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Modelling of S1 Subunits of Three Different Avian Infectious Bronchitis Coronavirus Strains

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Short Abstract: Avian Infectious Bronchitis (AIB) is a disease of economic importance. The development of drugs and vaccines depends on the existence molecular models. The S1 subunits of the spike of three strains was modeled by conventional homology. The analysis of models suggest the localization of the relevant regions for their activity.

Long Abstract:
The recent fears of an burst of an atypical in-influenza, known as avian influenza, has forced the related communities to review the current strategies and resources to nullify not only this but many other infective agents. Despite the consequent public health problems associated to this kind of zoonosis the economic impacts of these illnesses remains unknown. The avian infectious bronchitis (AIB), in spite of this absence of the headlines is also a zoonosis that inflicts heavy economic loses in avian industry annually and carrying out a succession social consequences. The need of well characterize the AIB coronavírus at molecular level is carried out by the necessity of its control and the mitigation of its effects on the avian production. The genetic identification of AIB coronavirus represented a milestone in this worldwide effort. Vaccines for AIB has been produced for a long time. However the use of vaccines demands a more complete knowledge about the molecular nature of the specificities of the virus that the producer is dealing with. Nowadays, due the technological advances, is possible to identify genetically the virus that is causing the outbreak. But due the high rate of mutations presented by coronaviridae the vaccines need to be specific in order to be effective. The production of more specific vaccines demands a good understanding of the characteristics of a selected molecular target. In this way, the development of efficient vaccines and/or specific antiviral drugs would represent the second milestone. The recent consortia among biological sciences and computer sciences lead to the emergence of Bioinformatics which tools are playing an important role in the development of new classes of drugs. So far, the search for drugs against AIB coronavirus, could be carried out on the basis of its molecular structure. In this respect, the development of specific antivirals, designed on the basis of structural knowledge of target proteins cannot be synthesized yet. In spite of the already abundant genomic information few crystal structures for the viral proteins are available so far. The main reason for the apparent contradiction between the abundance of experimental data and lack of crystallographic structures comes from the technical difficulties in getting crystals of these proteins. The elaboration of computational models of these structures is the mostly feasible alternative to deal with these impediments. Recently, Spiga et.al., in a excellent work, presented a 3D molecular model of S1 spike protein of SARS coronavirus that is available in the Protein Data Bank under code 1Q4Z.

In coronaviridae, the spike glycoproteins are translated as a large polypeptides that are subsequently cleaved by virus-encoded or host-encoded proteases to produce two functional subunits, S1 and S2. The S1 subunit lies as the peripheral fragment and S2 a the membrane-spanning fragment of the spike. Both S proteins seems to be responsible for the fusogenic process when expressed individually. The spike is believed to be type I transmembrane protein, with N-terminal ectodomains and C-terminal hydrophobic anchor, and with an unusual cysteine-rich domain that bridges the putative junction of the anchor and the cytoplasmic tail. The type I glycoprotein S of coronavirus, whose trimers constitute the typical viral spikes, is assembled into virions through non-covalent interactions with the M protein. Similar to other viral membrane proteins, the S1 glycoprotein subunit of AIB should play an important role in the interaction of the virus with its host cell receptor, having a primary role in eliciting antibodies in the host species. Thus, a comprehensive 3D model of S protein would be of great value in the search for a vaccine, anti-viral drugs and in designing novel diagnostic tools.

Here, we present the modelling of the S1 subunits of the spike glycoprotein of AIB, a highly antigenic viral envelope protein, involved in the host cell infection. These three different S1 subunits are derived from the vaccinal species M41, H120 and H52

These models were elaborated by homology taking as model the SARS S glycoprotein model given the great philogenetic proximity of AIB and SARS virus. The AIB S1 subunit model was validated using consensual methods. In order to establish the validity of the models some expected structural and immunogenic features was successfully mapped over these models corroborating their good quality. At consequence these models can potentially be useful for future researches for alternative drugs against this agent. These models are presently deposited in PDB under the accession codes 2GOS, 2GOR and 2GOQ.