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Genomic Benefits of COVID-19 Vaccines

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ABOUT THE STUDY

COVID-19 vaccines can help prevent SARS-CoV-2 infections if they are effective and, more importantly, have no side effects. They may have immediate or long-term effects on COVID-19-related illnesses, and may even result in the emergence of new SARS-CoV-2 subtypes. We examine the benefits and drawbacks of the BNT162b2 vaccine using previously published data and a group of highly effective COVID-19 genetic biomarkers (*MND1, CDC6, ZNF282*). We discovered that the COVID-19 illness and the genomic signature patterns identified in the literature are biologically equivalent, and that the vaccine increased *ZNF282* expression while decreasing *MND1* and *CDC6* expression in SARS-CoV-2-naive patients. The genetic biomarkers increased *MND1* and *CDC6* expression levels in SARS-CoV-2-naive patients. *MND1* and *CDC6* expression levels were increased in SARS-CoV-2-naive patients by the genetic biomarkers. By increasing expression levels, some side effects emerge, raising serious concerns about whether COVID-19 convalescent individuals should continue to use the current vaccine. These findings demonstrate the genomic level, which aids in the development of next-generation vaccines, antiviral drugs, and pandemic response strategies.

As a result, the COVID-19 pandemic continues, with new sub variants of Omicron BA.5 and possibly new variants on the way. Knowledge of virus structures at the protein level has been obtained since the pandemic began, and many informative publications have been provided. Meanwhile, publications on SARS-CoV-2 genetics and vaccine effectiveness provided many valuable insights for future research and practice, including pandemic management. However, there have been reports that SARS-CoV-2 variants evade immune response and vaccines cause adverse effects, raising concerns about the decreased effectiveness and increased adverse effects of current vaccines. Furthermore, knowledge of COVID-19's pathological causes, virus formation, and gene interactions is still limited. The powerful new genomic study method is used to establish the geometry of the COVID-19 genome space, which establishes biological equivalence between the disease and the three genomic signature patterns and seven subtypes of the disease. These developments give the campaign against the COVID-19 pandemic renewed hope.

Many studies have evaluated the effectiveness of vaccines using antibody responses to SARS-CoV-2 and its variations. We recently identified a crucial set of genes that can cluster COVID-19 infected people into sub groups and perfectly or almost perfectly categorize individuals into their respective groups. This excellent performance allowed for the reliable identification of COVID-19 disease biomarkers using blood sample data and SARS-CoV-2 biomarkers utilizing NP/OP swap PCR sample data. In this study, we evaluated the genomic advantages and hazards of the BNT162b2 vaccine in COVID-19 convalescent octogenarians and SARS-CoV-2 naive persons using high performance gene biomarkers. Indicating the genomic (*MND1, CDC6, ZNF282*) advantages and disadvantages of the COVID-19 vaccine BNT162b2 in two heterogeneous populations, pointing to a new COVID-19 study focus, namely gene interactions, and identifying a potential target for next-generation vaccines, antiviral medications, treatments, and management are the three contributions made by this paper. We found that in people with SARS-CoV-2 naïve, the vaccine increased the expression of *ZNF282* while decreasing the expression of *MND1* and *CDC6*, which is compatible with the biological equivalence between the COVID-19 disease and the patterns of genomic markers identified in the literature. The vaccine, however, had a negative effect on COVID-19 convalescent octogenarians. *MND1* and *CDC6* expression levels were increased. Furthermore, it decreased *ZNF282* expression levels. Such side effects raise serious concerns about the current vaccine and when it should be prescribed to COVID-19 patients.

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