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Johns Hopkins Blue J(cluster)s: Ejimix and Shiloh(s) expand the diversity of mycobacteriophages on campus.

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Since 2008, the J cluster has grown to include 34 sequenced phages including 4 new genomes in the last year. One of these new J-cluster genomes is that of Ejimix, a temperate siphoviridae isolated on the campus of Johns Hopkins University. Like other J-cluster genomes, the Ejimix genome is nearly twice as long as the average siphoviridae genome, comprised of 111,924 base pairs and 242 genes. Ejimix shows significant homology and synteny with other J-cluster phages BAKA and Wanda and has the programmed frameshift and intron found in other genomes in the J cluster. We highlight several regions in which the Ejimix genome departs from synteny with these related genomes. We also examine several instances in which Glimmer and GeneMark called for overlapping forward and reverse genes and present our determinations. Ejimix is a temperate phage, which distinguishes it from Shiloh-1 and -2, J-cluster phages isolated together at JHU in 2016. This work adds to our understanding of conservation among these surprisingly long siphoviridae mycobacteriophage genomes and offers guidance for future J-cluster annotation projects.