CONSIDER FOR TALK

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Characterization of Gordonia phages with the help of DOGEMS

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Using Gordonia terrae as the bacterial host, our phage hunting started with soil collected from the UWF campus. Out of twenty soil samples collected independently, students have isolated and purified 10 phages: Griffith, YellowGate, Pogo, Semowler, Tetu, Fury, Spicyboi, Pleakley, HuiMin, and Forcado. Based on the whole genome sequence information, Fury and Pleakley are CR5 phages. The CR5 phages have lytic life cycle. To determine the cluster categories of the other eight phages isolated, we took the DOGEMS approach, sequencing the mixed DNAs of Griffith, YellowGate, Pogo, Spicyboi, HuiMin, and Forcado. The sequence information derived from the phage DNA mixture result indicated at least an additional CR5 phage was among these six, and maybe phages of clusters CR4, DI, DL, and DR. We were able to design 3 sets of cluster CR5-specific primers to identify phages Griffith, YellowGate, Pogo, Spicyboi, and HuiMin are CR5 phages as well. This result is consistent with the observation that these 7 CR5 phages all produce medium to large clear plaques. These 7 CR5 phages have their phage tail length at the range of 260-465 nm. We also designed primers based on other small contigs matched to clusters DI, DL, and DR for identifying the other three phages Semowler, Tetu, and Forcado. The results of these three phages’ identification were not as conclusive as the CR5 phages; however, the results so far suggested these three phages might belong to cluster DL. These three phages Semowler, Tetu, and Forcado, all produced very small plaques and have their phage tails longer than 650 nm. Further exploration of phage Tetu will be carried out during the coming summer. While carrying out the DOGEMS project, we noticed a few supposed to be DI- or DL cluster specific primers also gave rise to PCR products out of CR5 phages. These PCR products appeared to have a larger size than original prediction. By observing the patterns of these PCR products derived from the CR5 phages, one could not help but to roughly profile these phages, that Griffith, YellowGate, and HuiMin are more similar to each other; the next kin would be phage Pogo, and then followed by Spicyboi. It might be worthy of exploring the application of the DOGEMS approach, that by using a more elaborated experimental design based on a series of PCR and sequencing experiments, one may be able to profile phages without the whole genome sequence information.