

عنوان مقاله:

فاسیولا ژیگانتیکا نشخوارکنندگان: تجزیه و تحلیل شجره شناسی بر اساس ترادف COX1

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خلاصه مقاله:

BACKGROUND: Fasciola species are parasitic trematode with world wide distribution that infects wild and domesticated herbivores, particularly ruminants. The aim of the present study was to investigate the intra species variations of *F. gigantica*, from goats and buffalos isolates in two common geographic climates of Iran. **METHODS:** Fasciola species were collected from goat, buffalo, sheep, and cattle in different regions. Cytochrome c oxidase I (COX1) of mitochondrial DNA (mt-DNA) was amplified from individual trematodes by polymerase chain reaction (PCR), using universal primers, and the amplicons were consequently sequenced and sequencing data were analyzed, using Clustal W software against the GenBank database. **RESULTS:** A monomorphic DNA segment of approximately 499bp was seen in Fasciola isolates. The results of the amino acid sequence alignment defined strictly conserved amino acid residues in buffalo isolates of *F. gigantica* and partially conserved residues for goat isolates of *F. gigantica*. There are four tandem amino-acid replacements in the goat isolates at the position of 135-138, where Leucine (L), F (Phenylalanine), T (Threonine), and D (Aspartate) sequences changed into S (Serine), L (Leucine), H (Histidine), and L (Leucine), respectively. Furthermore, a replacement in the sequence of amino acid was found in isolates from buffalo at the position of 154, where Serine (S) was transformed into Leucine (L). **CONCLUSION:** The findings of our study indicate that the variants of goat and buffalo can be responsible for persistence of Fasciola infection in the endemic areas of Iran. It seems that biological differences could be occurred by considering a variety of *F. gigantica*-hosts in Iran. Thus, suitable approaches are required for effective treatments and useful control strategies.

کلمات کلیدی:

COX1, Fasciola gigantica, phylogenetic, Ruminants, Sequence

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