GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Deep sequencing-based analysis of gene expression in bovine mammary epithelial cells after *Staphylococcus aureus*, *Escherichia coli*, and *Klebsiella pneumoniae* infection

L. Xiu, Y.B. Fu, Y. Deng, X.J. Shi, Z.Y. Bian, A. Ruhan and X. Wang

College of Life Sciences, Inner Mongolia University, Hohhot, China

Corresponding author: X. Wang
E-mail: wxiao2008@gmail.com

Genet. Mol. Res. 14 (4): 16948-16965 (2015)
Received January 14, 2015
Accepted May 25, 2015
Published December 15, 2015
DOI http://dx.doi.org/10.4238/2015.December.15.1

ABSTRACT. The goal of this study was to characterize the transcriptome of primary bovine mammalian epithelial cells (pBMECs) and to identify candidate genes for response and resistance to *Staphylococcus aureus* (strain S108), *Escherichia coli* (strain E23), and *Klebsiella pneumoniae* (strain K96) infection. Using Solexa sequencing, approximately 4.9 million total sequence tags were obtained from each of the three infected libraries and the control library. Gene Ontology (GO) analysis of the S108-infected pBMECs showed differentially expressed genes (DEGs) were significantly involved in metabolic processes. In E23-infected pBMECs, DEGs were predominantly associated with cell death and programmed cell death GO terms, while in K96-infected pBMECs, DEGs were primarily involved in metabolic processes and in utero embryonic development. Analysis of the cluster of orthologous groups of proteins showed that the S108-infected, E23-infected and K96-infected pBMECs were significantly involved in "Translation, ribosomal structure and biogenesis", "General function prediction only" and "Replication, recombination and repair". The transcriptome sequences were also annotated for KEGG orthology, and it was found that DEGs in S108-infected pBMECs were significantly

involved in oxidative phosphorylation and Parkinson's disease. The clustered pathway terms of the DEGs of the E23-infected pBMECs were found to involve the NOD-like receptor signaling pathway and oxidative phosphorylation, while those of the K96-infected pBMECs were primarily involved in oxidative phosphorylation and apoptosis. Our results have identified a number of immune-related genes that showed changes in gene expression after bacterial infection, and provided insight into the interactions between pBMECs and the bacteria.

Key words: Bovine mammary epithelial cells; Deep sequencing; *Escherichia coli*; Gene expression; *Klebsiella pneumoniae*; *Staphylococcus aureus*

