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FLAGELLAR ASSEMBLY IN *SALMONELLA FLHA* DELETED STRAIN AND ITS ROLE IN BIOFILM FORMATION

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Biofilms formation is a major hazardous problem from both clinical and environmental perspective. Flagellum-mediated motility is important for biofilm formation by several gram-negative bacteria. More than 50 genes are involved in flagellar biosynthesis and function in *Salmonella typhimurium*. The flagella basal body is a representative of type III protein secretion systems; used by several gram-negative bacterial pathogens to colonize foreign tissues and substrates. The mechanism of flagellar assembly was analyzed in *S.typhimurium*, using bioinformatics analysis to identify conserved structural elements. In this study, FliI a flagellar protein that is needed for flagellar assembly and may be involved in a specialized protein export pathway was cloned and overexpressed. *FlhA* deleted mutant *Salmonella* strain SJW1616 was used to transform *FliI* overproducing plasmid by electroporation. Using vital dyes (Alexaflour 488), visualization of motility was observed in wild type, SJW1616 (Δ*flhA*) and *FlhA* transductant strain which was further assessed by biofilm formation ability. Swimming, swarming motility along with significantly reduced biofilm formation was observed in SJW1616 (Δ*flhA*) compared to wild type and *FlhA* transductant strains. This study will extend initial evidence that *FliI* plays important role in flagellar export system and flagellum-mediated rotation is critical for swimming, swarming motility and biofilm formation. The flagellar basal body is a particularly convenient drug target, since the architecture of most its components has been determined near atomic resolution and it is an ancient evolutionarily conserved macromolecular assembly. The knowledge gained will also have implications for elucidation of the mechanistic design principles underlying protein secretion complexes.

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