

Conclusions:
From the sequenced viral isolates (36.6% from all isolates) and those where the NA inhibition assay was performed (50.3%), we can conclude that the majority of isolated viral strains were sensitive to oseltamivir.

The unique case of NI resistance detected in Portuguese viral strains apparently was developed during the oseltamivir treatment in a landscape of other clinical complications. The association between the oseltamivir therapy and the development of the H275Y mutation has been widely documented (Wang et al., 2010; Hanvall et al., 2010; MMWR, 2009). At February 2009, these cases represented 38% of all oseltamivir-resistant pandemic influenza cases (WER, 2010). We didn’t detect in the studied strains other mutations, involved in resistance to NA, such as E119V, I223V, Q136K. Conventional sequencing can provide a rapid tool for monitoring the molecular markers of antiviral resistance in influenza A virus and for an early detection of antiviral resistant strains.