Acta Scientific Veterinary Sciences (ISSN: 2582-3183)

Volume 2 Issue 12 December 2020

Editorial

The Principle of Interaction of the Peptides for Protection from Coronavirus disease (COVID-19)

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Received: August 26, 2020

Published: October 30, 2020

The human being of the modern world is experiencing most destructive and profound economic shocks in recent history in the wake of the novel coronavirus disease (COVID-19) pandemic. Despite efforts to contain the virus, the number of cases positive to it are only increasing by the day. The need of the days is to ensure that all attempts in cohesion for a win-win situation.

History of identification of the coronavirus disease (COVID-19) goes to Middle East Respiratory Syndrome-Coronavirus (MERS-CoV) from Saudi Arabia in 2012. The coronavirus belongs to family: Coronaviridae and mostly reported among the Middle Eastern people. Middle East Respiratory Syndrome (MERS) is the disease caused by this virus. According to Melnik., *et al*. (2011), bats are the reservoir of this coronavirus. Severeness of coronavirus disease (COVID-19) causes the necessity of the effective therapeutic treatments. In this scenario, the antimicrobial peptides (AMP) can serve as potential treatment option for MERS. It has been shown that the antimicrobial peptides (AMP) act as modulators in viral diseases. On the basis of results of laboratory experimentations, and on the basis of the Wimley-White interfacial hydrophobicity scale (WWIHS), Melnik., *et al*. (2011) shortlisted antimicrobial peptides (AMP). These antimicrobial peptides (AMP) had greater than fifty percent inhibition of human cytomegalovirus. Further, Melnik., *et al*. (2011) reported several peptides with WWIHS = 5.2 inhibited multiple strains of influenza with the half maximal inhibitory concentration (IC50) of 1 μM. By and large, other antimicrobial peptides (AMP) with positive WWIHS values have been shown to inhibit various viruses such as Dengue, White Nile (Hrobowski., *et al*. 2005); SARS (Sainz., *et al*. 2006) and Rift Valley Fever (Koehler., *et al*. 2013). Badani., *et al*. (2014) opined the possible mechanism of inhibition of viral pathogen by the antimicrobial peptides (AMP) is by the interfering with fusion of host cellular and viral membrane of glycoprotein. This potential of the antimicrobial peptides (AMP) is the background for this editorial attempt for the proposal of their utilization as effective therapeutic agents against the novel coronavirus disease (COVID-19) pandemic.

In order to target coronavirus, the knowledge of structural and nonstructural proteins is significant. The spike protein of coronavirus is a multifunctional machine of biomolecules. The spike protein use to mediate the entry of coronavirus into the body of host cells. In very first step, through the subunit of spike protein: S1, the coronavirus use to bind to a receptor present on the surface of host cell. In the second step, through the subunit of spike protein: S2, there is fusion of the membrane of viral particle with the membrane of host cell. According to Fang Li (2016), the two domains in S1 from different coronaviruses are with potential to recognize a variety of receptors of host cells and leading to viral attachment. The prefusion and postfusion are the two structurally distinct conformations of the spike protein. The membrane fusion is the result of triggering of the transition from prefusion conformation of the spike protein to postfusion conformation of the spike protein.

The marvelous features of the proteins lie in interaction with other proteins. The protein interactions are in order to perform various tasks for the sustainable life through welfare of the cell. This is the foundation principle for the knowledge to proceed for the development of therapeutics. The research on this line should consider a set of the antimicrobial peptides (AMPs) in order to identify their role as putative modulators for the proteins of coronavirus. More specifically, research on this line should aim at evaluating the inhibitory mechanism of a set of the antimicrobial peptides (AMPs) with specific physicochemical properties. In order to determine accuracy of the antimicrobial peptides (AMPs) in binding with spike fusion core of coronavirus, it should employ peptide-protein interaction.