

2nd International Conference on **Influenza**

September 12-13, 2016 Berlin, Germany

Molecular epidemiology of virus influenza B in Parana state, Southern Brazil from 2000 to 2015: Implications in immunizations strategy for influenza

Sonia Mara Raboni, Bruna Lapinski, Luciane A Pereira, Meri B Nogueira and Luine R Vidal
Universidade Federal do Parana, Brazil

Influenza (flu) is an acute infectious respiratory disease caused by a global spread of influenza virus type A, B and to a lesser extent type C. Children, the elderly and immunocompromised patients with chronic diseases are the most likely groups to severe disease (severe acute respiratory syndrome), responsible for high rates of hospitalization and death that occur annually in 10% of the world population. Epidemiological indicators have shown how the impact of influenza B is substantial, both on the number of childhood deaths but also in the development of severe disease with high numbers of admissions in ICU. In Brazil, the vaccine provided by the National Immunization Program is trivalent, consisting of only one of the two influenza B lineages, which co-circulate annually. In this cross-sectional study, we have characterized by molecular methods the influenza B strains detected from clinical samples stored at the Virology Laboratory/HC-UFPR from 2000 to 2015 and evaluated a possible mismatch between annual prevalent lineage and vaccinal lineage. B lineages (Victoria & Yamagata) were identified by qRT-PCR. From a total of 7,258 respiratory samples investigated for flu B in the period of the study, 74 were positives. Of these, 64 samples were differentiated by lineage. We have observed in 2000 (n=2) and 2001 (n=8) 100% Yamagata; in 2003 (n=7) 43% Yamagata and 28% Victoria; in 2003 (n=5) 80% Victoria and 20% Yamagata; in 2004 (n=2) 50% each lineage; in 2006 (n=6) 66% Yamagata and 34% Victoria; in 2008 (n=17) 41% Yamagata and 29% Victoria; in 2009 (n=2) 100% Yamagata; in 2010 (n=3) 66% Yamagata and 33% Victoria; 2012 (n=3) and 2013 (n=7) 100% Victoria; 2015 (n=6) 100% Yamagata. In the years 2005, 2007, 2011, 2014 none flu B was identified. Two of the years with a high number of cases (2001 and 2008) have presented Yamagata prevalence, while in 2013 there was Victoria lineage prevalence. However, only in 2013 there was a substantial vaccine mismatching. In general, we have also observed that the lineages Yamagata and Victoria co-circulated in an incidence of 60% and 40% respectively. Studies on epidemiological and molecular characteristics of influenza infections are essential for the introduction of preventive and therapeutic intervention by health surveillance units. The identification of strains circulating in the community is a great benefit, providing the information needed for the definition of the annual composition of vaccines.

sraboni@ufpr.br