

Accepted Manuscript

Identification of *Pasteurella multocida* transcribed genes in porcine lungs through RNAseq

Cristiane Silva Chitarra, João Xavier de Oliveira Filho, Nelson Morés, Mayara Inácio Vincenzi da Silva, Stefhano Luis Cândido, Paula Gabriela Cezarino, Luciano Nakazato, Valéria Dutra

PII: S0882-4010(17)31018-5

DOI: [10.1016/j.micpath.2018.06.014](https://doi.org/10.1016/j.micpath.2018.06.014)

Reference: YMPAT 3007

To appear in: *Microbial Pathogenesis*

Received Date: 16 August 2017

Revised Date: 11 May 2018

Accepted Date: 8 June 2018

Please cite this article as: Chitarra CS, de Oliveira Filho JoãXavier, Morés N, da Silva MayaraInáVincenzi, Cândido SL, Cezarino PG, Nakazato L, Dutra Valé, Identification of *Pasteurella multocida* transcribed genes in porcine lungs through RNAseq, *Microbial Pathogenesis* (2018), doi: 10.1016/j.micpath.2018.06.014.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



IDENTIFICATION OF *Pasteurella multocida* TRANSCRIBED GENES IN PORCINE LUNGS THROUGH RNAseq

Cristiane Silva Chitarra^a, João Xavier de Oliveira Filho^b, Nelson Morés^c, Mayara Inácio
Vincenzi da Silva^a, Stefhano Luis Cândido^a, Paula Gabriela Cezarino^a, Luciano
Nakazato^a, Valéria Dutra^a

Avenida Fernando Corrêa da Costa, nº 2367 - Bairro Boa Esperança - Cuiabá – Mato
Grosso – CEP: 78060-900, Brazil.^a

Avenida Paulo Gama, 110 - Bairro Farroupilha - Porto Alegre - Rio Grande do Sul
CEP: 90040-060, Brazil.^b

Rodovia BR-153, Km 110, Distrito de Tamanduá Caixa Postal: 321 - Concórdia – Santa
Catarina CEP: 89715-899, Brazil.^c

ABSTRACT

Pasteurella multocida is one of the most important pathogen that causes pneumonia in swine. Although several virulence factors are known, the pathogenesis of this bacterium is not well-studied. Therefore, to study the pathogenesis of *P. multocida* infection in porcine lung, next-generation RNA sequencing was used to compare the transcriptomes of *P. multocida* grown *in vivo* and *in vitro*, respectively. After *P. multocida* infection a total of 704 genes were expressed *in vitro*, 1422 genes were expressed *in vivo*, and 237 genes were differentially expressed based on statistical analyses, *p*adj of ≤ 0.1 . Genes encoding ribosomal proteins or other products that function in the regulation of transcription and translation were downregulated, whereas genes whose products affected

Download English Version:

<https://daneshyari.com/en/article/8749310>

Download Persian Version:

<https://daneshyari.com/article/8749310>

[Daneshyari.com](https://daneshyari.com)