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Genomic Analysis of Mycobacteriophage Smeadley

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Smeadley was found in 2011 in Conyers, GA by Krystle McMinn student of Georgia State University. We received its genome through adopt a phage program, annotated it and looked at some of its genes more closely. Smeadley belongs to the subclaster A8 together with four other phages: Astro, Saintus, Expelliarmus and Roary. Two of them are submitted to the Gene Bank: Astro and Saintus. Saintus is also from Georgia, Astro is from South Carolina and Expelliarmus is from Michigan. Smeadley has a genome with a length of 52392 bps and has 98 predicted genes. This genome is very packed, with few long gaps and multiple instances of a 3 base pair overlap. Another feature of Smeadley genome is that the first half of the genome is forward and the second is reversed similarly to all A cluster phages. BLAST of the full genome of Smeadley returns 99% identity with Astro. BLAST of individual genes revealed that 48 of Smeadley’s putative genes have genes from Astro as their best match, 31 have Saintus and 19 have Fredward that is not a part of Phagesdb. Smeadley has 1 tRNA gene, corresponding to tryptophan. The first part of the genome contains many genes with well predicted functions such as structural proteins: minor tail subunit, major tail subunit, tai assembly chaperone, tapemeasure, portal and terminase and functional proteins: lysin A, lysin B, integrase, protease. We identified programmed frameshift in front of the tapemeasure. The end of the genome has many short genes that don’t have functional domains. Smeadley does not have any unique genes or genes matching other clusters than A.