

Detection and Identification of More Than One Species of Leishmania in Human from Endemic Focus of Zoonotic Cutaneous Leishmaniasis in Abarkouh

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Background & Objectives: Leishmaniasis is one of six important diseases which are great problems in global public health. In Iran, 15 out of 32 provinces have endemic regions for zoonotic cutaneous leishmaniasis (ZCL) where *L. major* have been reported as the main causative agent of this form of disease.

Methods: Samples were collected from suspected people to ZCL in different villages and cities of Abarkouh in 2010 and 2011. Stained Smears were examined under a light microscope and classified based on number of Leishmania amastigotes. DNA of parasite extracted and ITS-rDNA gene amplified by PCR. The PCR product digested with BsuRI restriction enzyme which was selected based on in-silico analysis using CLC DNA software.

Results: Samples were collected from lesions of 85 suspected people, 62 slides were microscopy-positive, 58 out of 85 were positive after amplifying ITS-rDNA gene. Using RFLP, most of the samples identified as *L. major* and those identified as *non-L. major*, were sent for sequencing and all Leishmania species will confirm in congress.

Conclusion: According to our finding, Leishmania major has been definitely recognized as the causative agent of ZCL in Abarkouh. The exact identification of Leishmania species in human cases is necessary for treating and controlling disease to help local health authorities

Keywords: *Leishmania major*; ITS; rDNA; PCR_RFLP; Abarkouh; Iran