

عنوان مقاله:

MULTILOCUS SEQUENCE TYPING AND GENETIC STRUCTURE OF FASCIOLA ISOLATES FROM LIVESTOCK
IN KERMANSHAH, IRAN

محل انتشار:

نوزدهمین کنگره بین المللی میکروب شناسی ایران (سال: 1397)

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خلاصه مقاله:

Background and Aim: fasciolosis is a parasitic disease caused by liver fluke species of the genus *Fasciola*, *Fasciola hepatica* and *Fasciola gigantica*. There is limited information about the diversity of the genus *Fasciola* in Iran. Implementation of molecular strategies for parasite typing, particularly multilocus sequence typing (MLST) represents an improved approach for genetic variability and population dynamics analyses. For the first time, we introduce a Multilocus Sequence Typing (MLST) method to genetically characterize *Fasciola* species. **Methods:** Thirty-four *Fasciola* species isolated from livestock and from Kermanshah province were characterized using MLST approach. DNA fragments (500-800 bp) from 5 housekeeping genes were sequenced. A MLST analysis was developed based on the genes Cyt b, ND1, HSP 70, Pold, Pepck. Phylogeny analysis was conducted both on concatenated MLST loci and on each individual locus. **Results:** A total of 3154 bp were analyzed for each isolate. In all, 52 and 72 polymorphic sites were identified for *Fasciola hepatica* and *Fasciola gigantica*, respectively. The neutrality hypothesis could not be rejected. The overall MLST scheme exhibited a high level of discrimination (Simpson Index = 0.9929) for *Fasciola hepatica* and *Fasciola gigantica*. **Conclusion:** We suggest that MLST will have a strong impact on molecular epidemiological studies of fasciolosis disease and the phylogenetics of its causative agent.

کلمات کلیدی:

Fasciola, genotyping, livestock, MLST, Iran

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