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