

## **Stress-responsive proteins are upregulated in *Streptococcus mutans* during acid tolerance.**

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*Streptococcus mutans* is an important pathogen in the initiation of dental caries as the bacterium remains metabolically active when the environment becomes acidic. The mechanisms underlying this ability to survive and proliferate at low pH remain an area of intense investigation. Differential two-dimensional electrophoretic proteome analysis of *S. mutans* grown at steady state in continuous culture at pH 7.0 or pH 5.0 enabled the resolution of 199 cellular and extracellular protein spots with altered levels of expression. Matrix-assisted laser desorption ionization time-of-flight mass spectrometry identified 167 of these protein spots. Sixty-one were associated with stress-responsive pathways involved in DNA replication, transcription, translation, protein folding and proteolysis. The 61 protein spots represented isoforms or cleavage products of 30 different proteins, of which 25 were either upregulated or uniquely expressed during acid-tolerant growth at pH 5.0. Among the unique and upregulated proteins were five that have not been previously identified as being associated with acid tolerance in *S. mutans* and/or which have not been studied in any detail in oral streptococci. These were the single-stranded DNA-binding protein, Ssb, the transcription elongation factor, GreA, the RNA exonuclease, polyribonucleotide nucleotidyltransferase (PnpA), and two proteinases, the ATP-binding subunit, ClpL, of the Clp family of proteinases and a proteinase encoded by the pep gene family with properties similar to the dipeptidase, PepD, of *Lactobacillus helveticus*. **The identification of these and other differentially expressed proteins associated with an acid-tolerant-growth phenotype provides new information on targets for mutagenic studies that will allow the future assessment of their physiological significance in the survival and proliferation of *S. mutans* in low pH environments.**

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