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2024 SEA Faculty Meeting Abstract

Coastal Carolina University

Conway SC

Corresponding Faculty Member: Daniel Williams (dwilliams@coastal.edu)



Daniel C Williams

Partitioning systems of non-integrating temperate phages

Daniel C Williams

Phages in the A cluster are designated as being temperate, but many of them lack an identifiable integrase gene. Prophages of these viruses exist as low-copy number extrachromosomal elements, which are replicated and partitioned into daughter cells during host cell division. The genome of these “phagemid-like” viruses contain a *parABS* system made up of three adjacent genetic elements; a centromere like binding protein (ParB), a ATPase partitioning protein (ParA), and centromere-like DNA site (*parS*). ParB specifically binds to replicated DNA at *parS* sites and through a series of interactions with ParA distributes DNA cargo to both ends of the dividing cell. Consistent with interactions between Par proteins mediating prophage maintenance, all *parABS* cassette containing genomes have both ParA and ParB genes. Although *parABS* cassettes are unevenly distributed in various A sub-clusters, the ParA genes are restricted to a single pham while the ParB genes are distributed into two phams; a large one of 148 phamly members, such as EmyBug, and a much smaller one of 4 genes; 40AC, Anon, Echild, and Refuge. EmyBug readily forms lysogens that can be stably maintained. However, attempts to generate stably maintained lysogens of Refuge have been unsuccessful. Similar observations have been made with 40AC and Echild, suggesting lack of a functional ParB gene in these genomes. Further bioinformatic and functional analysis of these distinct ParB gene phams will provide insight into phage parABS systems mechanism of prophage maintenance of non-integrating viruses.