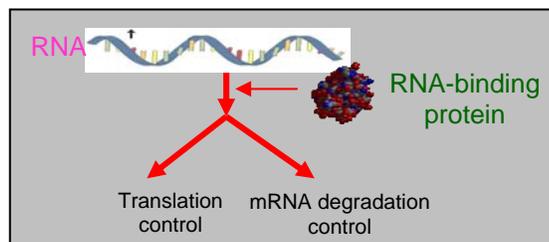


Match Game

Sample-matched transcriptomic and proteomic measurements offer insight into Salmonella virulence

Post-transcriptional regulation plays an unexpectedly prominent role in the pathogenic bacteria *Salmonella*'s ability to infect its host, as indicated by a new study conducted by researchers from Pacific Northwest National Laboratory, Oregon Health Sciences University, and the Sidney Kimmel Cancer Center.

Using resources at the Department of Energy's EMSL, the research team collected proteomics data from *Salmonella* mutant strains lacking specific RNA-binding proteins that mediate the translation of RNA into protein (post-transcriptional control) and the isogenic parent strain grown under four different conditions. Specifically, the research team investigated the *Salmonella* RNA-binding virulence proteins Hfq and SmpB. The team then compared the proteomics data to sample-matched transcriptomics data, analyzed at the Sidney Kimmel Cancer, to characterize the global control of gene expression at the post-transcriptional level. The comparison, *one of the most complete analyses of global post-transcriptional regulatory mechanisms in any organism*, revealed that a relatively high percentage of all the annotated *Salmonella* genes ($\geq 20\%$) are regulated post-transcriptionally. The extent of global regulation of translation observed is much greater than previously thought with profound effects in all stages of *Salmonella*'s life cycle, including a variety of housekeeping pathways and known and novel virulence factors. The team's findings have implications for human health and agriculture. This research offers insight into the ability of pathogens to rapidly adapt to a changing environment, such as in the infection of a human host.



A surprising percentage of genes are post-transcriptionally regulated in Salmonella.

Scientific Impact: While the role that DNA-binding proteins play in regulating gene expression is well understood, how RNA-binding proteins control gene expression remains unclear. The team's work provides one of the first quantitative global analyses of the role RNA-binding proteins play in regulating gene expression and makes a significant contribution to knowledge of this regulatory process. This work also supports EMSL's goal to predict biological functions from molecular and chemical data.

Societal Impact: Hfq and SmpB are proteins essential for virulence in a wide range of pathogenic bacteria including *Salmonella*, a leading cause of foodborne illness. Understanding how proteins Hfq and SmpB mediate virulence is important for protecting human health and agriculture.

For more information, contact EMSL Communications Manager Mary Ann Showalter (509-371-6017).

Reference: Ansong C, H Yoon, S Porwollik, H Mottaz-Brewer, BO Petritis, N Jaitly, JN Adkins, M McClelland, F Heffron, and R Smith. 2009. "Global Systems-Level Analysis of Hfq and SmpB Deletion Mutants in *Salmonella*: Implications for Virulence and Global Protein Translation." *PLoS ONE* 4(3):e4809. DOI:10.1371/journal.pone.0004809

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