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SPACE-TIME CLUSTER ANALYSIS OF MALARIA IN FARS PROVINCE, IRAN

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Background: Malaria is a human infectious disease transmitted by protozoan parasites from plasmodium family, which is prevalent in tropical and semi-tropical zones. This disease is important due to high frequency and severe lethality. Malaria is distributed from Sub-Saharan Africa, Asia, to Latin America. Totally, 214 million malaria cases were seen in 2015 universally ending up in 4,34,000 deaths, 90% of which occurred in Africa. Iran is a potentially suitable endemic site for malaria, with the incidence rate of 10-100 cases per 1,00,000 inhabitants. Indeed, almost 90% of cases are detected in southern parts of the country.

Study Objective: The objective of this research is to detect space-time clusters of malaria in Fars province, Iran.

Materials & Methods: Using time-series data including 357 malaria cases recorded during 1/1/2011 to 31/12/2015 in Fars province, space-time cluster analysis was done retrospectively to testify if the cases were distributed randomly over time and space. Thereafter, subgroup analysis was done to detect significant clusters within clusters. Space-time permutation model using scan statistics was employed using SaTScan software.

Results: The results indicated statistically significant space-time clusters of malaria ($p<0.05$). The most likely cluster included 6 cases from 1/7/2015 to 31/7/2015. However, no significant sub-clusters were observed within clusters in the study ($p>0.05$).

Conclusion: Malaria could have a space-time feature in Fars province, Iran. This can have an important effect on future studies on malaria prevention and prediction.

Biography

Marjan Zare pursued MS in Biostatistics and is a PhD student in Epidemiology. He 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 centre 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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