

MONITORING PROTEIN EXPRESSION CHANGES IN *SALMONELLA ENTERICA* WHEN EXPOSED TO OSMOTIC STRESS

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Salmonella enterica is a facultative intracellular pathogen that remains a significant health problem, causing an estimated three million fatalities per year due to acute gastroenteritis and diarrhoea, and a further 600,000 deaths per year due to typhoid fever. Over 2000 serovars have been described, reflecting the vast host range of this organism. *S. enterica* serovar Typhimurium (formerly, *S. typhimurium*) is the leading serotype associated with gastroenteritis in humans and causes a typhoid-like disease in susceptible mice.

Understanding how, when, where and why virulence proteins are controlled in vivo is crucial to understanding how *Salmonella* causes disease, and ultimately, in designing more effective vaccines and antimicrobial agents.

In this study we have investigated the response of *Salmonella* to osmotic stress. Specifically, we have looked at the change in protein expression profiles when *Salmonella* is exposed to high concentrations of NaCl. Protein extracts were digested with sequencing grade trypsin and analysed by replicate LC-MS experiments on a Q-ToF Premier mass spectrometer. These datasets were then processed and searched against a non-redundant *Salmonella* species-specific databank to identify the constituent proteins. Tryptic peptide intensities of all identified peptides were then normalised, using exogenous internal standard peptide signals. This allowed quantitative comparison of peptide intensities between the two samples to determine expression differences. To date this approach has identified 14 proteins that are either up or down regulated in response to osmotic stress. This includes several membrane related proteins, including integral membrane proteins. Finally, data has been compared and contrasted to that of using a traditional 2D PAGE protein separation in combination with *in-gel* tryptic digestion and MS based protein identification.