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Characterization of a temperate Cluster FA phage 'Pucara' from the host Arthrobacter, and a lytic Cluster EF phage 'Snakehole' that infects Microbacterium foliorum.

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The bacteriophage Pucara was isolated from a soil sample collected in Southern Connecticut State University's campus in New Haven, Connecticut in 2023, and enriched on the host *Arthrobacter*. After three rounds of purification, TEM was performed on, and genomic DNA was isolated from this temperate bacteriophage. This Cluster FA phage has a long flexible non-contractile tail of 157.9 nm long, and a capsid length and width of 57.98 nm. Pucara has an interesting potential lipase that is only present in one other Cluster EM2 phage genome. A second bacteriophage named Snakehole was isolated using the host *Microbacterium foliorum*, and analyzed similarly. It was determined to be a Cluster EF member, lytic, and has a circularly permuted genome organization. Snakehole's genome length is 56,035 base pairs, with approximately 83 predicted genes.