



Towards A Better Understanding of The Flagellar FlgM Secretion Signal

Atoosa M. Samani (Kelly T. Hughes)

Department of Biology

The bacterial flagellum represents a remarkable evolutionary achievement in nature, which is constructed from more than thirty different protein components. Driven by an ion-powered rotary motor, the rigid flagellar filament rotates at speeds of up to 1,200 cycles per second and propels bacteria through liquid environments and across hydrated surfaces. By changing direction of filament rotation (clockwise vs counter-clockwise) a bacterium can change the direction of its movement, and swim towards nutrient sources available in the environment and away from toxic substances. The flagellum consists of three principal structures: (1) a basal body that crosses both the inner and outer membranes and acts as the rotary motor, (2) an external universal joint that connects the drive shaft of the basal body to the (3) external filament.

The genes in the flagellar transcriptional hierarchy are temporarily regulated in response to assembly, and are organized into three promoter classes: I, II, and III. Class I includes the *flhDC* operon, also known as the flagellar master operon, and activates transcription of the class II promoters. Class II genes encode the proteins that make up the HBB, FlgM, and its chaperone σ^{28} . Twenty percent of FlgM will be produced by class II promoter, and the rest is expressed by a class III promoter. The FlgM and σ^{28} interaction regulate the activation of class III gene transcription. When the HBB structure is completed, FlgM is released from σ^{28} and secreted outside the cell. Free σ^{28} will then activate transcription of the class III genes (Figure 1).

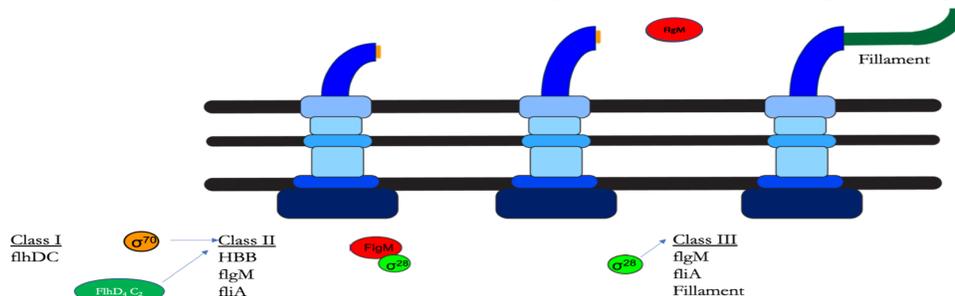


Figure 1. Flagellar assembly and transcriptional hierarchy.

The flagellum employs a type III secretion (T3S) system for protein export. The flagellar T3S that is located at the cytoplasmic base of the HBB facilitates the export of substrates into a central channel, which then diffuses to the tip of the growing structure and self-assembles into place. Exported proteins exit the cell as unfolded polypeptides during the secretion process; however, they fold in place as they exit the tip of the growing organelle. By taking advantage of FlgM-bla fusion, I was able to recognize the regions on FlgM that are important for its secretion. β -Lactamase (Bla) confers ampicillin resistance to cells when it is secreted into the periplasm through the type two secretion (T2S) system where it folds into an active conformation. The full-length FlgM protein can replace the Bla T2S signal and allow for secretion of FlgM-Bla through the flagellar T3S system into the periplasm in *flk* mutant strains, where it can fold and confer ampicillin resistance. Data from my experiments suggest that the secretion signal of FlgM can be found near the N-terminal of the protein. Further targeted mutagenesis experiments are planned to investigate the T3S signal of FlgM further.