TITLE: STUDY OF REGULATORY REGION SHARED BY TWO TRANSCRIPTION FACTORS QseB, TWO-COMPONENT SYSTEM AND YgiV, A REGULATOR OF THE AraC FAMILY IN *Salmonella enterica* serovar Typhimurium

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ABSTRACT:

Salmonella enterica serovar Typhimurium is a Gram-negative bacillus responsible for most cases of food poisoning in several countries. It is an important enteric pathogen, which causes self-limited human gastroenteritis, but some more invasive strains can cause typhoid fever. The great success in the pathogenicity of this bacterium occurs through the complex temporal regulation of its virulence genes. Thus, there are several mechanisms involved in the regulation of these virulence factors as the two-component QseBC system is involved in the detection of these signals and functions as a global virulence regulator. QseC responds to autoinducer-3, epinephrine and norepinephrine. The *visP* encodes a Virulence and stress-related Periplasmic protein that has been associated with virulence by several mechanisms. Moreover, *ygiV* encodes a transcription regulator of the AraC family, which is co-transcribed with *visP* in *S.* Typhimurium and is being characterized by our group. This work aims to study the expression and regulatory region shared by the *qseBC* and *ygiV*/*visP* operons, besides to investigate whether the regulators YgiV or QseB regulated these operons in different stress conditions. First, we analyzed the genomic organization of *ygiV/visP* operon, and between those genes there are 71 pb noncoding, indicating a potential promoter. It was cloned in front of the *lacZ* reporter gene and by β-Galactosidase activity assays showed that it is not induced in different conditions, indicating the absence of a promoter in this region. After that, to the mapping of the regulatory regions of the *qseBC* and *ygiV/visP*, different fragments corresponding to these regulatory regions were PCR amplified and were cloned in front of the *lacZ* reporter gene. We observed that the expression pattern of the *qseBC*, only P1 was induced during the stationary phase and QseB showed to participate of this regulation. QseC mutant is more resistant than the wild type to polymyxin B and only P6 showed expression induction by this antibiotic. The expression pattern of *ygiV/visP* showed an increase during stationary phase only in P4, however independently of the regulation by QseB or YgiV. The constructs P1 to P4 showed increased expression under low oxygen conditions in static growth and this can be partially attributed to two regulators. Finally, in other stress conditions such as H_2O_2, NaCl and Bile, only in the presence of 3% Bile that the four constructs presented expression increase.

Keywords: Transcription factors, QseBC, two-component system, AraC family regulator, regulation and gene expression.

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