MOLECULAR ANALYSIS OF GENE ENCODING VirB11 PROTEIN OF *Brucella abortus* LOCAL ISOLATES AND VACCINE STRAINS

Maria Gladis Bupu Meze

ABSTRACT

Brucellosis in cattle is a disease caused by *Brucella abortus* due to the reduction in livestock population caused by abortion, stillbirth, weak birth, infertility and sterility. *virB11 gene* that encodes VirB11 protein is an important virulence factor acts as an ATPase for assembling organelles when the bacteria replicate, helping to complete the bacterial cycle and agress to another cells. The objective of this study are to detect and analyze the structure nucleotide and amino acid, the phylogenetic, homology and prediction of B cell epitope of the partial *virB11* gene as encoding of *B. abortus* VirB11 protein in isolates from Pinrang, NTT, strain vaccines S19 and RB51. The isolates *B. abortus* were recultured and followed by microscopic and biochemical tested, PCR, sequencing, homology, phylogenetic tree and prediction of B cell epitope. The PCR result showed *virB11* gene have DNA band 720 bp. The homology results of the *B. abortus virB11* partial gene from Pinrang, NTT, strain vaccines S19 and RB51 were 100% and in the same clusters. *B. abortus virB11* partial genes from Pinrang, NTT, strain vaccines S19 and RB51 also have more than 99,86% similarity with *B. abortus virB11* genes in China, Italy and USA. Partial genes encoding VirB11 protein from Pinrang, NTT, strain vaccines S19 and RB51 had 12 epitopes. Base on log score the epitope with TEVCVN structure peptides has the most immunogenic epitope caused it has highest log score.

Key words : *Brucella abortus* Pinrang isolate, *Brucella abortus* NTT isolate, S19 Strain, RB51 Strain, *virB11* gene