

PROTEOMICS EVALUATION OF MOLECULAR MECHANISMS INVOLVED IN PATHOGENESIS OF SALMONELLA spp

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Salmonella species are an important group of enteric pathogens which could be penetrate the intestinal epithelial barrier and are capable of causing disease (i.e. they are pathogenic). Many foods, particularly foods of animal origin and other foods which may be subject to faecal contamination have been identified as vehicles for the transmission of this pathogen to humans. Those of particular importance include meat, poultry, eggs, milk, fruit and vegetables. Spread of this pathogen may occur in the food processing environment through cross contamination from raw food or infected food handlers.

The molecular bases for Salmonella adherence to and invasion of epithelial cells are distinct and complex and a large number of Salmonella genes are required for entry into cultured epithelial cells. Salmonella enterica serotypes are closely related genetically but they are significantly different in pathogenic potentials. Deep inside the relative responsible mechanisms may be a key to more general understanding of the invasiveness of intestinal bacterial infections.

This study represents a classic proteomic approach combining 2D gel electrophoresis and mass spectrometry for the comparative analysis of the proteomes of different species of Salmonella isolated from food with the principle aim to find biomarkers to understand pathogenesis mechanism.

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