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Lessons derived from three years of searching for Arthrobacteria phages in the Chihuahuan Desert

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This year, our Phage Hunters group continued attempting the isolation of *Arthrobacter sp*. phages from the Chihuahuan Desert. Out of 14 soil samples analyzed, 11 were collected in El Paso, TX, 2 in Cloudcroft, NM, and 1 in our border city of Ciudad Juarez, Mexico. Although Arthrobacteria are capable of growing under adverse conditions, our search for Arthrobacteria phages in our desert environment has continued to be largely unsuccessful: out of the 12 soil samples collected in the Chihuahuan desert, only 1 turned out positive. In sharp contrast, one of the two samples collected from Cloudcroft, NM, in the Lincoln National Forest, turned out positive. This finding, consistent with those of our previous Phage Hunters groups, indicates that Arthrobacteria phages are scarce in this geographical area. The possibility that Arthrobacter’s abundance might be affected by the extreme heat that predominates during the season in which the samples are collected will be taken into consideration as an important variable for future iterations of this laboratory.   
  
Due to issues related to the purification of DNA from the Arthrobacteria phages isolated by us, for the second part of the course, our group annotated the genomes of two *Mycobacterium smegmatis* bacteriophages isolated by students at Southern Maine Community College: Hegedechwinu and Anglerfish. Hegedechwinu, an F1-subcluster bacteriophage, has a 56,644 bp-long genome coding for 104 genes in the forward direction and 4 genes in the reverse direction; these reverse-direction genes were ignored by the automatic annotation performed using DNA Master and were found only during the manual annotation. Anglerfish, an A1-subcluster bacteriophage, has a 51,992 bp-long genome, coding for 38 genes in the forward direction and 56 genes in the reverse direction. Interestingly, neither of these phages contained tRNA genes. Considering that these phages were isolated in a very different environment from ours, we compared these phages with those previously isolated by UTEP students using *Mycobacterium smegmatis* in previous academic years. For Anglerfish we chose phages that belong to the A cluster, including Rebeuca, Airmid, Naca, and Yokurt. For Hegedechwinu we chose the only non-A cluster phages from UTEP, i.e., Leston (a K5 subcluster member), and Nicholasp3 (an L2 subcluster member). As expected, in spite of their different geographical origin, Anglerfish showed substantial similarities with the A-cluster phages isolated at UTEP. On the other hand, Hegedechwinu showed a similar functional gene arrangement as those observed in Leston and Nicholasp3 regardless of its different geographical origin and subcluster identity. Altogether, these findings emphasize the remarkable evolutionary relationships among bacteriophages in our biosphere.