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2023 SEA Symposium Abstract

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Characteristics of Mycobacteriophage Nergal and TiniBug

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The Nergal and TiniBug phages were isolated from M. smegmatis mc2155. The phages were annotated using the PECAAN program.   
Nergal was isolated from a soil sample at Bowling Green, KY. The name originated from the Babylonian God of war and pestilence, a reference to the metaphorical war between bacteria and bacteriophages. The Nergal genome is 51, 176 bp long and has 88 protein-encoding genes. Nergal is a temperate phage related to the K cluster phages Milly, Findley and BoostSeason with an 87% similarity as evidenced by NCBI-BLAST. The lysis cassette comprising the Lysin A, holin and three lysin B genes (genes 26-30) was located between 22,488bp-25,836bp. When compared to its closest relative Milly, Nergal exhibited massive rearrangements of the protein domains as evidenced in Pham maps on PECAAN. The genome comprised of several well-characterized genes such as Cap decoration protein LmD like, excise, hydrolase, WhiB family transcription factor, DNA helicase, DNAQ-like DNA polymerase gene, NrDH-like glutaredoxin and Antitoxin HlCB-like domain.  
TiniBug phage was isolated from a water sample from Bowling Green, KY. The TiniBug genome is 55, 792 bp long and has 85 protein-encoding genes. TiniBug is a temperate phage related to the K cluster phages DrHayes, SamuelLPlaqson and Urkel with a 98% similarity as evidenced by NCBI-BLAST. The lysis cassette comprising the lysin A, lysin B and holin genes (genes 29-31) was located between 24,766bp-27,702bp. The genome comprised of several well-characterized genes such as helix-turn-helix DNA binding domain MER-like, MRE-11 double stranded break exo/endonuclease, NrdH-like glutaredoxin, DNAE-like ds DNA polIII, RusA-like resolvase, SprT-like protease, Antitoxin HlCB-like domains and cas4 exonuclease. The mid-region of the genome (genes 42 and 44) housed the genes involved in life cycle regulation, the tyrosine integrase and the immunity repressor.