



Detection of Critical Genes Associated with Bovine *Staphylococcus aureus* (*S. aureus*) Subclinical Mastitis in Dairy Cattle

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Abstract: Bovine mastitis, is one of the most common diseases of dairy cattle which is responsible for the rate of elimination, low milk yield and poor milk quality; therefore, it induces significant economic losses in the dairy cattle industry [1]. *S. aureus*, a Gram-positive pathogenic bacterium, is a major subclinical mastitis-causing pathogen in dairy cattle which is usually asymptomatic, persistent, resistant to antibiotic treatment and easily reoccur [2]. In order to get a higher power of statistical analysis, meta-analysis were used in the current study to combine p-values obtained from individual analysis of datasets extracted from 10 microarray-based datasets which investigate transcriptomic data of mammary gland tissue infected by *S. aureus* in dairy cows. 185 genes showed significantly differentially expressed after meta-analysis (44 genes down and 141 genes up regulate respectively). Sub-Network Enrichment Analysis (SNEA) were used to predefine gene sets which have more significant expression changes downstream targets using pathway studio software [3] on differentially expressed genes. Direct regulatory network between the SENA gene seeds were retrieved and displayed by Pathway studio software. Twenty-two critical genes including extracellular proteins such as: *C-X-C motif chemokine ligand 8 (CXCL8)*, *Interleukine 10 (IL10)*, *C -C motif chemokine ligand 3 (CCL2)* and membrane protein such as: *Toll like receptor 2 (TLR2)* were detected through applying 12 different ranking algorithms of Cytohubba plugin in Cytoscape software on direct regulatory network of SNEA gene seeds .

Keywords: Meta-analysis; Microarray; Transcriptom; S.aureus; SNEA

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