

EVALUATION OF DIFFERENTIALLY REGULATED PROTEINS OF *FUSOBACTERIUM* SUBMITTED TO OXIDATIVE STRESS.

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Fusobacterium nucleatum is found as indigenous microbiota, but also frequently recovered from anaerobic infections. Since alterations in its cell morphology and virulence have been reported after oxidative stress, in this study, the hypothesis of differentially regulated proteins occurrence was evaluated. *F. nucleatum* ATCC 25586 and a derivative oxidative-stress-adapted strain were employed. The bacterial proteome was analyzed by 2D electrophoresis. Three protein spots up-regulated were excised and processed for ESI-Q/TOF MS. A significant change in the protein profiles were observed. According to the data base searching, the peptides submitted to ESI-Q/TOF MS were found to be NAD-specific glutamate dehydrogenase, phosphoglycerate kinase, and acyl-CoA dehydrogenase. Overall, differences of this magnitude may not have resulted from the accumulation of single point mutations and thus may be part of a broader program of genetic control to protect and prevent oxidative damage. These global changes while not entirely understood did have other significant effects, once some other systems might be involved. ESI-Q/TOF-MS, in addition to 2-DE, enable the opportunity to gain a more holistic view of the bacterial proteome and contribute to achieve a better understanding of species diversity and to elucidate the role of specific proteins in disease. Supported by CNPq and FAPEMIG.

Key words: *Fusobacterium*, oxidative stress, proteome, mass spectrometry