

عنوان مقاله:

Phylogenetic Evaluation and Molecular Variation of *Leishmania major* and *Leishmania tropica* Isolated from Different Parts of Iran

محل انتشار:

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خلاصه مقاله:

Aims The aim of this study was species identification and phylogenetic analysis of species of *Leishmania* isolated from clinical samples. **Materials & Methods** The samples were collected from patients that were infected from different parts of Iran. After microscopic examination, we used PCR method for amplify the ITS1 (internal transcribed spacer 1) gene. RFLP method (digestion with Apo1 restriction enzyme) and for phylogenetic construction, DNA sequencing of PCR product were used. **Findings** Two samples from Khorasan province (Mashhad) were *Leishmania tropica* (*L. tropica*), while others were *Leishmania major* (*L. major*). *L. tropica* samples are more variable compared with *L. major*. The molecular sequencing differences between *L. major* was related to geographical distribution. Based on the results of PCR product in the gel electrophoresis and DNA sequencing for *L. tropica* and *L. major*, the DNA sizes were between 350 and 369bp. The RFLP for *L. major* and *L. tropica* showed two and one bands, respectively. The sequences for all samples from central parts are the same, but there is difference with the samples isolated from North-East part of Iran. **Conclusion** The sequences of ITS1 gene of *Leishmania major* separated from Damghan and Esfarrayen are different from other samples. Similarity of DNA sequences of North-East part of Iran of *L. major* with samples from central parts was 99%. The similarity of two isolates of *L. tropica* was 96%. The most similarity of *Leishmania tropica* isolated was 95% with Indian isolate and the most similarity for *Leishmania major* was 99% with Friedlin strain

کلمات کلیدی:

Leishmania Major; PCR; RFLP; Sequencing; Phylogenetic Analysis; Iran

