

**TITLE:** UNVEILING THE REGULON OF THE MarR FAMILY TRANSCRIPTION FACTOR CV3905 OF *Chromobacterium violaceum*

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**ABSTRACT:** Transcription factors are regulatory proteins able to bind in specific regions of DNA in response to various signals to regulate gene expression. MarR family transcription factors, widely found in bacteria and archaea, control many processes, such as virulence, antibiotic resistance and oxidative stress response. *Chromobacterium violaceum* is a Gram-negative, free-living  $\beta$ -proteobacterium, able to act as a human opportunistic pathogen. The *C. violaceum* genome has fifteen predicted MarR family transcription factors, among them the protein encoded by CV3905. In this work, we identified genes regulated by the MarR family transcription factor CV3905 using microarray analysis. Comparison of transcriptome profiles of wild type and  $\Delta$ CV3905 mutant strains revealed a few differentially expressed genes. However, microarray analysis comparing the  $\Delta$ CV3905 mutant with a strain overexpressing CV3905, allowed identifying about two hundred differentially expressed genes. Many of these genes were previously found be regulated under cumene hydroperoxide stress in *C. violaceum*, suggesting that CV3905 could be a redox sensing transcription factor. Northern blot assay validated that CV3905 activates the *ohrA* gene, encoding an enzyme for organic hydroperoxide detoxification. Additionally, we verified *in vitro* that the purified CV3905 protein containing two cysteine residues formed intermolecular dimers in non-reducing SDS-PAGE gel, after exposure to cumene hydroperoxide, hydrogen peroxide and *tert*-Butyl hydroperoxide. Using EMSA assays, we demonstrated a redox-dependent binding of the CV3905 protein in the promoter regions of CV3905 and *ohrA* genes. Together, these results suggest that CV3905 is a redox-sensing transcription factor that controls expression of a large regulon required to defense against oxidative stress in *C. violaceum*.

**Keywords:** Bacterial genetics, Gene regulation, Transcription factors, *Chromobacterium violaceum*, MarR Family, Oxidative stress

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