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SPATIOTEMPORAL CLUSTERING OF CUTANEOUS LEISHMANIASIS IN FARS PROVINCE, IRAN

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Background: Cutaneous Leishmaniasis (CL) is an infectious endemic disease in most provinces of Iran, which is among public health problems. CL is prevalent in 88 countries in the world, infecting nearly 12 million individuals. Almost two million new leishmaniasis cases occur yearly, with CL accounting for 1500000 cases. Fars province is known to be an endemic area for CL.

Study objective: The objective of this study is to assess the spatiotemporal trait of CL in Fars province, Iran.

Materials & Methods: Spatiotemporal cluster analysis was done retrospectively to find spatiotemporal clusters of CL cases. Time-series data were recorded from 29201 cases in Fars province, Iran from 2010 to 2015, which were used to verify if the cases were distributed randomly over time and place. Then, subgroup analysis was applied to find significant sub-clusters within large clusters. Spatiotemporal permutation scans statistics in addition to subgroup analysis were implemented using SaTScan software.

Results: This study resulted in statistically significant spatiotemporal clusters of CL (p<0.05). The most likely cluster contained 350 cases from 1 July 2010 to 30 November 2010. Besides, 5 secondary clusters were detected in different periods of time. Finally, statistically significant sub-clusters were found within the three large clusters (p<0.05).

Conclusion: Transmission of CL followed spatiotemporal pattern in Fars province, Iran. This can have an important effect on future studies on prediction and prevention of CL.

Biography

Marjan Zare pursued MS in Biostatistics and is a PhD student in Epidemiology. She has expertise in statistical and epidemiological modelling, and has passion in improving health care and public health policies. She has been working for Shiraz Medical School research center for three years and she knows how to work with R, ITSM, CMA, Lisrel, Arc GIS, SaTScan, SPSS, Python language softwares to do ordinary statistical analysis. Also, she is interested in doing micro array analysis using Mega Data in field of genetics; hereby she knows how to work with the related softwares like Plink and Hoploview. The basis of this research is to predict the potential outbreaks in the future using Time-Series data.

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