M-004-22 **MOLECULAR ANALYSIS OF NEURAMINIDASE INHIBITORS RESISTANCE IN BRAZILIAN STRAINS OF INFLUENZA A(H1N1)PDM 09**

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Resumo

Treatment of Influenza viruses is based in two classes of drugs, M2 blockers (adamantanes) and neuraminidase inhibitors (NAI). High levels of resistance to M2 blockers have been identified in all Influenza viruses. Then, the NAI as oseltamivir (Tamiflu®) and zanamivir (Relenza®), which block the active site of the enzyme and inhibit viral release, are the most widely used drug to treat Influenza virus infections. However, the emergence of NAI resistance has been reported, being a growing problem both in clinical and in public health. Monitoring of antiviral resistance is essential for Influenza virus surveillance. Resistance can be monitored by genotypic assays using molecular markers that are associated with drug resistance. In our study, a total of 10 strains of Influenza A (H1N1) pdm 09 collected during June 2011 to May 2012 from Southeast and Central West of Brazil were tested for the presence of the oseltamivir resistance-conferring substitution in the neuraminidase (NA) gene by conventional sequencing. Sequence analysis of full-length NA gene was carried out to identify NAI molecular resistance markers. Our analyses showed that all Brazilian strains have the conserved histidine amino acid at position 275. All patients were oseltamivir-sensitive. The most frequent polymorphisms in the NA amino acid sequence identified were V106I (100%), V241I (100%), S299A (20%) and N369K (80%). In anyone specimen H275Y, I223K or I223R, molecular markers potentially associated with resistance to neuraminidase inhibitors, were detected. Until now, none oseltamivir-resistante Influenza A (H1N1) pdm 09 virus were observed in Brazil, but it is imperative the continuous surveillance. These data suggest that sequencing of complete NA gene is a powerful tool for detection of NAI resistant viruses.