Structural Studies of Human Influenza Virus X-31.

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Influenza is an acute respiratory disease caused by three types of virus belonging to *Orthomyxoviridae* family, which includes three genera of Influenza (A, B and C). They are enveloped negative-stranded RNA viruses that can be distinguished on the basis of antigenic differences in nucleocapsid (N) and matrix (M) proteins. Influenza A viruses are pleiomorfic with glycoprotein spikes on the surface and genome consisting of eight RNA fragments. The haemagglutinin (HA), neuraminidase (NA) and matrix (M2) proteins are embedded in the envelope lipid. HA and NA are critical for the biology of influenza virus. The Influenza subtype used in this project is the X-31 (A/Aichi/68), a recombinant human virus. To inactivate and study the stability of viral particles we used high hydrostatic pressure, in addition high and low temperatures, and chemical agents as urea and guanidine hydrocloride. Structural changes are accompanied by spectroscopy techniques and light scattering. We evaluated the effects or perturbing agents by hemagglutination title and neuraminidase activity. The purified samples showed no drop in hemagglutination title or in neuraminidase activity after 3 hours of pressurization. Spectroscopic measurements in the presence of denaturant agents showed small variations in the structure of the particles. Significant changes in emission of fluorescence and light scattering were observed only in the presence of high concentration of these chaotropic agents. As observed to H3N8, an avian subtype, X-31 shows a drop in hemagglutination title after 6 hour under 3,1 kbar, but in other hand, the neuraminidase activity was not altered. Study and understand stability of different subtypes of influenza is of crucial importance, due to the possibility of an influenza pandemic.

Key words: influenza, protein structure, X-31.
Supported by: CNPq, FAPERJ.