



Whole-Genome Sequence of the Novel *Enterobacter* Bacteriophage Arya with an Integrase Pseudogene, Isolated from the Gut of the Formosan Subterranean Termite

Chinmay Vijay Tikhe,^{a*} Chris R. Gissendanner,^b Claudia Husseneder^a

^aDepartment of Entomology, Louisiana State University Agricultural Center, Baton Rouge, Louisiana, USA

^bSchool of Science, University of Louisiana Monroe, Monroe, Louisiana, USA

ABSTRACT We isolated and sequenced the novel *Enterobacter* bacteriophage Arya from termite gut. The genome showed synteny to lytic bacteriophage genomes; however, the genome encodes a truncated, putatively nonfunctional integrase pseudogene. Lysogeny-related genes were previously observed in certain lytic phages, but their role and evolution remain unclear.

Previous studies suggest that the termite gut contains a population of unexplored novel bacteriophages (1, 2). In this study, we isolated a novel bacteriophage, Arya, infecting *Enterobacter* sp. CT7 (GenBank accession no. KT204538), which is the third bacteriophage isolated from the termite gut and the second to infect *Enterobacter* sp. CT7.

Bacteriophage Arya was isolated from the gut of the Formosan subterranean termite, *Coptotermes formosanus*. Phage isolation, DNA extraction, DNA sequencing and annotation, and electron microscopy were carried out as described previously (1). Bacteriophage Arya produced small but clear plaques on *Enterobacter* sp. CT7. DNA sequencing produced a linear contig with terminal redundancy. PCR and restriction digestion confirmed the DNA to be circularly permuted. Arya has a genome length of 41,918 bp, with a G+C content of 54%. The genome has a total of 64 predicted protein-coding sequences and an arginine tRNA gene. Of the 64 genes, 55 produced a match in the NCBI GenBank protein nr database. Based on similarity to sequences in the database, 22 proteins were assigned a putative function. The overall genome architecture is conserved, with a packaging module, a structural module, a DNA replication/metabolism module, and a lysis cassette. The genome of phage Arya showed a high level of synteny to *Escherichia* phage vB_EcoM_ECO1230-10 (3), *Escherichia* phage vB_EcoM-ep3 (4), and *Pseudomonas* phage PPpW-3 (5). The *Escherichia* bacteriophages vB_EcoM_ECO1230-10 and vB_EcoM-ep3 are lytic, and no integrase or other lysogeny genes are present in their genomes (3, 4). Despite being lytic, phage PPpW-3 harbors a predicted integrase pseudogene. The Arya genome also contains a predicted integrase pseudogene. It encodes a 43-amino-acid product which is small compared to products of other integrases and is most likely nonfunctional (6). Both the PPpW-3 and Arya genomes contain an arginine tRNA gene located next to the integrase pseudogene. Also, similar to phage PPpW-3, Arya did not show the presence of other essential lysogeny genes (repressor and antirepressor genes). The presence of an integrase pseudogene in phage PPpW-3 is hypothesized to be the result of a horizontal gene transfer event (3). Electron microscopy and VIRFAM (7) analysis confirmed phage Arya to be a member of the *Myoviridae* family.

In another study, we isolated bacteriophage Tyrion, which also infects *Enterobacter* sp. CT7 (2). Phage Tyrion is lysogenic and is predicted to alter the host cell receptors to provide superinfection immunity against the host. Isolation and sequencing of bacte-

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Address correspondence to Chinmay Vijay Tikhe, ctikhe1@jhu.edu.

* Present address: Chinmay Vijay Tikhe, W. Harry Feinstone Department of Molecular Microbiology and Immunology, Bloomberg School of Public Health, Johns Hopkins University, Baltimore, Maryland, USA.

riophage Arya provides us with a model system for studying superinfection immunity and the dynamics among a bacterial host, a lytic phage, and a lysogenic phage.

Accession number(s). The complete annotated sequence of the *Enterobacter* phage Arya genome can be accessed under the GenBank accession no. [KX231828](https://www.ncbi.nlm.nih.gov/GenBank/ accession/KX231828).

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