

## Gene Expression Profiling of Iron-Related Genes of *Pasteurella multocida* Serotype A Strain PMTB2.1

**Authors :** Shagufta Jabeen, Faez Jesse Firdaus Abdullah, Zunita Zakaria, Nurulfiza Mat Isa, Yung Chie Tan, Wai Yan Yee, Abdul Rahman Omar

**Abstract :** *Pasteurella multocida* is associated with acute, as well as, chronic infections in avian and bovine such as pasteurellosis and hemorrhagic septicemia (HS) in cattle and buffaloes. Iron is one of the most important nutrients for pathogenic bacteria including *Pasteurella* and acts as a cofactor or prosthetic group in several essential enzymes and is needed for amino acid, pyrimidine, and DNA biosynthesis. In our recent study, we showed that 2% of *Pasteurella multocida* serotype A strain PMTB2.1 encode for iron regulating genes (Accession number CP007205.1). Genome sequencing of other *Pasteurella multocida* serotypes namely PM70 and HB01 also indicated up to 2.5% of the respective genome encode for iron regulating genes, suggesting that *Pasteurella multocida* genome comprises of multiple systems for iron uptake. Since *P. multocida* PMTB2.1 has more than 40 CDs out of 2097 CDs (approximately 2%), encode for iron-regulated. The gene expression profiling of four iron-regulating genes namely *fbpb*, *yfea*, *fece* and *fur* were characterized under iron-restricted environment. The *P. multocida* strain PMTB2.1 was grown in broth with and without iron chelating agent and samples were collected at different time points. Relative mRNA expression profile of these genes was determined using Taqman probe based real-time PCR assay. The data analysis, normalization with two house-keeping genes and the quantification of fold changes were carried out using Bio-Rad CFX manager software version 3.1. Results of this study reflect that iron reduced environment has significant effect on expression profile of iron regulating genes ( $p < 0.05$ ) when compared to control (normal broth) and all evaluated genes act differently with response to iron reduction in media. The highest relative fold change of *fece* gene was observed at early stage of treatment indicating that PMTB2.1 may utilize its periplasmic protein at early stage to acquire iron. Furthermore, down-regulation expression of *fece* with the elevated expression of other genes at later time points suggests that PMTB2.1 control their iron requirements in response to iron availability by down-regulating the expression of iron proteins. Moreover, significantly high relative fold change ( $p \leq 0.05$ ) of *fbpb* gene is probably associated with the ability of *P. multocida* to directly use host iron complex such as hem, hemoglobin. In addition, the significant increase ( $p \leq 0.05$ ) in *fbpb* and *yfea* expressions also reflects the utilization of multiple iron systems in *P. multocida* strain PMTB2.1. The findings of this study are very much important as relative scarcity of free iron within hosts creates a major barrier to microbial growth inside host and utilization of outer-membrane proteins system in iron acquisition probably occurred at early stage of infection with *P. multocida*. In conclusion, the presence and utilization of multiple iron system in *P. multocida* strain PMTB2.1 revealed the importance of iron in the survival of *P. multocida*.

**Keywords :** iron-related genes, real-time PCR, gene expression profiling, fold changes

**Conference Title :** ICGMGA 2017 : International Conference on Genome Mapping and Genomics in Animals

**Conference Location :** Istanbul, Türkiye

**Conference Dates :** December 21-22, 2017