Abstract

Nearly all countries worldwide have been affected by the enormity of COVID-19 caused by SARS-CoV-2, including Indonesia. This pandemic has a variation in symptoms and the number of deaths among Indonesian COVID-19 patients, which could be explained by the nonspecific immunity provided by the cross-reactive epitopes from LAVs (BCG, OPV, and MMR). However, there is still a lack of base evidence showing the cross-reactivity between these LAVs and SARS-CoV-2 specific to the Indonesian population. Through *in silico* approach, the SARS-CoV-2 Wuhan-Hu-1 isolate T cell epitopes were predicted against HLA alleles specific to the Indonesian population. The generated epitopes were then compared with the OPV, BCG, and MMR sequence to identify similar patterns. The cross-reactive epitopes were further rechecked and inspected for their population coverage in Indonesia. Both BCG and MMR contain 15 and 7 strong binding cross-reactive epitopes specific to the Indonesian population, which have 2 to 4 amino acid substitutions compared with SARS-CoV-2 epitopes. Despite that, the cross-reactive epitopes are potentially able to induce either cross-reactive $CD8^+$ or $CD4^+$ T cells against SARS-CoV-2. Additionally, most cross-reactive epitopes have similar or higher population coverage than SARS-CoV-2 epitopes, ranging from 4.83% to 73.5%. In contrast, no cross-reactive epitopes were found from OPV specific to the Indonesian population, which may be due to the genome nature of poliovirus. Overall, these identified cross-reactive patterns may serve as a pillar for uncovering the full potential of beneficial cross-protection against SARS-CoV-2 and future pandemics.

Keywords: cross-reactivity, SARS-CoV-2, BCG, OPV, MMR, immune response