CONSIDER FOR TALK

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Analysis of OscarSo and Cece: Pioneering Phage Isolated from Microbacterium radiodurans

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Members of the bacterial genus *Microbacterium* are gram positive rods and have been isolated from a wide range of environments including soil, cheese and other dairy products, and plants. The majority of *Microbacterium* phages were isolated using *M. foliorum* as a host which was originally isolated from grass and we decided to try to isolate, identify and characterize other phages using another *Microbacterium* species. *Microbacterium radiodurans*, known for its radiation resistance was originally isolated from sand in the Gobi Desert and using this species we were able to isolate four phages from soil, two of which were sequenced, OscarSo and Cece. The two phages couldn’t be any more different. OscarSo has a genome of 33,432 bp with circularly permuted ends and Cece has one of the largest actinobacteriophage genomes with a genome size of 186,513 bp with direct terminal repeat ends. OscarSo has a G+C% content of 69.2% compared to Cece which has 59.6%. Although there is a significant difference in G+C% content, both are within the range of previously isolated Microbacterium phages which generally have G+C% content ranging from 51-71%. OscarSo is unrelated to any other sequenced phages with 50 predicted genes, 60% of which are orphams with no known close relatives and no tRNAs. On the other hand, Cece is a member of cluster GD and has 299 predicted genes, 24% of which are orphams and 46 tRNAs. In our presentation, we will present further bioinformatic analysis, host range data and other experimental analysis of OscarSo and Cece which are the only sequenced phages isolated using *M. radiodurans* as a host.