

Genetic polymorphism of *Leishmania major* in two hyper endemic regions of Iran revealed by PPIP-PCR and ITS- RFLP.

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Source

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Abstract

BACKGROUND:

Zoonotic cutaneous leishmaniasis (ZCL) is a polymorphic disease that may show various clinical manifestations. Although it is suggested that the genetic variability of the parasite is one of the factors influencing clinical manifestations of leishmaniasis, no data exists regarding genetic polymorphism of *Leishmania major* (L.major). This study investigates the determination of genetic variations within the species of L.major isolates from different cases of ZCL in two hyper-endemic areas of Iran.

METHODS:

A variety of nucleic acid detection methods that target both DNA and RNA have been developed. Among these, the polymerase chain reaction (PCR) method proved to be a highly sensitive and specific technique. Species identification was based on permissively primed intergenic polymorphic-polymerase chain reaction (PPIP-PCR) and restriction fragment length polymorphism analysis of amplified internal transcribed spacer (ITS-RFLP) in the ribosomal operon of L.major from clinically different forms of ZCL. The DNA products were amplified by PCR, followed by digestion of the PCR product with restriction enzymes. The profiles were visualized in agarose gel under ultraviolet (UV) light.

RESULTS:

The PCR product obtained for all isolates was about 1010 bp in size. Different patterns of PPIP-PCR and ITS-RFLP in the ribosomal operon were classified as I, II, III, IV, and V. This classification was according to the number and localization of bands. Results of this research detected the genetic and clinical polymorphism of L. major, and showed that strain A was more frequent than other strains.

CONCLUSION:

The L.major causing ZCL in Isfahan, Iran is genetically a highly polymorphic species and PPIP-PCR exposed more genetic polymorphism among clinical samples in Isfahan, Iran.