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Molecular Detection of Leishmania from the Phlebotomus Genus: Tendency towards Leishmaniasis Regression in Constantine, North-East of Algeria

Authors : K. Frahtia, I. Mihoubi, S. Picot

Abstract : Leishmaniasis is a group of parasitic disease with a varied clinical expression caused by flagellate protozoa of the Leishmania genus. These diseases are transmitted to humans and animals by the sting of a vector insect, the female sandfly. Among the groups of dipteral disease vectors, Phlebotominae occupy a prime position and play a significant role in human pathology, such as leishmaniasis that affects nearly 350 million people worldwide. The vector control operation launched by health services throughout the country proves to be effective since despite the prevalence of the disease remains high especially in rural areas, leishmaniasis appears to be declining in Algeria. In this context, this study mainly concerns molecular detection of Leishmania from the vector. Furthermore, a molecular diagnosis has also been made on skin samples taken from patients in the region of Constantine, located in the North-East of Algeria. Concerning the vector, 5858 sandflies were captured, including 4360 males and 1498 females. Male specimens were identified based on their morphological. The morphological identification highlighted the presence of the Phlebotomus genus with a prevalence of 93% against 7% represented by the Sergentomyia genus. About the identified species, P. perniciosus is the most abundant with 59.4% of the male identified population followed by P. longicuspis with 24.7% of the workforce. P. perfiliewi is poorly represented by 6.7% of specimens followed by P. papatasi with 2.2% and 1.5% S. dreyfussi. Concerning skin samples, 45/79 (56.96%) collected samples were found positive by real-time PCR. This rate appears to be in sharp decline compared to previous years (alert peak of 30,227 cases in 2005). Concerning the detection of Leishmania from sandflies by RT-PCR, the results show that 3/60 PCR performed genus are positive with melting temperatures corresponding to that of the reference strain (84.1 +/- 0.4 ° C for L. infantum). This proves that the vectors were parasitized. On the other side, identification by RT-PCR species did not give any results. This could be explained by the presence of an insufficient amount of leishmanian DNA in the vector, and therefore support the hypothesis of the regression of leishmaniasis in Constantine.

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