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A DNA-Based Identification of *Strongyloides stercoralis* Isolates from Iran

MR Nilforoushan, H Mirhendi, S Rezaie, M Rezaian, AR Meamar, EB Kia

Abstract:

Background: *Strongyloides stercoralis*, the etiological agent of strongyloidiasis, is one of the most common parasitic nematode with the unique ability to complete its life cycle and proliferate within the host. Although it is an endemic parasite in Iran, no molecular characterization is available on isolates originated from the country. Therefore, this study was conducted for molecular identification of human *Strongyloides* isolates in the three most prevalent provinces. Methods: After microscopical examination and agar plate culture of nearly 1500 stool samples, 20 isolates of *S. stercoralis* filariform larvae were recovered from (Gilan and Mazandaran in north and Khouzestan in south) of Iran. The genomic DNA was extracted from all these samples and two primer sets were selected for amplification. ITS1 region of the rDNA gene was amplified by a nested Polymerase Chain Reaction (nested-PCR). The PCR products were sequenced and analyzed in comparison with the sequences deposited in GenBank. Results: DNA sequence analysis of ITS1 region showed that all the 20 isolates were *S. stercoralis*. There was slight variation in the ITS1 region among the isolates. Conclusion: ITS1 sequencing seems to be a valid target for molecular identification of *S. stercoralis*.

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rDNA

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