

## **In silico annotation of the genes involved in biosynthesis of lipopolysaccharide for *Burkholderia pseudomallei*.**

### **ABSTRACT**

*Burkholderia pseudomallei* is the causative agent of melioidosis, a serious disease of man and animals. The high mortality of *B. pseudomallei* infections may be caused by lipopolysaccharides, an endotoxin. The biosynthesis of LPS is complex comprising three components, lipid A, core oligosaccharide and O-specific antigen. In the current study, by using the available *B. pseudomallei* genome database provided by Wellcome. The study demonstrated that the bioinformatics comparative technique was able to annotate LPS genes in *Burkholderia pseudomallei*. By developing a simple and easy flow chart including the use of Artemis software, a total of 44 putative ORFs involved in biosynthesis of lipopolysaccharide for *B. pseudomallei* and the genetic mapping for the ORFs have been successfully determined using bioinformatics and laboratory approaches. It is about 95.7% success for annotation based on the 46 genes that act as references. In the near future, a suitable vaccine or antimicrobial may be developed by targeting the genes encoding the various components essential in LPS biosynthesis and survival of the pathogen.

**Keyword:** Bioinformatics; *Burkholderia pseudomallei*; Data mining; Genes; Lipopolysaccharides; Melioidosis; Open reading frames.