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Hong Kong develops bioinformatics tool to predict COVID-19 vaccine effectiveness against variants

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Genetic distance on the receptor-binding domain of spike protein is highly predictive of vaccine protection



Timely evaluation of COVID-19 vaccine effectiveness (VE) is desperately needed to inform and update vaccine design as novel genetic variants continually emerge. A research team led by Professor Maggie Haitian WANG and Professor Benny Chung Ying ZEE, both from The Jockey Club School of Public Health and Primary Care at The Chinese University of Hong Kong's (CUHK) Faculty of Medicine (CU Medicine), has developed a computational approach that can rapidly predict the protective effects of COVID-19 vaccines by analysing genetic distance (GD).

Based on nearly two million SARS-CoV-2 sequences and 49 clinical trials and observational studies, researchers have recently developed new algorithms that can be used to rapidly evaluate the VE of different types of vaccines against symptomatic COVID-19 infection.

They found that the GD between the receptor-binding domain of the spike protein of the circulating viruses and the vaccine strain is highly predictive of vaccine protection. Their method demonstrated 95% VE prediction accuracy using genome analysis, validated on an independent dataset.

This approach can be applied to design vaccines with optimal estimated effectiveness, and improve vaccine clinical trial design and the evaluation of vaccines before they are deployed.