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Comprehensive Phylogenetic Analysis and Discovery Isolation of Enterococcus faecalis Phage from a Soil Sample in Florida

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Enterococcus faecalis is a commensal bacterium found in the gastrointestinal tract, oral cavity, and vagina of humans, which can transition to pathogenic states, leading to diverse infections. Many E. faecalis infections are becoming progressively challenging to treat, stemming from the lack of effective antibiotic therapies against its virulence factors, including biofilm formation and antibiotic resistance. Phage therapy emerges as a promising alternative, targeting bacteria with minimal impact on host flora. However, despite phages' ubiquitous presence and potential applications in medicine and biotechnology, their diversity and ecological niches are vastly understudied. Here, we investigated the diversity of sequenced E. faecalis phages and isolated a phage from a new environmental source. All phages belonged to either the Siphoviridae, Herellevirdia, Andrewesvirina, Rountreeviridae, or Autographiviridae family, and their genomes ranged between 16,954 and 151,985 base pairs. The phylogenetic analysis focused on single 'marker' genes, specifically the portal protein and terminase large subunit. Applying single-gene analysis yielded distinct clusters, each corresponding to specific families and genera. Furthermore, we successfully isolated a lytic phage from soil capable of infecting E. faecalis OG1RF. From our results, we conclude that a single gene has the potential to serve as a molecular marker for classifying phage taxonomy, as evidenced by the distinct clustering of phages. Additionally, our findings indicate soil as an additional source for isolating E. faecalis phages. Understanding the diversity of E. faecalis phages will aid in identifying alternative therapeutic targets to treat E. faecalis infections, thereby addressing the challenge of antibiotic resistance and enhancing treatment options for patients.