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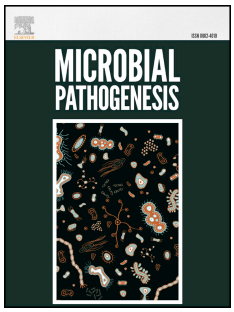

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Molecular characterization and differential expression analysis of interleukin 1β from *Ovis aries*

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Abstract

The interleukin-1 family is an important component of the innate immune system and plays an important role in regulating immune responses on the invasion of intracellular parasites in the acquired immune system. Interleukin 1β (IL-1β) is one of the members of the IL-1 family that predominantly activates downstream signaling pathways to play immunological functions of stimulating T and B lymphocyte activation and promoting the various syntheses of inflammatory substances in conjunction with other cytokines. Here, a full-length *IL-1β* cDNA (*OaIL-1β*) of sheep (*Ovis aries*) was cloned using rapid amplification of cDNA ends (RACE), which consists of 1494 bp and contains a 5'-UTR region with a length of 83 bp, a complete ORF of 801 bp in length, and a 3'-UTR region with a length of 642 bp. Recombinant protein OaIL-1β was expressed and purified, and the monoclonal antibody against IL-1β of sheep is prepared. Western blotting results showed that the sheep IL-1β protein was detected in the heart, liver, lung, kidney, stomach, intestine, muscle, lymph nodes and leukocytes with the highest expression in the muscle and the lowest expression in the lung. Different bacteria treating sheep white blood cells induced differential expression of *OaIL-1β*. Compared with the normal sheep, *OaIL-1β* in the buffy coat was differentially expressed in the *Brucella melitensis*-challenged group and the *B. suis* S2 strain-inoculated group. However, whether IL-1β may be considered as a molecular biomarker for differing *Brucella*-infected animals from brucellosis-vaccinated animals or not need to be further studied.

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