International E-Conference on New Horizons in

"Biochemistry, Microbiology and Food Technology - 2020"

Jointly Organized by

Yogi Vemana University

8

Universiti Malaysia Kelantan

ABSTRACTS





Department of Biochemistry and Microbiology, YVU, Kadapa India

8

Faculty of Agro-based Industry, UMK, Malaysia

12th & 13th October, 2020



EPP 74

MUTATIONS FROM AFRICA'S SARS-CoV-2 GENOME A LEAD TO A NOVEL VACCINE

NDAYAKO H. H 1*, IBRAHIM B. U1, GARA T. Y 2, AND SALIHU I. M1

1Department of Biological Sciences, Ibrahim Badamasi Babangida University Lapai. 2Department of Biochemistry Federal University of Technology Minna. *Corresponding Author's Email: hauwannadyadya@gmail.com, Phone: +2348036102000

The world is overwhelmed! This type of incidence will never be forgotten" it started in December when pneumonia-like symptoms was identified in Wuhan, China. The culprit was identified as beta-corona virus. The virus was named by WHO as SARS-CoV-2. SARS-CoV-2 is a positive strand RNA virus; the SARS-CoV-2 genome is made up of approximately 29,700 nucleotides. This comprises of a long ORF1ab polyprotein at the 5' end, which encodes 16 non-structural proteins. And 3' end encodes 4 major structural proteins including: the spike (S) protein, nucleocapsid (N) protein, membrane (M) protein and the envelope (E) protein. The disaster caused by Covid19 disease can't be over emphasized; it is spreading fast across the whole world. More than 33 million confirmed cases have been recorded across the globe. But interestingly Africa's covid19 cases have been on the decline since the month of July and 80% of the recorded cases are asymptomatic compared to the other continents. This poses lots of questions; What is making Africans thick in the skin against this virus? inference have been made to socio-ecological factors and hot-humid nature of the climate. But this can only be proven by the genomic make-up of the of complete sequence of the SARS-CoV-2 of the African populace. Mutations have been reported in the spike protein encoding gene of the SARS-CoV-2 in some regions of Africa through sequence alignment with sequence of SARS-CoV-2 isolated from Wuhan as the query. Keeping in mind that the spike protein plays is a very important role in the transmission of the disease, through the binding of its spike to angiotensin converting enzyme (ACE2) receptor at the surface of human cells. By the application of bioinformatic tools the site of mutations in the genome this will give possible insight on epitopes of t-cells which will show binding affinity to human leucocyte antigen (HLAs) of the Africans population which will in turn induce immune responses. Thus this review is an eye opener to make cognizance the potentials of the T-cells epitopes at the location of mutations in the genome of the SARS-CoV-2 from Africa. these could be the answer to eradicate the virus entirely from the globe, through the development of a novel vaccine.

Keywords: SARS-CoV-2, Spike protein, mutation, Epitopes, Bioinformatic tools.