CONSIDER FOR TALK

10th Annual SEA Symposium Abstract

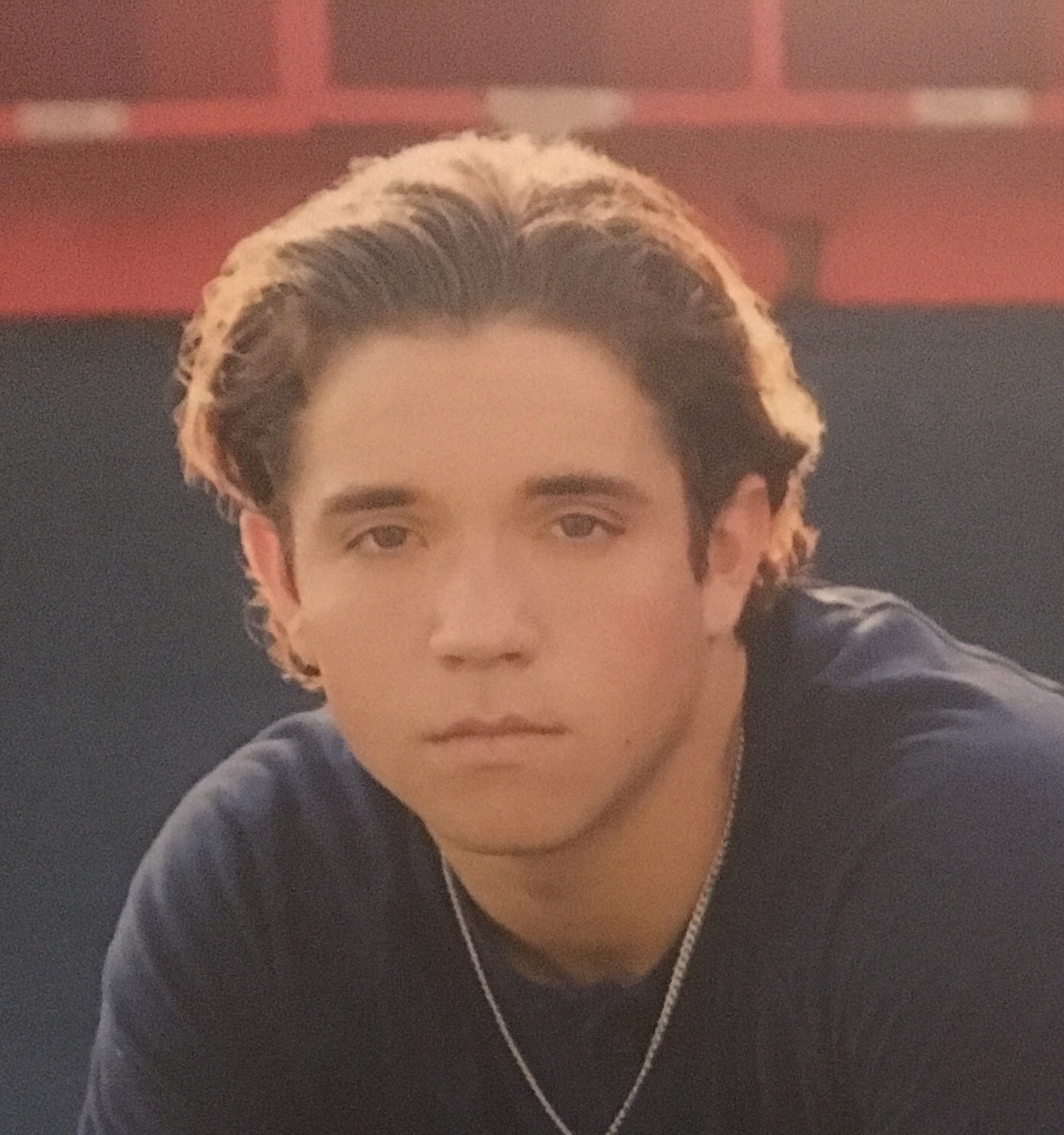
University of Alabama at Birmingham

Birmingham AL

Corresponding Faculty Member: Denise Monti (denise.monti@unf.edu)



Mckinley R Williams



Ote A Staton

Investigating Corynebacterium Phages: Similar Yet Very Unique

Mckinley R Williams, Ote A Staton, Adam R Aldaher, Katelin M Baird, Annisha Borah, Georgia E Haggard, Shriya Meesala, Sarah L Nealy, Aneesh Pathak, Raksha Ramdas, Manuel M Rocha, Sristi Das, Saakshi Thukral, Callie E Walls, Mohammad Waqas, Alexander K Winters, Katrina J Sahawneh, Denise L Monti

Over the past decade, the number of full-length phage genome sequences increased exponentially, in part, due to efforts of students in the HHMI SEA-PHAGES program. Although mycobacteriophages represent the largest group in the Actinomycetales database, several groups recently expanded efforts to isolate phages on alternate bacteria hosts, including Gordonia spp., Rhodococcus spp., Arthrobacter spp., and Microfloriorum spp., among others. For the past two years, students at the University of Alabama at Birmingham have studied phages infecting the host Corynebacterium. Here we report a comparison of Corynebacterium phages to those published in the Actinomycetales database and note unique characteristics of this group. Most *C. vitaeruminis* phages are lytic viruses and share a high degree of genetic similarity (>90% ANI). Moreover, most of these viruses share a common repeat region in the right arm not believed to be found in any previously isolated phage in the Actinomycetales database. Gradual degeneration of the consensus repeat sequence indicates this repeat may be a result of replication slippage. Unexpectedly, *C. vitaeruminis* phages do not all mediate cross-infection of the related bacterium *Corynebacterium pseudodiptheriticum* despite the high degree of genetic similarity among the *C. vitaeruminis* phages. To expand the pool of Corynebacterium viruses studied, we recently isolated five phages infecting the host *C. xerosis* and 3 additional *C. vitaeruminis* phages. In contrast to the *C. vitaeruminis* phages, all C. xerosis phages are likely temperate phages. Of the two viruses with complete full-genome sequences (Juicebox and SamW), both are singletons and appear to share a similar tyrosine integration system. Closer examination of the GC content across the genome revealed a significant drop in GC content particularly in the region of the integration complex for both Juicebox and SamW. Despite possibly sharing a similar integration complex, immunity studies show that *C. xerosis* phages are homoimmune. Future studies will expand isolation of Corynebacterium phages to further explore commonalities and differences of phages infecting this genus of bacteria. We are particularly interested in expanding phage isolation and sequencing efforts to the host *Corynebacterium glutamicum*, an important industrial microbe.