

OTR.16 - Characterization of Respiratory Syncytial Viruses circulating in the northeast Brazilian region: epidemiological and molecular surveillance within the Influenza surveillance program

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Introduction:

According to the WHO, lower respiratory tract infection is the leading cause of hospitalization among children under 5 years of age and the human respiratory syncytial virus (hRSV) is the main virus responsible for these infections. However, Influenza and other respiratory viruses also infect this population. Currently, prophylactic treatment with the monoclonal antibody Palivizumab is the only available option for hRSV infection, due to cost it is limited for high-risk populations. Several hRSV vaccine candidates are in advanced clinical trials and it is possible that in the near future we will have a safe and effective vaccine against hRSV. Given its impact on public health and the epidemiological characteristics of hRSV, one of the current priorities for WHO is to look to adapt the use of the influenza surveillance network to capture and monitor hRSV cases.

Objective:

The aim of this study was to characterize the clinical, epidemiological and molecular profile of hRSV within the already established Brazilian influenza surveillance network to inform the adoption (or not) of combined surveillance of Influenza and hRSV viruses.

Methodology:

In Sergipe State from February 2016 to October 2017 Nasopharyngeal aspirates collected from children under 6 years of age (240 Influenza-like illness, ILI, and 156 Severe Acute Respiratory Infection, SARI) were screened for Influenza and hRSV by real time RT-PCR. The G gene from hRSV strains identified were sequenced and characterized phylogenetically.

Results:

The Sergipe influenza surveillance program was able to detect hRSV cases in two epidemic waves from April to August of each year during the period of study, mainly in first year of life. hRSV was the most commonly detected virus (n = 124) followed by Influenza A (8 H1N1pdm09 and 3 H3N2) and influenza B (4 B/Victoria and 2 B/Yamagata). Coinfection was identified in 6 hRSV with Influenza A or B. Of the 396 cases analyzed, 364 reported the presence or absence of fever. When fever was present, 31% (103/336) were positive for RSV and 5% (18/336) for Influenza virus. Among cases that reported absence of fever, 54% (15/28) were positive for hRSV. However, even screening the majority of cases with fever, we could detect the hRSV in 19% (43/226) of the ILI cases and in 51% (60/156) of the SARI cases. We characterised some hRSV strains genetically and observed a co-circulation of RSV-A, genotype ON1-like and RSV-B, genotype BA-like.

Conclusion:

This study highlights that it is possible to characterize the seasonality, and the epidemiological and molecular characteristics of hRSV using the influenza surveillance program, it can be a valuable sentinel scheme. However, to better understand the impact and burden of hRSV disease it will be necessary to establish reference units to better characterize hRSV cases not captured by the Influenza case definition.

Keywords: Human Respiratory Syncytial Viruses; Influenza and hRSV surveillance; Respiratory infection in children