CONSIDER FOR TALK

10th Annual SEA Symposium Abstract

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 Potential of Mycobacteriophages as Candidates for Phage Therapy - Identification of Phage that Infect Nontuberculous Mycobacteria Pathogens

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Nontuberculous mycobacterial (NTM) infections cause a wide range of debilitating diseases and are increasing in prevalence in the U.S and worldwide. With the increased resistance to antibiotics by NTM pathogens, phage therapy is gaining attention as an alternative for the treatment of such infections. Over 7,000 bacteriophages that infect the non-pathogenic species *Mycobacterium smegmatis* have been isolated. Host-range tests have identified specific subclusters of phage that can infect multiple *M. smegmatis* strains and a non-pathogenic strain of *M. turberculosis*, indicating that they may exhibit broad host range and can possibly infect NTM pathogens. Members of the A3 subcluster have multiple phages that are potentially broad host range. In addition, these phage share a specific variant of a gene (GP5) encoding a putative minor tail protein. We have tested the ability of a large series of A3 phage to infect six pathogenic Mycobacterium species (*M. abscessus, M. chelonae, M.* *fortuitum, M. mageritense, M. porcinum*, and *M. septicum*) to determine if A3 broad host range extended to NTM species and if the infectivity correlates with the gene variant. In addition, as part of the SEA-PHAGES broad host-range project, we have identified the cluster AB mycobacteriophage Muddy as a broad host-range candidate that infects all six of the NTM pathogens tested.