

Table S1. Susceptibility of Selected Influenza A Virus Isolates to Neuraminidase Inhibitors

Variable	A/H1N1 275H	A/H1N1 275Y	A/H3N2
Isolates tested, no.	21	25	69
IC <sub>50</sub> oseltamivir	0.77±0.23	222±63	0.28±0.17
IC <sub>50</sub> zanamivir	0.85±0.28	0.70±0.17	0.88±0.64
Reference viruses	A/H1N1 (Brisbane/59/07)	...	A/H3N2 (Perth/16/09)
IC <sub>50</sub> oseltamivir	0.68±0.13	...	0.29±0.07
IC <sub>50</sub> zanamivir	0.77±0.15	...	0.75±0.37

Isolates were inoculated in Madin-Darby canine kidney cells, in the presence of increasing concentration of either oseltamivir or zanamivir.

Abbreviation: IC<sub>50</sub>, median infective dose.

Figure S1. Phylogenetic analysis of nucleotide sequences of the neuraminidase gene (nucleotide 1372) of influenza A virus subtype H1N1 isolates from Cameroon, Côte d'Ivoire, Madagascar, Senegal, and Seychelles, as well as reference viruses. The tree was constructed using an ML method. The scale bar shows the genetic distance expressed as nucleotide substitutions per site. A specific color is used for isolates from each country (red for Cameroon, green for Madagascar, orange for Senegal, light blue for Seychelles, and dark blue for Côte d'Ivoire). The strains name includes the isolation date (year\_month). Major genetic clades are indicated on the right.

Figure S2. Phylogenetic analysis of nucleotide sequence of the hemagglutinin 1 gene (nucleotide 1057) of influenza A virus subtype H3N2 isolates from Cameroon, Côte d'Ivoire, Madagascar, Niger, and Senegal, as well as reference viruses. The tree was constructed using an ML method. The scale bar shows the genetic distance expressed as nucleotide substitutions per site. A specific color is used for isolates from each country (red for Cameroon, green for Madagascar, orange for Senegal, light blue for Niger, and dark blue for Côte d'Ivoire). The strains name includes the isolation date (year\_month). Major genetic clades are indicated on the right.



