

**COMPARATION OF *pfhaB1* GENE *Pasteurella multocida* TYPE B ISOLATE LOCAL CATTLE AND BUFFALO FROM EAST NUSA TENGGARA (NTT)**

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**ABSTRACT**

Almost all regions in East Nusa Tenggara (NTT) Province Indonesia are endemic areas of *Septicaemia Epizootica* (SE), it is caused by *Pasteurella multocida* (*P. multocida*) Serotypes B: 2. The *pfhaB1* gene is the virulence factor of *P. multocida*. The objectives of this study were analysis the phylogenetic tree, homology and prediction B cell epitope of the gene a coding pfhA protein of isolates *P. multocida* from Buffalo and Cattle NTT. The isolates *P. multocida* were recultured and followed by microscopic and biochemical tested, PCR, sequencing, homology, phylogenetic tree, and also prediction of B cell epitope. The PCR result showed *pfhaB1* gene have DNA band 506 bp. The isolates *P. multocida* from Buffalo NTT and Cattle NTT are the same cluster and they have phylogenetic relatedness closely with Katha strain vaccine and also isolates from Iran and India. The isolate *P. multocida* from buffalo have four identical epitopes with Katha strain vaccine, but isolate from cattle have two identical epitopes with Katha strain vaccine. Between buffalo NTT, cattle NTT and Katha strain vaccine have two identical epitopes. Base on log score the epitope with NGYLLNELLQEL structure peptides from buffalo isolate has the most immunogenic epitope caused it has highest log score.

**Key words** : East Nusa Tenggara (NTT) Indonesia, Haemorrhagic Septicaemia, Katha Strain Vaccine, *Pasteurella multocida*, *pfhaB1* Gene