I. Introduction

SARS-CoV-2 is a +ssRNA virus of the family coronaviridae, originating in Wuhan, China. In late 2019, a series of cases associated with a seafood market in Wuhan were found to have originated from a novel coronavirus, now termed SARS-CoV2. The virus proceeded to spread rapidly across the world in the following months, with total cases numbering above 23 million and deaths exceeding 800,000 as of August 22, 2020 (WHO, 2020). As of time of writing, no clear cure or vaccine exists for SARS-CoV-2, while threats of a second wave of infection loom across the globe.

Currently, it is known that the virus targets one or both of two proteins: ACE2 and TMPRSS2 in order to facilitate the entry of the viral genome into the cytoplasm. Being a positive sense ssRNA virus, the genome is readily recognized by the ribosome and translated into proteins. The proteins are processed and then presented to T cells. This eventually results in a CD8 T-cell response, which kills infected cells, thereby preventing further viral reproduction and CD4 T cells which help B cells produce antibodies. T-cells are thus central to an immune response to SARS-CoV-2, and with no cure or vaccine currently available, research the immune response upon infection is one way to combat SARS-CoV-2. (Azkur et al., 2020)

T-cells consist of two main types: CD4 and CD8. These two types of T-cell recognize peptides from a pathogen which is presented by Major Histocompatibility Complex (MHC) molecules on the surface of antigen presenting or infected cells. The CD8 T-cells recognize the epitopes presented by MHC class I, whereas CD4 T-cells recognize peptides presented by MHC class II. The MHC, or Major Histocompatibility Complex, are membrane proteins on antigen-presenting cells (APCs, which include the likes of dendritic cells and normal cells such as endothelial cells). MHCs are also termed HLAs (Human Leukocyte Antigens) when referring to human MHCs, as MHCs are present in all mammals. MHCs present 8 or 9 amino acids for MHC class I or 10 to 30 amino acids for MHC class II.

These peptides are key in determining the immune response, as they derived from the of pathogens proteome that have been processed by a cell

HLA genes are the most polymorphic genes in the human genome. HLA allotypes vary from population to population. These varying allotypes result in different epitope recognition patterns, and as such each allotype will present different epitopes produced from the same proteins. This thesis will thus focus on the HLA allotypes of Javanese population predict the peptides from SARS-CoV-2 which will be presented by these alleles. (Gonzalez-Galarza et al., 2019)

SARS-CoV-2 is still in the same family of viruses as the common cold coronaviruses, and it has been postulated that this may result in the presence of memory T cells that could in turn protect against severe COVID-19. Healthy donors and patients have been found to have CD4 and CD8 T-cells that were already reactive to the SARS-CoV-2-derived peptides, demonstrating T cell cross-reactivity as these patients had no prior history of being infected by SARS-CoV-2. (Braun et al., 2020) (Mateus et al., 2020) (Grifoni et al., 2020) A set of epitopes in SARS-CoV are identical to that of SARS-CoV-2, highlighting the potential for prior work on other viruses to result in a productive vaccine. (Ahmed, Quadeer, McKay, 2020)

a. Objectives

The aim of this thesis is to predict T cell epitopes from SARS-CoV-2 which will be presented by HLA alleles of the Indonesian Javanese population and comparison of epitopes produced by SARS-CoV-2 with epitopes from common cold coronaviruses.

b. Scope of Work

As a dry lab thesis, and no laboratory experiments to be conducted. The scope of this work is purely a computer-based prediction followed by comparison of strong binding between epitopes-

derived from SARS-CoV-2 and the epitopes derived from the typical common cold coronaviruses presented by the HLA alleles of the Javanese population.

c. Research Question

Are there common epitopes between SARS-CoV-2, HCoV-OC43, and HCoV-HKU1 which are presented by HLA allelotypes common in the Indonesian Austronesian population?