کارگاه‌های آموزشی مرکز اطلاعات علمی

مقاله نویسی علوم انسانی

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آموزش مهارت های کاربردی در تدوین و چاپ مقاله
Original Article

Molecular Detection of *Leishmania infantum* in Naturally Infected *Phlebotomus perfiliewi transcaucasicus* in Bilesavar District, Northwestern Iran

A Sanei Dehkordi, Y Rassi, MA Oshaghi, MR Abai, S Rafizadeh, MR Yaghoobi-Ershadi, M Mohebali, Z Zarei, F Mohtarami, B Jafarzadeh, A Ranjbarkhah, E Javadian

1Department of Medical Entomology and Vector Control, School of Public Health, Tehran University of Medical Sciences, Iran
2Emergency Management Center (EMC) Ministry of Health and Medical Education, Iran
3Department of Parasitology and Mycology, School of Public Health, Tehran University of Medical Sciences, Iran
4Health Center of Bilesavar, Ardebil Province, Iran

(Received 16 Aug 2010; accepted 19 Feb 2011)

Abstract

Background: Visceral leishmaniasis is caused by *Leishmania infantum*, transmitted to humans by bites of phlebotomine sand flies and is one of the most important public health problems in Iran. To identify the vector(s), an investigation was carried out in Bilesavar District, one of the important foci of the disease in Ardebil Province in northwestern Iran, during July–September 2008.

Methods: Using sticky papers, 2,110 sand flies were collected from indoors (bedroom, guestroom, toilet and stable) and outdoors (wall cracks, crevices and animal burrows) and identified morphologically. Species-specific amplification of promastigotes revealed specific PCR products of *L. infantum* DNA.

Results: Six sand fly species were found in the district, including: *Phlebotomus perfiliewi transcaucasicus, P. papatasi, P. tobbi, P. sergenti, Sergentomyia dentata* and *S. sintoni*. *Phlebotomus perfiliewi transcaucasicus* was the dominant species of the genus *Phlebotomus* (62.8%). Of 270 female dissected *P. perfiliewi transcaucasicus*, 4 (1.5%) were found naturally infected with promastigotes.

Conclusion: Based on natural infections of *P. perfiliewi transcaucasicus* with *L. infantum* and the fact that it was the only species found infected with *L. infantum*, it seems, this sand fly could be the principal vector of visceral leishmaniasis in the region.

Keywords: *Leishmania infantum, Phlebotomus perfiliewi transcaucasicus, nested PCR, Iran*

Introduction

Leishmaniases are parasitic diseases of multifaceted clinical manifestations caused by infections with species of *Leishmania*. These diseases are widespread in the Old and New Worlds with great epidemiological diversity. Approximately, 700 species of sand flies are known but only 10% of these serve as disease vectors. Further, only about 30 species are important from a public health standpoint (WHO 1990, Desjeux 2000, Sharma 2008).

Visceral leishmaniasis (VL), commonly caused by *Leishmania infantum* in the Mediterranean region, the middle east and Latin America, affects approximately half a million new patients each year (Lachaud 2002). In the Mediterranean basin, domestic dogs (*Canis fa-
miliaris) are the principle reservoir host and some species of sand-flies belonging to the subgenus Larroussius are the primary vectors (Oshaghi et al. 2009a).

Although VL occurs sporadically throughout Iran, the disease is endemic in several parts of northwestern Iran (Nadim et al. 1978, Davies et al. 1999, Mohebali et al. 1999, Rassi et al. 2004, 2005, 2009, Oshaghi et al. 2009b). The rate of infected sand flies in endemic areas and the identification of the infecting Leishmania parasites in the determined phlebotomine species are of prime importance in vectorial and epidemiological studies of leishmaniasis (Rodriguz et al. 1994). Three sand fly species, Phlebotomus perfiliewi transcaucasicus, P. (Larroussius) kandelakii Shchurenkova and P. (Larroussius) major Annandale are proven vectors in Iran (Rassi 2004, 2005, Azizi et al. 2008).

Two other species, P. (Larroussius) keshishiani Shchurenkova and P. (Paraphlebotomus) alexandri Sinton have been found naturally infected with promastigotes and are suspected vectors of VL in Iran (Seyyedi-Rashti et al. 1963, Schönian et al. 2003, Azizi et al. 2006). Leishmania parasites are directly detected by microscopic examination and all Leishmania species are very similar and their species identification is not possible morphologically (Schönian et al. 2003, Oshaghi et al. 2009a) therefore we used nested PCR and PCR-RFLP methods in this study, because the main advantages of these methods are their sensitivity and specificity, independently of the number, stage and localization of the parasite in the digestive tract of the vector (Perez et al. 1994).

