

VAC 03 - Challenges in Influenza B vaccination in Brazil: from vaccine mismatches to viral evolutionary dynamics

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Introduction

Vaccination against influenza plays a key role in averting severe disease and reducing morbidity, mortality and the socioeconomic costs allied with primary and secondary infections. Since trivalent Influenza B vaccine comprises only a viral lineage, a successful intervention relies on the agreement between circulating viruses and vaccine-selected strains. Furthermore, available data show two yearly Influenza epidemic peaks in Brazil, whereas national vaccination campaigns are carried out in a single period, after the first epi-peak in the North and part of Northeast regions.

Objective:

We investigated the distribution of influenza B lineages and their match with vaccine-strains in Brazil, along 2010-2016 influenza seasons. In addition, temporal and geographical patterns of viral circulation were explored and their putative impact on timely vaccination and vaccine composition are discussed

Methodology:

Influenza B lineage was determined by CDC real time RT-PCR and/or DNA sequencing in 669 clinical samples from different Brazilian regions, distributed as follows: South, 246; Southeast, 210; Center, 35; Northeast, 125 and North, 83. Samples from the Southern states, Southeast (except Sao Paulo) and Northeast (Bahia, Alagoas, Sergipe) were sequenced at the WHO/National Influenza Center (NIC), Rio de Janeiro. Sequences from

other states were downloaded from GISAID database. Maximum likelihood phylogenetic trees were reconstructed using a Maximum Likelihood algorithm (PhyML), with a GTR+I+G nucleotide substitution model. Viral dynamics along time-space was explored using using GMRF Bayesian skyride coalescent model, with a relaxed clock (Beast 1.8.0).

Results:

Key mismatches between the Southern Hemisphere vaccine and the most prevalent circulating viruses were identified in 2010 (except for the Northeast), 2013 and 2014 (Southeast and South), imposing a challenge for the trivalent vaccine usage. Our preliminary analyses suggest a strong spatial structure, with regional patterns of lineage distribution within the country. Although Yamagata and Victoria lineages present distinct evolutionary dynamics, different antigenic groups can be simultaneously observed. Moreover, viruses circulating in the South and Southeast regions were identified in the North only one year later, with putative implications for the use of a single vaccine composition within Brazil in the same influenza season.

Conclusion:

Our findings corroborate the international literature on the poor concordance between vaccine and circulating Influenza B strains. The introduction of the quadrivalent vaccine in the Brazilian calendar would avoid challenging predictions and their respective public health consequences.

Future phylodynamics and phylogeographic studies, including a representative sample of the North and Northeast, are critical to confirm these initial findings. Understanding the viral and epidemiological dynamics within Brazil is pivotal to tailor the public preventive policies.

Keywords: Influenza B; vaccine mismatch; phylogeny²¹