

ASSOCIATION BETWEEN *BmoR* AND *OxyR* TRANSCRIPTIONAL REGULATORS AND PHENOTYPICAL CHARACTERISTICS OF *Bacteroides fragilis* STRAINS

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Bacteroides fragilis is a Gram-negative rod that is found predominantly in the gastrointestinal tract as part of the human microbiota, but can become a pathogen leading to various clinical conditions. This bacterium is the strict anaerobe most commonly isolated from endogenous infections, and this may be due to the expression of virulence factors and its high resistance to oxidative stress. Among anaerobes, *B. fragilis* is one of the most resistant to oxygen exposure and can survive for up to 72 hours in an aerobic environment. One of the consequences of oxygen exposure is the formation of free radicals of oxygen that are harmful to the microorganism. *B. fragilis* has a strong response against this oxidative stress, which controls the expression of several genes, such those encoding detoxifying enzymes like superoxide dismutase and catalase. Much of the expression of these genes is controlled by the regulator *OxyR*, but there is another regulator, *BmoR*, which belongs to the MarR family of transcriptional regulators, that also participate in this response and is expressed independently of *OxyR*. However, it is not clear what is the mechanism involved in this response. Therefore, the aim of this study is to evaluate the prevalence of *bmoR* and *oxyR* in *B. fragilis* strains as well as their phenotypic characteristics. Initially, the genes *bmoR* and *oxyR* were identified by PCR in a set of *B. fragilis* strains and it was observed that not all the strains carried those genes. These same strains were exposed to oxidants such as atmospheric O₂ and hydrogen peroxide. It was not possible however, to establish a causal relationship between the presence of those genes and the observed phenotype. Mutant strains of *B. fragilis* were used to perform *in vitro* and *in vivo* tests. When these strains were exposed to peritoneal and medullar macrophages, there were no difference in the survival of any of the mutants when compared to the wild-type strain independent of the cell to which they were exposed, but when we evaluated the ability to form abscesses in C57BL/6 mice it was observed that the absence of *oxyR* led to decreased virulence. We hope that this study results helps to clarify how the *BmoR* and *OxyR* regulators acts on phenotypic characteristics of *B. fragilis* strains and how these regulators would be related to the ability of *B. fragilis* to prevail in infectious processes.

Key-words: *Bacteroides fragilis*, transcriptional regulation, oxidative stress, anaerobic bacteria