This study was carried out during Jul-Sep 2008 in rural areas of Bilesavar District, in northwestern Iran at an altitude of 1311 m (Fig.1). The total population of the Bilesavar was about 55000 in 2008. The climate is very hot (up to 40°C) in the summer and quite cold (-27°C) during the winter. The summers are short, lasting from mid May to mid September. The main activities of the people are agriculture and animal husbandry.

Sand fly collection
Sand flies were collected biweekly from indoors (bedroom, guestroom, toilet and stable) and outdoors (wall cracks and crevices and animal burrows) using sticky papers (100 papers per village, 50 papers in outdoors and 50 papers indoors) during July–September 2008. Collected sand flies were removed from sticky papers using needles or fine brushes, dipped in 70% ethanol, were stored in 96% ethanol, and kept in -20 °C before dissection.

Sandfly identification
The sandfly specimens were washed in 1% detergent then twice in sterile distilled water. Each specimen was then dissected in fresh drop of sterile normal saline by cutting off the head and abdominal terminalia with sterilized forceps and single used mounted needles. The remainder of the body was stored in the sterile Eppendorf microtubes for DNA extraction. Specimens were mounted in Puri’s medium and identified using the identification keys of Theodor and Mesghali (1964) and Lewis (1982).

DNA extraction
DNA was extracted by using the Bioneer Genomic DNA Extraction Kit. Extraction was carried out by grinding of individual sand flies in a microtube using glass pestle and followed by kit protocol and stored at 4°C.

Detection and identification of Leishmania species
Initial screening of sand flies was performed by nested-PCR amplification of kinetoplast DNA (kDNA) using the protocol and primers (Table 1) already explained by Noyes
et al. (1996). Amplification was carried out in two steps, both in the same tube. This PCR is able to identify promastigote infection of sand flies by producing a 680 bp for *L. infantum/L. donovani*, 560 bp for *L. major*, and a 750 bp for *L. tropica*.

Further identification of the *Leishmania* parasites was done by using the ITS1-PCR (El Tai et al., 2000) followed by HaeIII digestion of the resulting amplicons described by Schonian et al. (2003). The set of primers (Table 1) forward LITSR and reverse L5.8S was used to amplify 340 bp of rDNA including parts of 3’ end of 18S rDNA gene, complete ITS1, and part of 5’ end of 5.8S rDNA gene. All of the amplification reactions were analyzed by 1–1.5% agarose gel electrophoresis, followed by ethidium bromide staining and visualization under UV light. Standard DNA fragments (100 bp ladder, Fermentas) were used to permit sizing.

PCR products (15 µl) were digested with HaeIII without prior purification using conditions recommended by the supplier (Cinagen, Tehran, Iran). The restriction fragments were subjected to electrophoresis in 2% agarose and visualized under ultraviolet light after staining for 15 min in ethidium bromide (0.5 µg/ml). HaeIII digestion of ITS1 PCR reveals two fragments of 220 and 140 bp for *L. major*, the fragments of 200, 80 and 60 bp for *L. infantum* complex, and two fragments of 200 and a 60 bp for *L. tropica*.

**Results**

Altogether, 2,110 sand flies were collected and identified including *P. perfiliewi transcaucasicus* (62.8%), *P. papatasi* Scopoli (19.1%), *P. tobbi* Adler and theodor (3.9%), *P. sergenti* (10%), *S. dentata* Sinton and (1.8%), *S. sintoni* Pringle (2.4%). Among the collected specimens 433 females belonging to six species were screened for *Leishmania* infections (Table 2). Only 4 of 270 *P. perfiliewi transcaucasicus* (1.5%) were observed to be naturally infected with *L. infantum* using nested PCR against minicircle kDNA molecules with 680 bp (Fig. 2). Furthermore ITS1 amplification by PCR primers followed by PCR-RFLP technique confirmed the *L. infantum* DNA in two infected *P. perfiliewi transcaucasicus* with 340 bp (Fig.3). ITS1-PCR products were digested by HaeIII, for the *Leishmania* characterization. Since the length of PCR products for different species is different, for example, it is 360 bp for *L. major* and 340 bp for *L. infantum*, therefore the RFLP pattern is polymorphic for each species. The fragments of 220 and 140 bp for *L. major*, and the fragments of 200, 80 and 60 bp for *L. infantum* and two fragments of 200 and 60 bp were observed for *L. tropica* were diagnosed (Fig. 4). This is the first report of naturally infected of *P. perfiliewi transcaucasicus* to *L. infantum* in Bilesavar District, Northwestern Iran.

