Genetic diversity of influenza A(H1)pdm09 viruses, detected in Portugal since the 2009 pandemic

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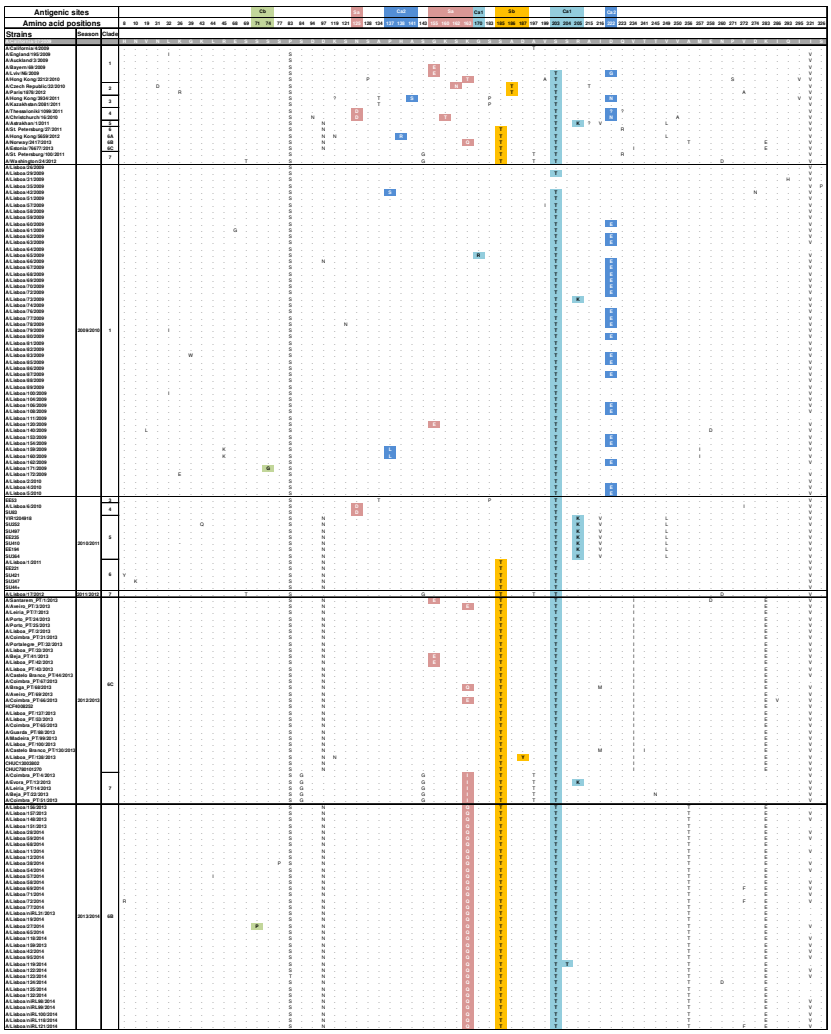
Background:

The antigenic drift of circulating influenza viruses requires a continuous monitoring of their antigenic and genetic properties in order to detect any changes that may justify the selection of different vaccine candidates, as well as changes in antiviral recommendations. Since its emergence in 2009, A(H1)pdm09 viruses show a constant antigenic pattern. However, in the post pandemic seasons these viruses revealed an increasing genetic diversity.

Material and Methods:

From the 2009 pandemic until the end of the 2013/2014 season, the Portuguese NIC has detected 1214 influenza A(H1)pdm09 viruses in the scope of the Portuguese Influenza Surveillance Programme. 416 viruses were isolated and characterised antigenically by HI assays. The HA1 genetic characterisation was performed for 138 viruses.

Table I - Amino acid substitutions observed in the HA1 subunit of influenza A(H1)pdm09 viruses comparing to the vaccine strain A/California/7/2009. Hemagglutinin antigenic sites are highlighted.



