

EFFECT OF POINT MUTATIONS IN THE *InvF* *Salmonella* TYPHIMURIUM TRANSCRIPTIONAL ACTIVATOR

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Salmonella enterica is known to be a causative agent of food- and water-borne illnesses. The virulence of *S. enterica* ser. Typhimurium depends on two type III secretion systems (T3SS-1 and T3SS-2); T3SS-1 is required to initiate intestinal infection while T3SS-2 is required for systemic infection. The regulation of virulence genes ensures that these T3SSs are appropriately expressed during infection. *InvF* is a transcriptional regulator of the AraC/XylS family and is important for the expression of invasion genes in *Salmonella* by acting as a classical regulator. *InvF* interacts with SicA and with the alpha subunit of RNA polymerase, but it is unknown through which amino acid residues it does so. Here we generated *InvF* point mutants and determine their effect on gene expression and cell invasion. Mutants obtained with different strategies are: R14A, K230A, S171A-K230A, I148V, I148V-G184A-P222L, Δ 146W-I148V-E166K-G185R, I148V-I229T W146A, R176A and R181A. The expression of SopB-FLAG was detected as well as the effect on cell invasion by using HeLa cells. Results showed which residues have a role in the expression of *sopB* and which have a role in invasion. The results of this project demonstrate that changes in specific positions of the CTD are important for the activation of *InvF*-dependent genes.