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CONTENTS

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Editorial Team of JABLM

Sl No.	Name of Editor	Qualifications	Current Affiliation	Official Address	Official Email Id
6.	Dr. Sharmistha Choudhuri 	MD Biochemistry (AIIMS, New Delhi), PGDIP Hospital Management (National Institute of Health and Family Welfare (NIHFW), New Delhi)	Assistant Professor	Department of Biochemistry, RG Kar Medical College 1 Khudiram Bose Sarani Kolkata -700004	sharmistha_choudhuri@yahoo.in
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From the desk of Editor-In-Chief

Newer strategies of vaccine development: facing the challenge of newly mutated covid-19 strains:

Since 2019, the novel COVID-19 virus has been the most important biological factor for large scale morbidity, mortality and increased financial crisis throughout the world. Keeping at pace with this crisis, the human intelligence has been seeking an optimum and effective long term remedial measure against this microbial menace. As in other similar previous challenges, development of a robust and effective vaccination system has been planned and implemented since last two years. But, with the recent outbreak of BF.7 variant of the COVID-19 in some parts of the world, the vaccination strategies which are being undertaken throughout the world since last two years are facing some crucial challenge and indicate strongly that these strategies are still under evolution for attaining more competence.

Regarding the peptide vaccines, till now the envelope proteins have been the common targets for development of vaccines and the major manufacturers of covid vaccines like Oxford University and Astrazeneca, Pfizer and BioNTech have prepared SARS-CoV-2 vaccines against the spike protein gene which is an important component of the envelope proteins of the virus. These vaccines have worked well and have been extremely beneficial for their potentiality of being used wide scale with limited side effects among all age groups throughout the world. But with continuous advent of newer strains of viruses, the ensuing changes in their envelope coding genes have been marked also. The most plausible reason for this frequent mutation in envelope proteins is their constant exposure to the exterior environment where they go through a continuous selection pressure of evolution. The alpha variants (B.1.1.7), delta variants (B.1.617), and the omicron variant (B.1.1.529) are classical examples of different variants that have evolved through mutation in the spike proteins in their envelope. The recent BF.7 variant, also known as BA.5.2.1.7 is also a subvariant of omicron sub-lineage B.A.5. All these facts herald an uncertainty about the long lasting efficacy of the present vaccines produced against the envelope proteins against forthcoming newer strains of the covid-19 virus.

In contrast to the envelope proteins, the nucleocapsid proteins of the virus are much more deeply buried withing the core of the virus and so are spared from a continuous exposure to the exterior surface where they might be detected by surveillance mechanisms of the host cells inducing them to mutate and thereby avoid future detection. Due to the deep burial, the genes for the nucleocapsid proteins do not face a constant evolutionary selection pressure and so are much more stable and do not mutate readily. Indeed, the nucleocapsid proteins show highly conserved areas among different strains of coronaviruses. Moreover, these highly conserved regions are very competent immune inducers in humans and are highly expressed during the infectious stages. The lower rate of mutagenicity in these proteins is further supplemented by their significant proneness to be discovered by our immune surveillance cells as the circulating CD4+ AND CD8+ cells have been found to recognise a lot of domains of nucleocapsid proteins and thereby are capable to generate a long lasting immunity against the virus for many decades. So, identification of the peptide target regions on these nucleocapsid proteins are becoming significantly important for newer vaccine development strategies. But the major challenge is to identify the peptide regions of the nucleocapsid proteins are to find a highly conserved region throughout the globe for fighting a global pandemic like Covid-19. However, with advent of science and highly developed computational techniques at a state of art level, this challenging task seems possible in vaccine developing labs. When this computational techniques are applied to widespread analysis of conserved sequence areas of the peptides using the sequence based method for vaccine development, the cognate regions on nucleocapsid peptides can be easily discovered which are recognised by the MHC I and II receptors. Moreover, the computational methods can also delineate the structure function relationships between the immunogenic peptide regions and their cognate MHC binding sites by analysing the peptide bound HLA structural characteristics i.e the p-HLA structural features in their bound states.

Thus, the combined use of sequence based analysis and structural characteristics of the p-HLA have created the potentiality for developing several p-HLA arena environments which with the help of advanced computational techniques are paving ways for developing newer effective vaccines using the nucleocapsid peptides with longer term efficacy against the novel corona viruses.

The well known capability of SARS-2 Covid 19 virus to recombine and mutate is a challenge for us. But with the advent of computational techniques in sequence based analysis and combinatorial approach for vaccine development, vaccines with long lasting efficacy against these frequent mutations are being developed producing a sigh of relief among billions of us throughout the world.