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Poster #37: Unveiling the regulatory landscape of the double-stranded RNA phage φ6 using ribosome profiling

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Regulation of gene expression is a key aspect of phage biology. DNA phages primarily rely on transcriptional regulatory mechanisms to modulate protein output both temporally and quantitatively. By contrast, phages with RNA genomes do not undergo a DNA stage during replication and therefore must rely on post-transcriptional regulation. These circuits, however, remain largely unexplored, particularly in phages with double-stranded RNA genomes.

To address this, we combine ribosome profiling and total RNA-seq to uncover the translational and transcriptional dynamics of the dsRNA phage φ6 during infection of its host Pseudomonas savastanoi. We determine the translational efficiency of each host and phage gene and identify potential regulatory events such as ribosome pausing. We further observe unexpected active translation within regions of both the phage genome and the host genome that are annotated as non-coding, thus suggesting the presence of novel ORFs.

This work reveals the sophisticated post-transcriptional regulatory network orchestrated by φ6 during infection, which appears to employ regulatory strategies reminiscent of ssRNA phages and eukaryotic RNA viruses. These findings expand our understanding of RNA phage biology and highlight the broader significance of post-transcriptional regulation, an emerging conceptual framework relevant for both RNA and DNA phages.

Reference #1

Reference #2

Reference #3

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