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11th Annual SEA Symposium Abstract

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Phinding Phages a Good Home: A Comparative Genomic Survey of 7 adopted Cluster A Mycobacterium smegmatis phages

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While considerable work has been done by SEA-PHAGES and other groups to characterize *Mycobacterium smegmatis* cluster A phages, a large number of isolated cluster A phages remain uncharacterized and could potentially add invaluable insights to bacteriophage evolution and lifestyle. In this spirit, we adopted 7 cluster A *M. smegmatis* bacteriophages from SEA-PHAGES (Rutherferd (A1), Whabigail7 (A2), Veracruz (A3), Bumblebee11 (A4), Scorpia (A5), Jordennis (A6), Expelliarmus (A8)) and did a comparative genomic annotation of the group. As shown by previous SEA-PHAGES work, all 7 phages displayed similar sizes and overall genomic architecture despite their discoveries from disparate locations across the United States. Despite these overall similarities, our study also revealed unique features in individual or subgroups of the 7 phages. Among these features were a 430 basepair gap in the Veracruz genome revealed by BLAST to represent a transfer event from the *M. smegmatis* genome, immunity repressor proteins in similar locations near the back ends of the Expelliarmus and Bumblebee11 genomes, and a section of the Rutherferd genome that defied the traditional front-half/back-half opposing direction of ORFs traditionally found in this cluster. Taken together, this study reinforces what has been previously revealed about the genomic architecture of *M. smegmatis* cluster A phages while revealing potentially intriguing individual adaptations that individual phages have made across different geographical locations.