Dicrocoelium* genus in the livestock of the city of Qazvin. Further research studies are needed to determine the intermediate host of the parasites in the region.