

Characteristics of influenza viruses in the 2018-2019 season

"The season in Sardinia was marked by the exclusive circulation of type A influenza viruses with a prevalence of the subtype H3N2 viruses. In particular, 63.87% of the isolated and/or identified viruses were found to belong to the subtype H3N2, while the H1N1pdm strains represented 36.13% of the total. There was no circulation of type B strains for the entire season. Also at national level there was an almost exclusive circulation of virus A (99.8%), while the viral identifications attributable to type B strains (0.2%) were extremely limited, with only 9 cases. Within type A, viruses belonging to the two subtypes H3N2 and H1N1pdm09 have always co-circulated, although the H1N1pdm09 strains were prevalent in the first week of the epidemic season while the H3N2 strains prevailed from mid-February onwards. Like every year, in Sardinia subjects aged between 0 and 4 years old (34%) were mainly affected, followed, to a lesser extent, by those aged between 15 and 64 (25%). Unlike previous years, the 5 to 14 year-old age group was less affected (21%). As expected, also this year the least affected subjects were adults over 64 years of age (20%). Viral isolation in culture gave positive results in 49 samples, i.e. 64.47% of the 119 samples tested positive in RT-Real Time PCR, all of type H3N2, whereas for the H1N1pdm samples, isolates could not be obtained. In order to investigate more closely the analysis on the characteristics of the viruses circulating in Sardinia, regarding the H3N2 samples, haemagglutinin gene sequencing was performed from the viral isolates; as regards the H1N1pdm, however, it was not possible to obtain isolates, therefore the RNAs of the clinical samples were amplified and sequenced. The sequences obtained were subsequently sent to the Virology laboratory of the *Istituto Superiore di Sanità* (ISS – National Health Institute) for subsequent processing together with the others received from the various national surveillance centres of the Influenza network. As for the subtype A (H1N1) pdm09 viruses sent to the ISS for characterisation, 11 of the 12 viral strains were identified in Sassari; in particular, 7 viruses were found to belong to sub-clade 6B.1A5 and 4 to sub-clade 6B.1A7. For one, it was not possible to trace the sub-clade, given the limited sequenced portion of the HA gene. The molecular characterisation analyses of the HA gene, carried out by the NIC-ISS have shown that the aforementioned viruses belong to the genetic subgroup 6B.1A, defined in particular by the additional amino acid substitutions in HA1, S74R, S164T and I295V, compared to the vaccine strain A/Michigan/45/2015. Part of the analysed strains present the further substitution in HA1, S183P, as the new vaccine strain selected for the 2019/2020 season, A/Brisbane/02/2019; these viruses also have N260D substitution, which defines the sub-clade 6B.1A5, together with the further mutations N129D and T185I. In four of the other viruses (Sardegna/07/85/2019, Sardegna /07/117/2019, Sardegna /07/131/2019 and Sardegna /11/206/2019), on the other hand, the substitution in HA1, K302T, was highlighted in association with three others in HA2 (I404M, N496S and E506D), and therefore fall under sub-clade 6B.1A7. As regards the viruses of subtype A (H3N2), the known problems related to the antigenic characterisation of these viruses remain, due to reduced or lack of ability to agglutinate the red blood cells of different animal species. Molecular and phylogenetic analyses, performed on the HA gene of A (H3N2) strains of 24 of the 25 viral strains identified in Sassari showed that 18 viruses belong to the sub-clade 3C.2a1b and 6 to the sub-clade 3C.3a. For only one strain it was not possible to trace the sub-clade. The molecular characterisation analyses of the HA gene, carried out by the NIC-ISS showed that most of the aforementioned viruses belong to the genetic subgroup 3C.2a1, defined by the amino acid substitutions N121K, N171K in HA1 and I406V and G484E in HA2. These viruses also have the additional changes K92R and H311Q, which identify the sub-clade 3C.2a1b. A minority of viruses, however, are grouped in the 3C.3a sub-clade, characterised by the substitutions S91N, N144K, F193S and K326R, which also includes the new vaccine strain selected for the 2019/2020 season, A/Kansas/14/2017. In light of these results and given the antigenic and molecular characteristics of the viruses circulating in Italy, Europe and the USA, the composition of the quadrivalent vaccine of the 2018-2019 season that was given by the component

A/Michigan/45/2015 (H1N1) pdm09, A/Singapore/INFIMH-16-0019/2016 (H3N2), B/Colorado/06/2017 (lineage B/Victoria/2/87) and B/Phuket/3073/2013 (lineage B/Yamagata/16/88) is modified to the 2019/2020 season and is given by the antigen analogous to strain A/Brisbane/02/2018 (H1N1) pdm09, antigen analogous to strain A/Kansas/14/2017 (H3N2), antigen analogous to strain B/Colorado/06/2017 (lineage B/Victoria/2/87), antigen analogous to strain B/Phuket/3073/2013-like (lineage B/Yamagata/16/88). The vaccine for the 2019-2020 season will therefore contain two new type A antigenic variants: one of subtype H1N1 (A/Brisbane/02/2018) which will replace strain A/Michigan/45/2015, and one of subtype H3N2 (A/Kansas/14/2017) which will replace strain A/Singapore/INFIMH-16-0019/2016. "

By Prof. Caterina Serra
Department of Biomedical Sciences - UNISS
Microbiology and Virology Unit AOU SS
Regional Reference Centre for the InluNet Virological Surveillance Network