

Homology Analysis, Phylogenetics and Prediction of Epitope Genes Encoding for Protein Type 4 Fimbriae A (PtfA) *Pasteurella multocida* Isolate from East Nusa Tenggara

ABSTRACT

Septicaemia Epizootica (SE), in Indonesia is a fatal acute disease in cattle and buffalo caused by *Pasteurella multocida*. Protein Type 4 Fimbriae A (PtfA) becomes one of the most important bacterial antigens and promising candidates for the development of SE vaccines and diagnostic kits. The aim of this study is to find out the homology of nucleotide sequence of Protein Type 4 Fimbriae A (PtfA) gene of *P. multocida* of isolate from NTT with vaccine strain (Katha strain) and 8 referen isolates and predict epitope gene Protein Type 4 Fimbriae A (PtfA) *P. multocida* of local isolate from NTT. Detection of PtfA gene of *P. multocida* from NTT and vaccine strain was done using PCR and then sequenced to obtain nucleotide sequence. Homology analysis of nucleotide sequences and amino acid sequences was performed on the BLAST program at NCBI. Epitope prediction analysis of PtfA genes *P. multocida* from NTT was performed using the online programme B Cell Epitope Prediction Tools. The results showed that the PtfA gene of *P. multocida* from NTT has 99% homology to isolate from China, Iran, India, France, UK, Khazakstan, Denmark and 98% homology to isolat from USA and PtfA gene of *P. multocida* isolate from NTT were likely to be immunogen candidates based on B cell epitope that had 4 epitopes, from both NTT isolate which had logscore value above 1. These findings indicate that *P. multocida* isolate from NTT has a chance as immunogen candidate, which can be developed as a vaccine candidate and diagnostic kit for SE.

Key word: *P. multocida*, PtfA, Nusa Tenggara Timur, PCR, sequence