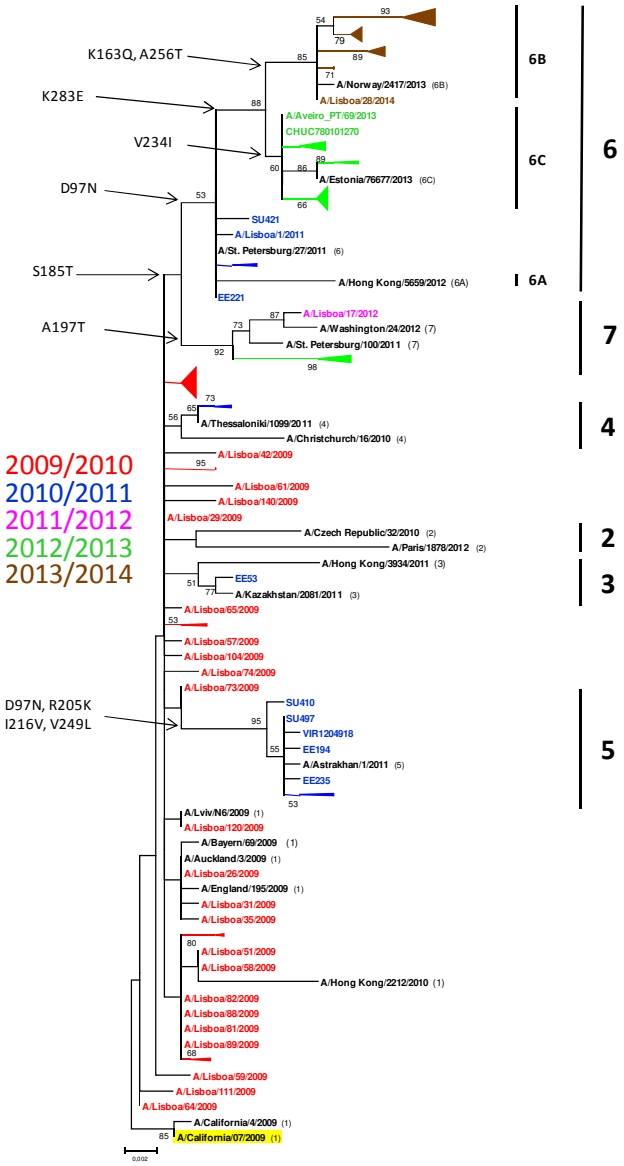


Figure 1 – Maximum likelihood phylogenetic tree of HA1 nucleotide sequences from influenza A(H1)pdm09 viruses, detected in Portugal since the 2009 pandemic until the 2013/2014 winter season. Bootstrap values above 50 are shown (500 replicates). Strains analysed are represented by different colours according to the season of detection: red (2009/2010), blue (2010/2011), pink (2011/2012), green (2012/2013 and brown (2013/2014). The vaccine strain is highlighted in yellow, and the reference strains in black.

Results:

All studied A(H1)pdm09 viruses revealed no antigenic diversity, being antigenically similar to the vaccine strain A/California/7/2009. In the pandemic season, when H1pdm09 viruses were introduced in the human population, they showed a very small genetic diversity and belonged to the genetic group 1 (A/Hong Kong/2212/2010). In the 2010/2011 season, Portuguese pandemic viruses showed some genetic diversity, being distributed by 4 genetic groups: group 3 (A/Hong Kong/3934/2011), group 4 (A/Christchurch/16/2010), group 5 (A/Astrakhan/1/2011) and group 6 (A/St. Petersburg/27/2011). In the following 2011/2012 season, the only one A(H1)pdm09 virus detected, belonged to group 7 (A/St. Petersburg/100/2011). The pandemic viruses circulating in 2012/2013 belonged to this group and to the group 6 (subgroup 6C). Viruses detected in 2013/2014 clustered also into the group 6 (but into the subgroup 6B). Throughout the study period, most viral strains acquired 2 amino acid substitutions located in HA1 subunit antigenic sites. However, all 2013/2014 pandemic strains have already fixed 3 amino acid substitutions within antigenic sites (K163Q substitution in Sa antigenic site, specific for 6B group viruses; S185T in Sb shared by group 6 and 7 viruses and S203T in Ca1).

Conclusions:

Since its emergence in 2009, the majority of pandemic H1 viruses, was antigenically similar to the vaccine strain A/California/7/2009, however, in the studied period, the H1 pandemic viruses revealed an increasing genetic diversity. In Portugal, A(H1)pdm09 viruses represented different genetic groups in circulation over the 5 last seasons. A gradual fixation of amino acid substitutions in the hemagglutinin antigenic sites is observed among the currently circulating H1 viruses, meaning that in the near future, they may start to differ antigenically from the vaccine strain A/California/7/2009. The virological surveillance of influenza A(H1)pdm09 highlights the importance of the genetic characterisation to understand possible pathways of evolution and antigenic drift of these viruses.

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