CHAPTER I

INTRODUCTION

1.1 Background

In late 2019, the world was suffering from a new global pandemic that was caused by the novel COVID-19 is widely known to be caused by the newest addition of coronaviridae family called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Li *et al*., 2020). This highly contagious virus has left a great impact in a worldwide level, resulting in more than 5.2 million mortalities and could be seen as a severe threat to public health around the world, including Indonesia (World Health Organization, 2021; Djalante *et al.,* 2020; Cascella *et al*., 2021). It was predicted that Indonesia would feel the significant impact of COVID-19 in an extended period due to its large population (Cascella *et al*., 2021). Currently, there are no specific therapeutic drugs to treat the patients (Lotfi *et al*., 2020; Cascella *et al*., 2021). Thus, an immediate step to develop an effective system to lower down the spread of COVID-19. One strategy that is being highlighted in recent literature is vaccine development and its implementation.

This strategy has been developed and implemented in many countries since the completion of vaccine development with hopes to achieve herd immunity in the population (Bethesda, 2020). Currently, three main types of vaccines are already available in the market; (1) mRNA vaccine like Moderna and Pfizer/BioNTech, (2) Non-Replicating Viral Vector vaccine like Janssen, AstraZeneca, and Covishield, (3) Inactivated vaccine like Sinopharm, and Sinovac (McGill, 2021; Bethesda, 2020). However, these vaccine's developments are not based on the T-cell epitopes and studies about T-cell epitope. In addition, the vaccine's analyses are mostly based on SARS-CoV-2 sequences and human leukocyte antigen (HLA) allele outside Indonesia. Thus, making it not specific enough for the Indonesian population.

The general SARS-CoV-2 genome is consisting in around 30 kb which encodes for more than 20 non-structural protein that involves in transcription and replication of the virus and 13 open reading frames (ORF), including structural protein such as N protein, M protein, S protein, E protein, and other non-structural protein (Poran *et al*., 2020). These proteins may become the potential candidate for developing a vaccine to induce robust T cell immune response.

This project's objective was to construct a T-cell epitope-based vaccine using HLA allele in the Indonesian population and Indonesian isolate SARS-CoV-2 sequences to have a more specific and effective vaccine for Indonesian people. The strategy to do the vaccine design is started by using immunoinformatic methods due to their method effectiveness in designing computer-based vaccines against viral disease (Yashvardhini *et al*., 2021). Furthermore, this type of method is preferable in the initial step of viral vaccine development due to its remarkable advantages, such as being highly specific, less time-consuming, safe, cost-effective, maintaining long-lasting innate and adaptive immunity, and capable of evading undesired immune responses (Yashvardhini *et al*., 2021).

1.2 Objectives

This project aimed to identify the nonameric peptides from SARS-CoV-2 that are conserved, immunogenic, have no resemblance with human peptides or human microbiomes, and generate SARS-CoV-2 T-cell epitope-based vaccines specific for the Indonesia population.

1.3 Research Scope

This research was going to be conducted fully online which will have no laboratory experiment activity. This project was done fully computer-based followed by the prediction of strong binding affinity of SARS-CoV-2 peptides to MHC molecules (both class I and II) and B cells epitopes using Indonesian HLA alleles to construct a specific peptide-vaccine design for Indonesian people.