JAMES OOI, National Research Council Canada

Mathematical modelling of COVID-19 vaccine-induced immune response

At the onset of the COVID-19 pandemic, several vaccine candidates were approved for emergency use guided by clinical trial data performed within a limited study time frame. The vaccine candidates include adenovirus vector, mRNA and protein subunit vaccine are being administered to mitigate the effects of the pandemic. Due to the limited study time frame of the clinical trials, there exist gaps in understanding various aspects of these vaccines, including but not limited to immunogenicity beyond the study time frame, varying doses, age, sex and effects of adjuvants. By applying published clinical trial data, we developed within-host mathematical models for various vaccine types that are currently in use or in final stages of clinical trials in Canada and analyse its associated humoral and cellular adaptive immune response. The vaccine-induced immune response investigated includes the antibodies, T helper cells, cytokines and cytotoxic T lymphocytes. The models' prediction allows for a better understanding of relationship between immune cells and cytokines while parameter sensitivity analysis establish the factors that contributes to peak immune response of different vaccine types. The long-term antibody prediction shows a discernible degradation. This finding supports the current third dose booster guidelines. Our within-host models guide the vaccination strategy by health authorities to optimize the vaccine rollout and serve as an in-silico tool for future vaccine re-formulation.