UNIVERSITI TEKNOLOGI MARA

APPLICATION OF BIOINFORMATICS TO *HELICOBACTER PYLORI* VACCINOLOGY

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ABSTRACT

Helicobacter pylori is a gram-negative and a microaerophilic bacterium. It has a shape of a spiral. It primarily lives in the human stomach as it requires acidic environment to survive. As a result of living in the human stomach, it causes gastric and duodenal ulcer including as a precursor of gastric carcinoma.Vaccine, a preparation of special antigenic material that is able to stimulate the production of antibodies against the infection caused by *Helicobacter pylori* is required. Conventional method of preparing vaccine requires the cultivation and dissection of the bacteria's main component before testing their ability to trigger the immune system. However Reverse Vaccinology searches the immunogenic antigens from *in silico* analyses from the genome pathway instead of culturing the microorganism. To yield a vaccine that has high selectivity against Helicobacter pylori, specific target of antigenic sequence need to be selected. The target should not have any well-conserved homolog in the human host. In this study, we focus on recognizing the toxin-like outer membrane protein (ID:O25331) in Helicobacter pylori including its secondary structure and predicting the antigen's epitopes that is able to bind to Major Histocompatibility Class-II molecules using a-TEPITOPE-based algorithm. The infection caused by the bacteria is widely spreading in developing countries including Malaysia. A target antigenic sequence using bioinformatic tools need to developed in order to fight against the pathogen. The physicochemical characteristic of the sequence includes its molecular weight was 30893, while it is slightly basic due the theoretical pI being 8.97; the sequence had the highest amount of leucine. It was characterise as hydrophobic due to its GRAVY value which was less than 1 as determined by ProtParam tool. The motif region predicted by SCAN PROSITE tool was from the ABC _TM1 family. PSIPRED found that its secondary structure consists of 77.86 % of α-helix and 22.14 % of coil. Region "IVLLLVICA" has binding affinity for most alleles used in the query entered in the ProPred tool, as a result it can be a potential candidate for vaccine development. "IVLLLVICA" can be utilized as a potential sequence for the vaccine against *Helicobacter pylori*. This research is an essential work in the fields of bioinformatic analysis and helps to put forward a new way for bioinformatic analysis of other genes.

CHAPTER 1

INTRODUCTION

1.1 Introduction

1.1.1 *Helicobacter pylori*

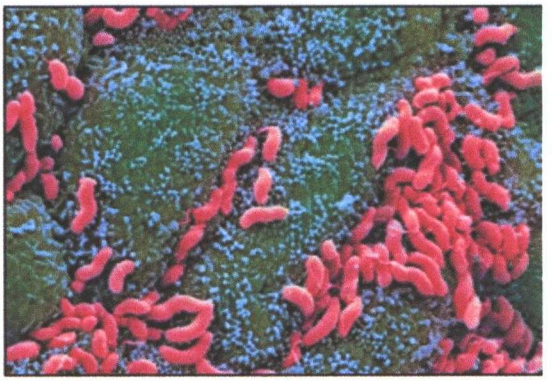

Plate 1.1 *Helicobacter pylori*. Image obtained from ***www.thelancet.com/oncology***

Human stomach has become the primary habitat for *Helicobacter pylori* even though it is too harsh for most bacteria (Talaro, 2005). *Helicobacter pylori* are micro-aerophilic, spiral and gram-negative bacillus (Zheng, *et al.*, 2002). It is first isolated from human gastric antral epithelium in 1982 (Michetti, *et al.*, 1999). Urease is its most important enzyme and it act as a potent multisubunit (Mobley, *et al.*, 1995) is crucial for its survival at acidic pH environment and its successful colonization in the gastric environment (Cover, *et al.*, 1996). Only few other microbes can colonize and