Genetic variability of influenza virus and vaccine effectiveness

Background
Euroeva is the portuguese component of the multicentric study I-MOVE (influenza monitoring vaccine effectiveness in Europe) that aims to estimate influenza vaccine effectiveness in Europe.
As an higher VE is expected when circulating viruses are similar to the vaccine strains, this study aims to describe circulating strains and amino acid substitutions in antigenic sites in order to better understand VE changes along seasons.

Methods
For this study, we used laboratory surveillance data from the last five seasons and VE estimated by EuroEVA that uses the test negative design.
Reference laboratory to influenza performed genetic characterization by phylogenetic analysis of the subunit 1 of haemaglutinin gene.

Results
Overall VE was low to moderate in all studied seasons. Higher VE was observed when Influenza B circulated which is in line with the higher VE estimated for Influenza B in all studied seasons, even when several amino acid substitutions in antigenic sites were observed.
Sub-optimal VE was estimated when Influenza A(H3) was dominant or co-dominant. The lowest VE was observed against influenza A(H3) in the last season.
Also low VE was estimated against Influenza A(H1)pdm09.
For both subtypes of influenza A the acquisition of substitutions in antigenic sites that correlates with higher differences when comparing with vaccine strains was observed.

Conclusions
For influenza B, VE was always higher than for influenza A, even when the circulating lineage was different from the vaccine selected virus and the acquisition of mutations in influenza B viruses had a moderate effect in decreasing VE. This fact could be explained by the cross-immunity between different influenza B strains. VE for A(H1)pdm09 did not reflect their genetic variability maybe because they remained antigenically similar to the vaccine strains but for A(H3) a dramatically reduction in VE was observed in last season when the drift virus dissimilar to the vaccine strain circulated.
Antigenic and genetic characteristics of circulating viruses are an important clue for VE prediction and interpretation, however there are individual immunological factors as cellular immunity and waning immunity that should be considered.