Bacteriophage Tripp is a Siphoviridae phage that infects Paenibacillus larvae, the bacterium responsible for American Foulbrood disease (AFB) in honey bee larvae.

Tripp was isolated from an AFB diseased hive in North Carolina. Its genome is 54,441 bp, 48% G+C, has 92 genes, and has 378 bp terminal repeats. It is distinct from all other P. larvae phages.

**The Tripp genome and two other P. larvae phage genomes**

During annotation of the Tripp genome, we found two consecutive genes (24 & 25) that appeared as partial transposases. If joined, the two genes would encode a typical full-length transposase. We present evidence to suggest there is an uncommon -2 programmed translational frameshift linking these two gene products.

**The Proposed Frameshift Site in the Genome of Tripp**

A programmed translational frameshift in the tail assembly region is conserved among many dsDNA phages, including mycobacteriophages, and is typically a ±1 shift. This type of frameshift is not observed in P. larvae phages sequenced to date. Among seven P. larvae phages from NC, and others, Tripp is the only phage where a programmed frameshift has been seen. Interestingly, the proposed frameshift is in a transposase gene and appears to be a -2 shift.

**The -2 Frameshift Sequence**

- The region spans the end of gene 25 (frame 1) and the beginning of gene 24 (frame 2).
- If joined in this region, the resulting 124 amino acid protein has 98% identity with a P. larvae transposase. Transposases with other types of frameshifts have been identified.
- The proposed “shifty region” has features seen in other -2 frameshift sites.

**The -2 Frameshift Site Includes a Pseudoknot**

The proposed “shifty region” has features seen in other -2 frameshift sites. If joined in this region, the resulting 124 amino acid protein has 98% identity with a P. larvae transposase. Pseudoknot-prediction software strongly suggests the formation of a pseudoknot immediately following the slippery sequence.

Together, the slippery sequence, RNA pseudoknot, and alignment with a P. larvae transposase strongly suggest the presence of a -2 programmed translational frameshift between genes 24 and 25 of bacteriophage Tripp.

**Conclusions & Future Work**

The transposase gene with its frameshift may have been acquired from the P. larvae host. Characterizing the frameshift features may aid in understanding the unique aspects of this frameshift.

We hope to analyze the pseudoknot and experimentally demonstrate the frameshift product.

**References**


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