

Patterns of cutaneous leishmaniasis during the COVID-19 pandemic in four endemic regions of Iran

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Abstract

Background: Both zoonotic cutaneous leishmaniasis (ZCL) and anthroponotic cutaneous leishmaniasis are endemic in different regions of Iran. It is important to know the type of cutaneous leishmaniasis (CL) for prevention strategies. On the other hand, Iran is one of the countries that was severely affected by the coronavirus 2019 (COVID-19) pandemic. However, little is known about the causative agents of CL during the COVID-19 pandemic in Iran.

Methods: In this study, a total of 181 samples were isolated from patients with CL lesions in four different endemic cities of Iran (Jahrom, Juyom, Kashan and Shoushtar) during the COVID-19 pandemic (the summer and autumn of 2021). The nested-PCR targeting kinetoplast DNA (*kDNA*) minicircles was applied for species identification of the parasite and the internal transcribed spacer-1 (*ITS-1*) gene was applied for sequencing and phylogenetic analysis.

Results: Molecular detection of *kDNA* minicircles revealed that all isolates from the four cities were *Leishmania major*, indicating the ZCL pattern. Ten isolates were sequenced by the *ITS-1* gene and deposited in GenBank [accession numbers: OL627363–72]. Sequencing and phylogenetic analysis displayed a high similarity rate of the isolates with sequences from other parts of Iran and Iraq. Over half of the patients (53.59%) had a single lesion, while 17.12, 14.92, 2.21 and 12.16% of cases had two, three, four and more than four lesions, respectively. About half of the patients (50.27%) had lesions on their hands, while the rest had lesions on multiple locations (19.34%), legs (16.58%), face (9.94%), ears (1.66%) and waist (2.21%).

Conclusions: This study revealed the occurrence of ZCL during the COVID-19 pandemic in four endemic regions of Iran. Strategies for prevention and control of the disease should be considered to mitigate the occurrence of ZCL.

Keywords: ACL, COVID-19, cutaneous leishmaniasis, Iran, SARS-CoV-2, ZCL