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Community incidence of pandemic influenza (A/H1N1, 2009) in Sao Paulo, Brazil, 2009

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Background: The aim of the present study is to describe the incidence of pandemic influenza (A/H1N1, 2009), in São Paulo, Brazil, during the 2009 influenza season. Data on incidence were obtained from a community trial to evaluate the influenza vaccine indirect effectiveness.

Methods: The data used in the present study were obtained from a community trial to assess the indirect effectiveness of influenza vaccination in schoolchildren, to protect their household contacts from influenza. 2009 Southern Hemisphere seasonal influenza vaccine and a control vaccine were used. After vaccination, participants were followed up for six months. Acute respiratory infections (ARI) were detected by telephone calls and samples of respiratory secretions of ARI cases were collected in the household for virologic diagnosis. Influenza diagnosis was made by PCR.

Results: We identified 631 cases of ARI and 101 cases of laboratory-confirmed influenza A(H1N1)2009. 61 of these were female; and 78 were under 20 years old (43.56% above 10 and 14 years old). Overall incidence of ARI and influenza A(H1N1)2009 were 8.83 and 1.41 per 100 participants, respectively. Among schoolchildren the incidence of influenza A(H1N1)2009 was 2.76 and 0.98 per 100 participants among household contacts. Pandemic influenza incidence was significantly lower ($p < 0.05$) among household contacts of schoolchildren vaccinated with the seasonal vaccine (0.70), when compared to the contacts of the control group (1.41).

Among the schoolchildren, incidence was significantly associated with the number of people living in the household, as well as with the number of people sharing the bedroom with the index child. For household contacts, incidence was significantly associated with age and with the number of people living in the household.

Conclusion: Few studies have reported the incidence of ARI and influenza in tropical regions. The observed incidence of ARI and laboratory-confirmed pandemic influenza were much lower than reported elsewhere.

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Molecular phylogenetic study on S-segment of Crimean–Congo Hemorrhagic Fever (CCHF) virus genome isolated from ticks in West Azerbaijan and Sistan and Baluchestan provinces, Iran, 2010

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Background: Crimean-Congo Hemorrhagic Fever (CCHF) virus is a tick-borne virus (Genus *Nairovirus*, Family *Bunyaviridae*) with negative-sense, single-stranded, three segmented RNA genome (L, M, S). The virus is transmitted through the bite of an infected tick, or by direct contact with CCHFV-infected patients or the products of infected livestock. The disease with 30% fatality rate occurs sporadically throughout much of Africa, Asia, and Europe. During recent years, an increasing number of human CCHF cases have been diagnosed in Iran. This study was undertaken to study the genetic relationship and distribution of CCHF Virus in the tick population of West Azerbaijan province and Sistan - Baluchistan Provinces in Iran as two critical epidemiologic areas in Iran, 2010.

Methods: In this study, 60 samples of ticks randomly collected from this region and were examined for presence CCHF virus by RT-PCR method (Based on S Segment). Two Positive samples have been sent for sequencing and bioinformatics analysis through MEGA4.

Results: CCHFV genome was found in 8.33% of ticks. Phylogenetic study reveal that the recent genome isolated from tick is located in Drosdov strain clade. (With 97% Identities). All sequence are available in Gene Bank in Accession Number JF798866 - JF798869.

Conclusion: It is the first report of emerging of new genetic group in Iran. The present investigation illustrates that two CCHF virus lineages are circulating in the Iran (Asian and Russia-Like Clades). Also, Vector control programs should be applied for reducing population density of potential tick vectors in this province. Further surveys are indicated in these regions to provide a better view of the distribution and epidemiology of the virus. In order to gain an insight into the topology of the strain in the CCHFV phylogenetic trees, the full-length S, M and L segments were additionally sequenced and analyzed.

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