

SIGNIFICANCE OF STUDYING THE TYPES OF IRRESOLUTE T CELL- IMMUNE MEMORY RESPONSES AND SYMPTOMS OF VARIOUS CLADES OF SARS-COV-2 IN RECOVERED 2019-NCOV ACUTE RESPIRATORY DISEASE PATIENTS OF ODISHA

***Akanksha Rout and Sitaram Swain**

Department of Zoology, Centurion University of Technology and Management, Odisha, India

ABSTRACT

The Severe acute respiratory syndrome coronavirus-2(SARS-CoV-2) is a newly emerged infectious disease that led to millions of infected patients and millions of deaths. The main causal agent of this syndrome, a novel coronavirus termed SARS coronavirus 2 (SARS-CoV-2) has been identified. The pandemic is eventually being tried to bring under control still, its high fear to comorbidity, asymptomatic nature and its ongoing changes of strain is making it more difficult to develop effective vaccine yet to prevent the disease. The immune system plays a vital role in the defence against SARS-CoV-2 infection, since none of the drugs employed to treat SARS is able to inhibit viral replication in vivo. Studies suggest that the novel coronavirus presents little variability, approximately seven mutations per sample. Even common influenza has a variability rate that is more than double and it is detected that the virus is presumably already optimised to affect human beings and this shows its low evolutionary change. Strong humoral responses have been found in most SARS patients while certain patients are completely asymptomatic. Sera from recovered SARS-2 patients could be used to treat newly infected individuals and passive transfer immune serum can prevent replication confirming the protective nature of the anti-SARS-CoV-2 serum Abs. A doubt arises whether T cell memory can form following SARS-CoV-2 infection or vaccination. Vaccination trial data will help us get to know this but the early data from recovered patients are encouraging as the memory CD4+ T cells and CD8+ cells were detected in 100% and 70% of patients recovered respectively. Further, defining how T cell memory forms in patients who experience mild symptoms of COVID-19 versus severe disease will be important. Moreover, the five clades detected in Odisha 19A, 19 B, 20A, 20B, 20C .19B clade was found to be more prevalent (17 per cent) in analyzed samples as compared to other clades reported so far in the country. The phylogenetic analysis of various reports showed that clades 20A and 20B evolved quite rapidly and are major source of disease transmission. Whereas 20C strain is rarely detected and appeared to be less adapted or somehow contracted at early stages of infection .These findings are thus showing the mutating types of the virus makes it more fascinating to hold more findings how each clade type responds and thus, the data of such T cell immune responses and detection of further details and symptoms of patients of each clade type will further give an important implication for developing SARS vaccines.

Keywords: SARS, coronavirus, pandemic, asymptomatic, T cells, clade, vaccine.

INTRODUCTION

In this revolutionizing world, it is known that with various diseases coming into demand, a new disease came into demand in the late December 31, 2019. Since Dec 31, 2019, the Chinese city of Wuhan of Hubei Province has reported an outbreak of a typical pneumonia caused by the zoonotic 2019 novel coronavirus (2019-nCoV) which then showed multiple cases of a type of pneumonia with a mysterious and undetermined causes.

Data from Dec 31, 2019 to Jan 28, 2020 were seen to export the number of cases from Wuhan internationally and China became one of the outbreaks epicentre as the epidemic grew slowly into pandemic by growing exponentially in multiple major cities of China with a lag time behind the Wuhan outbreak of about 1-2 weeks.

Then later various studies done in the Wuhan Lab and by WHO (World Health Organisation) confirmed that this typical form of pneumonia like disease is seen to be related to a certain positive stranded RNA virus synonymously known as the severe acute respiratory syndrome coronavirus 2, SARS-CoV-2, which is seen to be linked to the previous 2007 strain of it i.e., seen to have a phylogenetic similarity to the severe acute respiratory syndrome coronavirus (SARS-CoV) (Na Zhu et al., 2020).