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Original Article


Detection of *Leishmania major* In Naturally Infected Sand Flies Using Semi Nested-PCR

*MA Oshaghi¹, MR Yaghobi-Ershadi¹, M Abbassi¹, P Parvizi², AA Akhavan¹, A Rahimi Foroshani³, AR Zahraei¹, Y Rassi¹, F Mohtarami¹

¹Dept. of Medical Entomology and Vector Control, Faculty of Health & Institute of Health Research, Tehran University of Medical Sciences, Iran

²Dept. of Parasitology, Pasteur Institute of Iran, Tehran, Iran

³Dept. of Biostatistics & Epidemiology, School of Public Health, Tehran University of Medical Sciences, Iran

 Corresponding Author:

MA Oshaghi

Tel: +98 21 88951393, Fax: +98 21 88951393, E-mail: oshaghima@yahoo.com

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Abstract:

Background: The aim of this study was to assess *Leishmania* infection in sand fly species from areas where leishmaniasis is endemic. This is important for prediction of the risk and expansion of the disease.

Methods: In this cross-sectional study we used a PCR-based method for detection of *Leishmania* minicircle DNA within individual sand flies from Orzoleh, a new endemic leishmaniasis focus in southern Iran.

Results: We detected minicircle DNA in 6 of 92 (6.5%) *Phlebotomus (Phlebotomus) papatasi* collected indoor, while all of previous microscopic examination of sand flies specimens was negative for *Leishmania* promastigotes in the region. The species were identified as *Leishmania (Leishmania) major* by comparison of PCR products with a *L. major* positive control. All the *Leishmania*-positive sand flies were confirmed as *P. (P.) papatasi* by using a morphological key of Iranian sand flies.

Conclusion: Since PCR method is relatively easy and can process a large number of samples, it will be a powerful tool for the rapid identification of *Leishmania* species as well as monitoring the infection rate in sand fly populations in areas of low endemicity of leishmaniasis.

Keywords:

[Leishmania major](#) , [Sand fly](#) , [Leishmaniasis](#) , [PCR](#) , [Iran](#)

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