**Table 1.** Primers used in this study

| kDNA          | First step | Second step |
|---------------|------------|-------------|
|               | CSB2XF(forward): 5´-CGAGTA GCAGAAACTCCCGTTCA-3´ | LITSR(forward): 5´-CTGGATCATTTTCCCGATG-3´ |
|               | CSB1XR(reverse): 5´-ATTTTTTCGCGATTTTCGCAGAACG-3´ | L5.8S (reverse): 5´-TGATACCACCCATTATCGC-3´ |
|               | 13Z(forward): 5´ (ACTGGGGGTTGGTGTAAAATAG-3´ | |
|               | LIR(reverse): 5´-TCGCAGAAGCCCT-3´ | |

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Table 2. Fauna and PCR results of collected sand flies in Bilesavar District, 2008

| Species                  | Male No | Male (%) | Female No | Female (%) | kDNA | ITS | Leishmania species |
|--------------------------|---------|----------|-----------|------------|------|-----|--------------------|
| *P. perfiliewi trancaucasicus* | 1055    | 62.91    | 270       | 62.35      | 4    | 2   | *L. infantum*      |
| *P. papatasi*            | 356     | 21.22    | 47        | 10.85      | 0    | 0   |                    |
| *P. sergenti*            | 179     | 10.67    | 33        | 7.62       | 0    | 0   |                    |
| *P. tobbi*               | 45      | 2.69     | 35        | 8.09       | 0    | 0   |                    |
| *S. sintoni*             | 17      | 1.01     | 34        | 7.85       | 0    | 0   |                    |
| *S. dentate*             | 25      | 1.5      | 14        | 3.24       | 0    | 0   |                    |
| **Total**                | **1677**| **100**  | **433**   | **100**    | **4**| **2**|                   |

![Map of the study area located in Ardebil Province](image1)

**Fig. 1.** Map of the study area located in Ardebil Province

![kDNA PCR amplification of Leishmania stocks and L. infantum in P. perfiliewi transcaucasicus using nested-PCR](image2)

**Fig. 2.** kDNA PCR amplification of *Leishmania* stocks and *L. infantum* in *P. perfiliewi trancaucasicus* using nested-PCR. Lane N, Negative control, Lanes 1, 2, 3 represent *L. infantum* in *P. perfiliewi trancaucasicus* (680 bp) and Lane 4 *L. infantum* (680 bp) positive control, M: 100 bp size marker (Fermentas)
Discussion

Control of leishmaniasis depends on ecological and epidemiological information pertaining to the disease such as identification of preferred hosts and detection of natural infections in the vector(s). Finding naturally infected wild-caught specimens that are anthropophilic fulfills two essential requirements for incriminating a sand fly vector (Killick-Kendrick 1990). In endemic areas where more than one Leishmania species is present, diagnostic tools are required for the detection of parasites directly in samples and distinguish all relevant Leishmania species (Schönian et al. 2003). Characterization of Leishmania species is important, because different species may require special remedial method. On the other hand, such information is also valuable in epidemiologic studies where the distribution of Leishmania species in hosts and insect vectors is a urgent item in the controlling programs (El Tai et al. 2000, Schönian et al. 2003). Recently, mo-
molecular techniques (PCR) have been employed for vector incrimination of sand flies (Oshaghi et al. 2009a). The highly sensitive technique of PCR has been used for detecting *Leishmania* in sand flies in many endemic areas including Iran and India (Azizi et al. 2006, De Bruijn and Barker 1992, Oshaghi et al. 2009b, Mukherjee et al. 1997, Rassi et al. 2004, 2005, 2009). In the present study, infection of *P. perfiliewi transcaucasicus* by *L. infantum* was confirmed using molecular methods. It needs to mention that *P. perfiliewi transcaucasicus* was first found naturally infected with *L. infantum* in Germi District (other important focus of VL) adjoining to our study area (with 30 kilometers distance) in northwestern Iran (Rassi et al. 2009). Our study in Germi District showed that, 1.1% of dissected *P. perfiliewi transcaucasicus* sand flies were positive to *L. infantum* with 36.5% hematophagy preference to human (Anthropophilic Index) indicating a strong preference for human blood (Rassi et al. 2009). The apparent secondary preference of this species for dogs (23.5%), the main domestic reservoir of disease, may indicate that this species also plays an important role in transmission of VL to dogs (Rassi et al. 2009).

Based on high density of *P. perfiliewi transcaucasicus*, natural infected with *Leishmania infantum*, and high degree of anthropophily, it seems that that *P. perfiliewi transcaucasicus* could be the principal vector of VL in Bilesavar District northwestern Iran. *Phlebotomus kandelakii* was the first sand fly incriminated as a vector of VL in Meshginshahr city in northwestern Iran (Rassi et al. 2005). The high prevalence of *P. perfiliewi transcaucasicus* revealed by this study is consistent with the reports of Lewis (1982) on the distribution of this species in Iran and the Republic of Azerbaijan, adjoining to our study area. This is the first report incriminating *P. perfiliewi transcaucasicus* as the main vector of VL due *L. infantum* in the region.

Acknowledgements

We are grateful to staff of Bilesavar Health center for providing facilities to conduct this research and cooperation in the field sampling. This study received financial support from the School of Public Health, Tehran University of Medical Sciences, MSPH Thesis, 2010. The authors declare that there is no conflict of interests.

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