

**ABSTRACT**

**Homology Analysis, Phylogenetic Tree and Epitope Prediction ompA 37 kDa  
Gene of *Pasteurella multocida* Isolates from Nusa Tenggara Timur**

Thirty seven kDa omp A gene of *Pasteurella multocida* isolates from NTT buffalo, NTT cattle, and Katha strains were analyzed nucleotide sequence homology and phylogenetic tree with ruminant isolates from various countries in the world: India, China, Iran, and USA from GenBank data and B cell epitope predictions from both NTT isolates. Three Nucleotide sequences from three isolates were homology analyzed using BLAST at NCBI then phylogenetic tree using MEGA-X program and epitope prediction by online program at IEDB. The results showed 93-100% homology, phylogenetic tree of buffalo isolate and strain Katha with bovine from India, China, and Iran; buffalo from India; yak from China; calf from India; and cattle from India. Prediction tools found 5 peptida from both NTT and strain Katha isolates which had a logscore value above 1.

**Key words:** *Pasteurella multocida*, 37 kDa ompA, Nusa Tenggara Timur