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GENOME SEQUENCES

Genome Sequences of Nine *Erwinia amylovora* Bacteriophages

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ABSTRACT *Erwinia amylovora* is a plant pathogen belonging to the *Enterobacteriaceae* family, a family containing many plant and animal pathogens. Herein, we announce nine genome sequences of *E. amylovora* bacteriophages isolated from infected apple trees along the Wasatch Front in Utah.

At an estimated total number of 10^{31}, phages are by far the most abundant biological entity on the planet (1–7). They dramatically influence the evolution of bacteria by their ability to infect and kill their hosts and to transfer genetic material. *Erwinia amylovora* is a rod-shaped facultative anaerobic member of the *Enterobacteriaceae* bacterial family, which includes many well-characterized Gram-negative plant and animal pathogens, such as *Salmonella* spp., *Escherichia coli*, and *Klebsiella* spp. As the causative agent of fire blight, *Erwinia amylovora* infects members of the Rosaceae plant family, causing diseased areas to appear burnt (8–10). The isolation and characterization of phages that infect *E. amylovora* may aid in our understanding of these bacteria and provide potential treatment for this devastating agricultural disease. Herein, we announce the genome sequences of nine *E. amylovora* bacteriophages, vB_EamM_Asesino, vB_EamM_Alexandra, vB_EamM_Bosolaphorus, vB_EamM_Desertfox, vB_EamM_MadMel, vB_EamM_Mortimer, vB_EamP_Pavtok, vB_EamM_SunLIRen, and vB_EamM_Wellington.

Phages were isolated from apple trees along the Wasatch Front in Utah that appeared to harbor fire blight infection. Phages were plaque purified through a minimum of three passages after amplification via enrichment culture (11). All nine phages reported in this announcement infect the *Erwinia amylovora* ATCC 29780 strain, as indicated by plaque assays, and their characteristics are summarized in Table 1. Genomic DNA was extracted (Phage DNA isolation kit; Norgen Biotek), a library was made using the Illumina TruSeq DNA Nano kit, and sample genomes were sequenced by Illumina HiSeq 2500 sequencing (250-bp paired end) and assembled with Geneious (12) version 8.1 using *de novo* assembly with medium-low sensitivity and various percentages of data. All phages circularized upon assembly and were annotated using DNA Master (http://cobamide2.bio.pitt.edu/computer.htm), giving preference for calls that gave full coding potential coverage.

The nine phages were grouped into five distinct clusters by genomic dot plot and average nucleotide identity analyses, as previously described (11), with the first three groups containing jumbo *Myoviridae*. The first jumbo group included four myoviruses, vB_EamM_Bosolaphorus, vB_EamM_Desertfox, vB_EamM_MadMel, and vB_EamM_Mortimer, which are similar to previously published *Erwinia* phage Ea35-70 (13), as well as other phages we have isolated (14). The second group included two jumbo myoviruses, vB_EamM_Asesino and vB_EamM_Wellington, with similarity to the well-characterized *Salmonella* SPN3US phage (15) and related phages. The third is a single

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† Deceased. Charles J. Webb did not see or approve the final version of this paper.

TABLE 1 Properties of nine *Erwinia amylovora* bacteriophage genomes

Name	GenBank accession no.	SRA accession no.	Total no. of reads	No. of reads used	Assembly fold coverage (range [mean])	Length (bp)	No. of ORFs[a]	No. of tRNAs	G+C content (%)
vB_EamP_Pavtok	MH426726	SRX4597602	1,301,332	386,192	492–2,086 (1,069)	61,401	62	0	36.9
vB_EamM_SunLIRen	MH426725	SRX4597606	1,301,332	386,192	8,249–42,422 (13,566)	84,559	141	22	36.3
vB_EamM_Wellington	MH426724	SRX4597603	626,048	372,488	133–514 (329.7)	244,950	295	8	50.3
vB_EamM_Asesino	KX397364	SRX4597609	2,222,038	1,022,382	512–1,378 (1,037.7)	246,290	289	12	51.2
vB_EamM_Alexandra	MH248138	SRX4597608	381,540	200,005	63–516 (166.3)	266,532	349	0	49.8
vB_EamM_Bosolaphorus	MG655267	SRX4597604	778,168	326,344	83–555 (248.4)	272,228	321	1	49.4
vB_EamM_Desertfox	MG655268	SRX4597605	1,930,470	1,138,933	115–612 (352.9)	272,458	320	0	49.6
vB_EamM_Mortimer	MG655270	SRX4616109	2,581,160	287,396	47–207 (129.4)	273,914	325	1	49.5
vB_EamM_MadMel	MG655269	SRX4597607	1,604,720	1,443,568	567–1,577 (1,213.9)	275,000	321	0	49.4

[a]ORFs, open reading frames based on current annotation.

jumbo myovirus, EamM_Alexandra, which has similarity to previously published *Erwinia* phages EamM_Yoloswag (14) and EamM_Y3 (16). Podovirus vB_EamP_Pavtok and myovirus vB_EamM_SunLIRen are similar to *Erwinia* phages PEp14 and phiEa21-4 (17), respectively. The three jumbo myovirus groups package DNA by headful packaging (14) based on homology to phage phiKZ terminase (18), and their bp 1 was chosen by alignment to their phage family. PhageTerm (19) was used to determine the packaging strategy of SunLIRen and Pavtok. SunLIRen appeared to have headful packaging, and its bp 1 was assigned based on homology alignment to *Erwinia* phage phiEa21-4, while the packaging strategy of Pavtok is unknown, and its bp 1 was assigned due to homology to PEp14.

Data availability. The GenBank and SRA accession numbers for the nine *Erwinia* bacteriophages are listed in Table 1.

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