OTR.21 - Diversity change of Influenza A (H3N2) strains circulating in Brazil during 2017-2018: what expect for the next coming winter?

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Introduction:

Influenza A(H3N2) subtype was the predominant strain during the early months of the 2017 influenza epidemic in Brazil. In contrast with the regular influenza activity in Brazil, in Australia the A(H3N2) was responsible for a large and prolonged epidemic, not seen since the 2009 pandemic. Influenza A(H3N2) also caused a significant epidemic in 2017/2018 in the Northern hemisphere season. Several genetic and antigenic A(H3N2) variants were circulating, which made the decision about which strain to incorporate into the influenza vaccine challenging. For the 2018 Southern Hemisphere trivalent vaccine the WHO selected the new strain A/Singapore/INFIMH-16-0019/2016-like (3C.2a1) to replace the strain A/HongKong/4801/2014-like (3C.2a).

Objective:

The aim of this study was to describe the genetic diversity of influenza A(H3N2) viruses circulating in Brazil between January 2017 and January 2018, checking the match between these circulating strains and vaccine strains. We also describe the Brazilian strains and strains circulating worldwide.

Methodology:

Genetic sequencing of the hemagglutinin gene of the influenza A(H3N2) were performed, followed by a phylogenetic reconstruction using sequences available in GISAID (Global Iniciative on Sharing All Influenza Data) for comparison with our dataset.

Results:

During the study period we observed a large diversity of A(H3N2) genetic clusters, including 3C.2a, 3C.2a1 and 3C.3a and their subgroups. During

the 2016-2017 interepidemic and 2017 epidemic period the cluster most frequently detected belonged to genetic clade 3C.2a1 (148/185; 80,0%), a distinct group related to the 2017 vaccine strain A/HongKong/4801/2014-like (3C.2a). However, the genetic profile changed during the study period and in the interepidemic season 2017-2018 the most commonly detected genetic group was the 3C.2a cluster (43/58; 74,1%). Inside this cluster the majority (34/43; 79.1%) of strains belonged to a single genetic 3C.2a subgroup 2, bearing antigenic substitutions T131K and R142K (site A) and R261Q (site E). The dominance of this 3C.2a subgroup 2 in the 2017-2018 interepidemic period in Brazil was similar to the 2017-2018 season in Europe and Canada, according to their surveillance data. On the other hand, the strong 2017 epidemic season in Australia was characterized by a greater mix of genetic clusters and only 7% of viruses belonged to the 3C.2a subgroup 2. We saw a similar pattern in Brazil where we detected only (6/36; 16,7%) of this subgroup. For the 2018 Southern hemisphere vaccine, a new strain (3C.2a1) was chosen and it has 5-6 antigenic changes in comparison to the predominant 3C2a subgroup 2 circulating in South America since September 2017 until now.

Conclusion:

It is possible that the vaccine mismatch will not protect the population against a majority of circulating strains. Surveillance of the vaccine effectiveness supported by antigenic and serological analysis is necessary to prove this hypothesis. However, this highlights the difficulty of vaccine strain selection and highlights the value of an universal influenza vaccine.

Keywords: Influenza vaccine; Influenza A (H3N2); Vaccine mismatch