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Detection process and genetic diversity determination of *Leishmania* species isolated from patients with cutaneous lesions referred to health centers of Ilam province, west of Iran

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Statement of the Problem: Zoonotic cutaneous leishmaniasis is a polymorphic disease which may show various clinical manifestations. Genetic diversity of the parasite is suggested to be one of the factors influenced on disease clinical manifestations. So, determination of parasite species and genetic variation of *Leishmania* in endemic areas of Iran (Ilam provinces, west of Iran, Border of Iraq Country) were investigated.

Methodology & Theoretical Orientation: Samples were taken from skin lesions of suspected persons to cutaneous leishmaniasis. Slides were prepared to find Leishman body using microscope and DNAs were extracted and kinetoplast DNA gene was amplified by standard PCR. Data were analyzed using the molecular and statistical software.

Findings: 200 samples were taken from suspected lesions to cutaneous leishmaniasis. Leishman body was found in all samples. Parasite species determined by kDNA gene sequencing. All species were *Leishmania* major. Molecular data was analysed using different Bio-softwares such as Pregap4 and MEGA6. All sequences were subjected to BLAST analysis to verify the isolates under study as *Leishmania* major. The plotted phylogenetic tree revealed four different clades for 22 specimens (Fig. 1).

Conclusion & Significance: Although all isolates were *Leishmania* major and belonging to different county in same geographic region (Ilam province) however analyzed isolates showed intra species genetic diversity and divided in four clades in dendrogram. This variation can have impact on strategies to drug resistance and control programs against parasite. It's probable that different species of sandflies and rodents are vector and reservoirs of parasite respectively but more studies are needed to prove this possibility.

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