

## **Genetic Polymorphism and Viral Load as Determinants of Therapeutic Response against COVID-19**

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### **ABSTRACT**

In this presentation, we would like to concentrate on the following aspects in relation to COVID-19. First of all, we think that the period since the appearance of COVID-19 as a pandemic issue is still relatively short. However, thousands of articles have been published. We were looking for research articles investigating the aspects of genetic polymorphism and viral load, but there is some sort of disturbance among researchers. We think that genetic polymorphism and viral load are crucial determinants in therapeutic responses against COVID-19. In-depth investigation of these two variables makes the core of developing therapeutic options. We have previous experience in HCV. In HCV, both viral load and genetic polymorphism are important features in treatment options. Viral load helps in identifying degree level of infecting potentiality. For example, two phenomena can be explained, the first phenomenon is why COVID-19 has various degrees of infectious potential. As an illustrating example, if the viral load is relatively low, then the infectious ability is limited, and if the viral load is high, then any one exposed can be infected. The second phenomenon is when the best time to initiate treatment against COVID-19. If treatment is initiated when viral load is limited, treatment is almost successful. Regarding genetic polymorphism, initial information about COVID-19 was related to respiratory system, particularly the lungs. Polymorphisms in ACE2 is thought to play a role in the infectious ability of COVID-19. The expression of ACE2 receptors was reported in various tissues including liver, and kidneys. Accordingly, we can explain the impacts of COVID-19 on other systems. Finally, we got the idea why diabetic patients and heart patients are more likely to have adverse effects by COVID-19. We think this is due to synergistic effects of having other viruses such as HPV and CMV in case of diabetes as we found experimentally. In heart cases, we also have previously found that Chlamydia pneumonia to exist in about 50% of patients with heart diseases. Synergism of the various pathogens in COVID-19 is worthy to be more investigated.

**Keywords:** COVID-19, Genetic polymorphism, Viral load, Infectious potential, Polymorphism

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