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Fazel, A Desert Phage in the DJ Cluster, Contains Seven Orphams

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Bacteriophages (phages) are the most abundant biological entity on Earth. They contribute to conserving and maintaining microbial life because they infect bacteria cells. Because of this phages have many medical and antibacterial implications. Fazel is a phage that infects the soil bacterium *Gordonia rubripertincta*. Fazel was isolated directly from soil under a rain gutter on the New Mexico Institution of Mining and Technology campus after a rain shower; the soil was described as wet and sandy. Fazel plaques were small and clear, with defined edges and an average diameter of 1.2 mm. Transmission Electron Microscopy (TEM) photos identified Fazel as a siphovirus with a symmetrical icosahedral head. The length of the Fazel tail was 295 nm and the capsid was 69 nm in diameter. Fazel is a lytic phage. DNA isolated from a high titer lysate of Fazel was sequenced on a Illumina MiSeq lane. The Fazel genome is double-stranded DNA that is 60,088 base pairs long with 52.0% G-C content. Based on sequence similarity, Fazel belongs to the DJ cluster of actinobacteriophages. Autoannotation of the genome predicted 96 protein-coding genes and no tRNAs. Following manual annotation, 90 genes were found on the forward strand and two on the reverse. Functions were assigned to 32 genes. Although Fazel shows similarity to a previously isolated DJ phage, Fazel contains seven additional orphams and 16 genes belonging to phams not seen in Mossy. Like Mossy and other DJ cluster phages, the middle region of Fazel’s genome contains several repeated motifs and multiple rearrangements. In this region, Fazel contains two predicted novel proteins, one of which is on the reverse strand. Given the differences in the genomes between Fazel and Mossy, future testing would involve comparing differences in ability to infect other bacterial hosts similar to *G. rubripertincta*.