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Discovery of a Potentially New Gene Function in Bacteriophages

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The use of Bioinformatics tools has greatly enhanced our ability to predict the location, start site
and function of many genes. However, even with the many softwares currently available, we are
only capable of determining the gene function of 30% of phage genes.
During the annotation process of the Lewando phage, we came across a mystery gene
with particular characteristics. It all started with a BLASTP hit to a gene whose function was
labeled as amidase. This was a particular match due to amidase not being found under the
approved functions list. Therefore, rather than calling it quits and labeling the gene as NFK,
further research in literature and bioinformatics tools were made.
To our surprise, our gene had a high probability score on HHPred with the Ospl protein.
OspI is a glutamine deamidase that selectively deamidates glutamine residues. In phages,
amidase domains are associated with helping the lysis of bacterial cell walls. It has been
previously shown that the presence of the amidase domain is necessary for effective lytic
activity.
Ospl contains a putative cysteine–histidine–aspartic acid catalytic triad. This catalytic
triad has been shown to be essential for the deamidation function of this protein. Comparison of
the mystery gene sequence with the Ospl sequence showed that our gene contained the necessary
catalytic triad found in Ospl. Additional comparison between glutamine deamidase domains
from other proteins also demonstrates that our gene contains many of the conserved nucleotides.
This evidence strongly suggests that the Lewando phage and possibly other phages may
contain glutamine deaminases in their genomes.