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Molecular characterization of Leishmania infection in sand flies from Al-madinah province, Western Saudi Arabia

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Cutaneous leishmaniasis (CL) is caused by various species of the genus Leishmania. The disease is considered a major health problem in different areas of Saudi Arabia including Al-madinah Al-munawarah province. We aimed to identify Leishmania species isolated from sand fly vectors by molecular analysis. Sand fly sampling was carried out from May 2010-October 2010 in province of Al-madinah Al-munawarah from four different localities. Female sand flies collected were subjected to DNA extraction followed by molecular analysis using the nested PCR and conventional PCR protocols, respectively, against minicircle kDNA and ribosomal internal transcribed spacer 1 (ITS1-rDNA). The PCR positive specimens against ITS1-rDNA locus were digested for further confirmation of species identification. A total of 2910 sand flies were collected. *P. papatasi* accounted for 93.8% (1673 male and 1057 female), however, the number of P. sergenti was only 180 (109 male and 71 female). Sixty-two out of 250 (23.7%) female *P. papatasi* tested for Leishmania parasite were positive for *L. major* using the semi-nested PCR method against kDNA. All of the 62 positive specimens produced a band size 650bp. A 31% of female P. sergenti were positive against kDNA of *L. tropica* and produced a 720bp band. These positive *P.sergenti* for *L. tropica* DNA produced ITS1-PCR-RFLP profile showed two bands of~200bp and 57bp which are specific for *L. tropica,* confirming the presence of *L. tropica* in *P. sergenti*. However, the ITS1-PCR-RFLP profile showed two bands of~203bp and 132bp which are specific for *L. major* in *P. papatasi*. We concluded that, the semi-nested PCR method against kDNA and the ITS1-PCR-RFLP analysis are useful tools for molecular identification of both *L. major* and *L. tropica.* A multicenter study is necessary in order to evaluate the extent of the disease and functional analysis of new Leishmania genes.

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Biography

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