Journal of Immunology Research and Therapy
JIRT, 5(S1): 03
www.scitcentral.com

ISSN: 2472-727X

Conference Proceedings: Open Access

The Acidic Stress Response of *Brucella melitensis*: New Insights from a Transcriptome Analysis

David Kornspan[1*] and Mali Salmon-Divon[2]

[*1]*Kimron Veterinary Institute, Israel*

[2]*Ariel University, Israel*

Published November 23rd, 2020

ABSTRACT

The intracellular pathogenic bacteria belonging to the genus *Brucella* must cope with acidic stress as they penetrate the host via the gastro intestinal route, and again during the initial stages of intracellular infection. Following their uptake by the host cell, *Brucella* replicate inside a membrane-bound compartment-the *Brucella*-containing vacuole-whose acidification is essential for the survival of the pathogen. Therefore, identifying the genes that contribute to the survival of *Brucella* in acidic environments will greatly assist our understanding of its molecular pathogenic mechanisms. In a comparative transcriptomic analysis of the attenuated vaccine *Brucella melitensis* strain Rev.1 against the virulent strain 16M in cultures grown under either neutral or acidic conditions, we found 403 genes that respond differently to acidic conditions in the two strains (FDR<0.05, fold change ≥ 2), involved in crucial cellular processes, including metabolic, biosynthetic, and transport processes (Salmon-Divon et al., Front Microbiol. 2019). Further analysis of the RNA-seq data of 16M by comparing it to published transcriptomic data of this strain from both an *in cellulo* and an *in vivo* model, revealed 588 genes that were exclusively differentially expressed in 16M grown under acidic versus neutral pH conditions, including 286 upregulated genes and 302 downregulated genes that were not differentially expressed in either the *in cellulo* or the *in vivo* model. Among them we detected 13 key genes that are known to be associated with a bacterial response to acidic stress and were highly upregulated under acidic conditions in our study (Kornspan et al., Genes. 2020). These genes provide new molecular insights into the mechanisms underlying the acid-resistance of *Brucella* within its host and may facilitate the design of new and improved brucellosis vaccines.

Keywords: *Brucella melitensis*, Acid stress, RNA-Seq, Transcriptomic analyses, Virulence

Corresponding author: David Kornspan, Department of Bacteriology, Kimron Veterinary Institute, Bet Dagan 50250, Israel, E-mail: davidko@moag.gov.il

Citation: Kornspan D & Salmon-Divon M (2020) The Acidic Stress Response of *Brucella melitensis*: New Insights from a Transcriptome Analysis.J Immunol Res Ther, 5(S1): 03.