Egypt. Acad. J. Biolog. Sci., 6(1): 79 - 88 (2013)
Email: egyptianacademic@yahoo.com
Received: 15/3/2013

A. Entomology
ISSN: 1687–8809
www.eajbs.eg.net

Individual Variations in *Phlebotomus papatasi* Collected from Different Localities in Saudi Arabia

Reem A. Al-Ajmi
Department of Zoology, King Saud University, Riyadh, Saudi Arabia

ABSTRACT

A method of typing *Phlebotomus* taxa in three areas in Saudi Arabia (Riyadh, Madinah and Asir) using morphological characteristics revealed that the phlebotomine species is *Phlebotomus papatasi*. This identification was confirmed by establishing a polymerase chain reaction (PCR) and direct partial sequences of 18S ribosomal RNA (rRNA) gene using specific designed Primers SandF1:5′-AGGCTCATTCAGTCGCTTTC-3′ and SandR1:5′-TGCAAGCTTATGACTCACACTT-3′. Morphological individual variations were also observed among some collected specimens. Nevertheless, genetic analysis confirmed that these specimens were also *P. papatasi*. PCR-amplified amplicons using ChromasPro. MEGA 5 program and neighbor joining (NJ) methods revealed several direct sequences for *P. papatasi* that were submitted in GenBank under the accession number JQ929125. In conclusion, the obtained results establish a powerful tool for the molecular taxonomy of *Phlebotomus* spp. in endemic areas to plan appropriate epidemiological surveillance programs that could be used to detect natural infections of sand fly vectors with pathogens.

Keywords: Phlebotomine sand flies, PCR, 18S ribosomal RNA gene, direct sequences, morphological characters, molecular characters, taxonomy.

INTRODUCTION

Zoonotic cutaneous leishmaniasis is caused by the parasitic protozoan *Leishmania major*, which is transmitted by the phlebotomine sand fly *Phlebotomus papatasi* in North Africa and Middle East (Lane, 1993). Also *P. papatasi* has been implicated in the transmission of *L. arabica* in Saudi Arabia (Peters *et al.*, 1986; Kllick-Kendrick, 1990), and of arboviruses in many countries (Javadian *et al.*, 1977; Tesh *et al.*, 1977). It is postulated that successful establishment of the disease in an endemic area is the outcome of a close association between the *Leishmania* parasite and its natural sand fly vector (Hamarsheh, 2011). Thus, identification of both sand fly and *Leishmania* is of great importance for predicting expansion of the disease in endemic areas, and also it helps in designing new strategic programs that limit spreading of such serious vectors (Kato *et al.*, 2007; Fujita *et al.*, 2012).

Sand fly identification based on morphological characters includes terminal genitalia of males and internal structures of females, such as spermatheca and cibarium and also pharynx in the head region (Lango, 2005; Singh and Philips-Singh, 2010). On the other hand, the development of alternative molecular data has been recently introduced as tools for the identification of sand flies. Among these techniques are the ribosomal RNA (rRNA) gene architecture and the highly conserved sequences of certain domains of the gene. These rRNA gene sequences have been used to reevaluate higher level relationships within the subfamily Phlebotominae and within the genera *Phlebotomus* and *Sergentomyia* (Aransay, 2000). The rRNA gene is a multicopy gene of tandem repeated transcription units. Each transcription unit