

Project Leader (PI): Attila Karsi

Co-PI(s): Mark Lawrence

Collaborator(s): None

Objectives:

- Identify differentially expressed high-risk *L. monocytogenes* genes before and after catfish fillet attachment

Milestones for FY 2016-17:

Title: Identification of genes involving in *Listeria monocytogenes* attachment to catfish fillets

Milestones fully met

Progress Report:

We completed the objective of our project successfully during the extension period. Briefly, all catfish fillet attachment experiments were completed, and total RNAs from the fillet-attached and media-grown *Listeria* were isolated. After successful rRNA depletion and sequencing library preparation, RNA sequencing (RNA-Seq) analysis was conducted successfully and data were analyzed to determine differentially expressed genes.

Accomplishments

RNA-Seq analysis was conducted successfully. 336 genes were upregulated, and 43 genes were downregulated in the fillet-attached group compared to media-grown control group. Flagellar genes were among the highly expressed genes (Fig. 1).

Significant Activities that Support Special Target Populations:

With the completion of highly challenging RNA-Seq experiments, we will have a clear understanding of the genes that may be required by *L. monocytogenes* to attach fish fillets.

Technology Transfer:

None

International Cooperation / Collaboration

None

Publications:

In preparation

Presentations:

Akgul, A., Al-Janabi, N., Abdelhamed, H., Lawrence, M., **Karsi, A.** (2017, June). Expression analysis of *Listeria monocytogenes* in response to catfish fillet attachment. American Society for Microbiology ASM Microbe 2017 Meeting, New Orleans, LA, USA.

Figure:

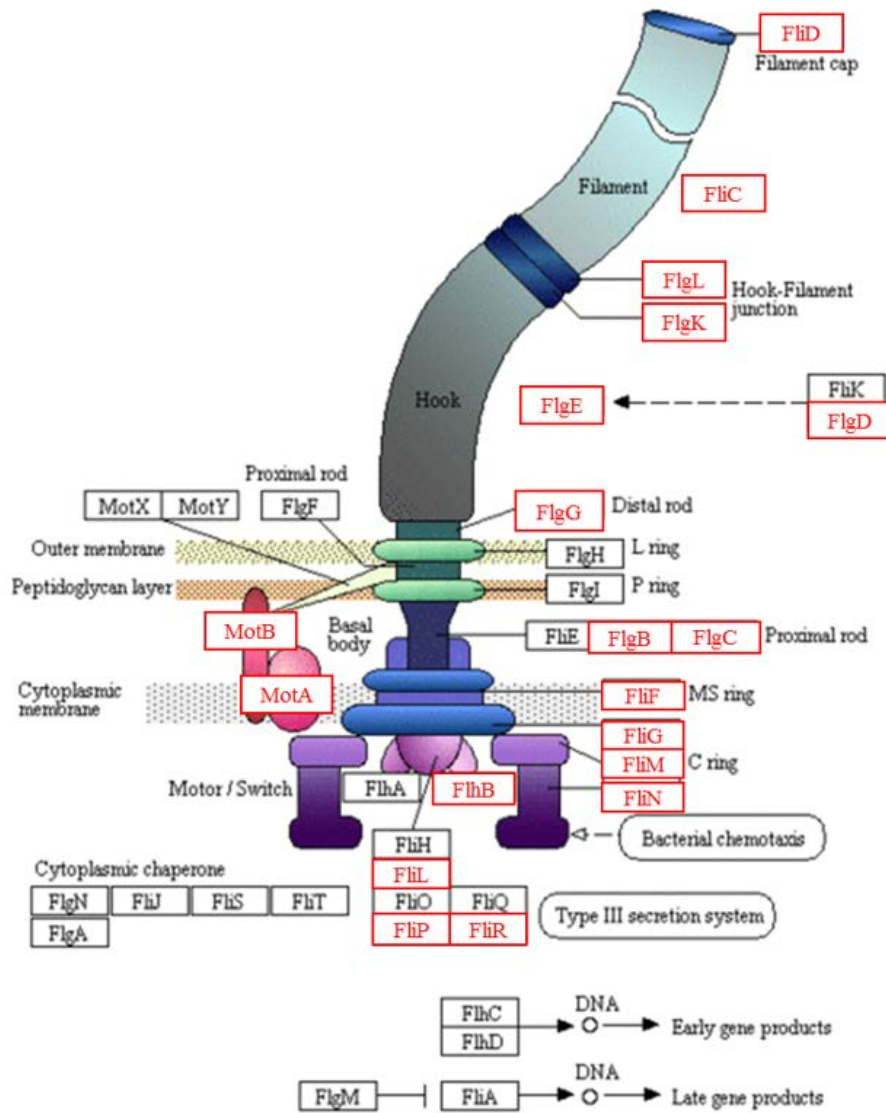


Fig. 1. *L. monocytogenes* flagellar structure. Red labels indicate highly expressed genes during catfish fillet attachment.