Title:	Characterization of Salmonella effector protein SteA using MS-Proteomics analysis, Flow Cytometry and Western Blotting
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Abstract:	Salmonella enterica serovar Typhimurium is one of the major foodborne pathogens that causes Salmonellosis in humans and Typhoid-like disease in mice. It spreads through contaminated food, poultry, eggs and meat and causes around 93.8 million cases of nontyphoidal Salmonella gastroenteritis and 155,000 deaths each year. Salmonella Typhimurium invades, survives and replicates inside host cells by effector proteins expressed by gene clusters known as Salmonella Pathogenicity Islands (SPI). Salmonella Typhimurium SteA is an effector protein under the regulation of both SPI-1 and SPI-2. SteA under SPI-1 condition performs immunosuppressive roles interfering with NF□B activation pathway. To explore other possible functions of SteA, Mass spectrometry-based proteomics analysis was performed using Perseus platform. STRING network and PANTHER classification system were used to assimilate the results from Perseus analysis. The analysis indicated the possibility that SteA could be involved in host cell death pathway. Further, Initial Flow cytometry-based apoptosis detection experiments show that SteA deletion in Salmonella Typhimurium causes a decrease in apoptosis in RAW264.7 macrophages on infection. Further experiments can help consolidate results and identify targets and mechanism involved.
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