CONSIDER FOR TALK

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Summary Of: Microbacterium Phages Clancy (EA1) & LilyLou (EK1); Arthrobacter Phage JEGGS (AM); Gordonia Phage Tangerine (DE1); and Mycobacterium Phages Mahavrat (F1), GroupThink (A3) & WideWale (A2).

Matthew P Johnson, Lily J Berry, Elizabeth K Guernsey, Wren A Jenkins, Deeya D Patel, Colleen S Jackson, Katie L Alexander, Sai P Boyareddygari, Jacquelyn V Buckley, Austin B Byrn, Norman T Chan, Akenpaul S Chani, Natalie G Cooper, Amara N Danturthi, Stephanie D Espinoza, Miranda L Estes, Edwin J Fields, Kacie N Gaekle, Brittney N Hackworth, Ansley N Harmon, Brandon C Hodge, Braden M Johnson, Matthew J Jones, Kelsey M Littrell, Lorenzo M Mahoney, Shifa Maryyam, Emily A McAffe, Grace M McClurg, Adam T McMahon, Logan O Mingus, Jacob M Moore, Elizabeth A Morgan, Maunil Mullick, Lukas R Negron, William J Newton, Hasitha Ramisetti, Johnthomas P Reagor, Miriam C Richardson, Nicholas R Sabotchick, Anna T Simpson, Hannah M Suter, Eleanor D Tarter, Matthew H Tauchert, Elisha P VanZant, Adrienne E Werle, Austin K White, Hope E Williams, Ashley K Wright, Bobby L Gaffney, Amanda K Staples, Naomi S Rowland, Rodney A King, Claire A Rinehart

Phages Clancy (EA1) and LilyLou (EK1) were isolated from mud and soil samples respectively, and were then enriched with *Microbacterium foliorum* where both exhibited turbid plaques. Even though the plaques were turbid, neither phage has an identifiable integrase nor repressor gene. Clancy is a Siphoviridae morphotype with a head diameter of 43 nm and tail length of 133 nm. LilyLou is a Podoviridae morphotype with a head diameter of 47 nm and a tail length of 17 nm. Clancy has a genome length of 41,555 bp and encodes 62 genes. LilyLou has a genome length of 54,388 bp and encodes 56 genes. Clancy is related to a large number of EA1 phages but LilyLou only matches one published phage, ArMaWen, another EK1 phage. An interesting feature of LilyLou, and other EK1 phages, is the length of gene 33 (13,482 bp coding for 4493 amino acids) which has no known function. EK1 phages have few known functions, not even a capsid nor protein.

JEGGS was isolated from a soil sample and enriched on *Arthrobacter sp*. ATCC 21022 and belongs to the AM cluster. It has a prolate head 37 x 60 nm and a 213 x 13 nm Siphoviridae type tail. It has a genome length of 58,287 bp that encodes 100 genes. It is a lytic phage but exhibits turbid plaques. It is most closely related to Heisenberger and Mudcat which also have prolate heads.

Tangerine was isolated from a soil sample and enriched on *Gordonia terrae* and belongs to the DE1 cluster. It is a member of the Siphoviridae family but has a flattened head that is 61 nm wide and 51 nm high (along the axis of the tail). The tail is 233 nm in length. Tangerine is a lytic phage and shows clear plaques with hazy halos near the edge of the plaque. It has a genome length of 57,306 bp and encodes 85 genes. It is related to the phage Ashertheman.

Mahavrat was isolated from a moist soil sample and was enriched and isolated using *Mycobacterium smegmatis* mc²155 as the host. Mahavrat belongs to the F1 cluster. It has a Siphoviridae morphology with a head diameter of 48 nm and a tail length of 308 nm. Mahavrat is a temperate phage with a genome of 55,945 bp. It has fairly clear plaques at 30°C.

GroupThink was isolated from a soil sample and was enriched and isolated using *Mycobacterium smegmatis* mc²155 as the host. GroupThink belongs to the A3 cluster. It has a Siphoviridae morphology with a head diameter of 42 nm and a tail length of 118 nm. GroupThink is a temperate phage with large cloudy plaques. The genome is 50,574 bp long and codes for 86 proteins and 3 tRNAs. Except at 29 bp, GroupThink is identical to Heliosoles.

WideWale was isolated from a soil sample and was enriched and isolated using *Mycobacterium smegmatis* mc²155 as the host. WideWale belongs to the A2 cluster with a Siphoviridae morphology that has a head diameter of 38 nm and a tail length of 103 nm.
The genome is 53,040 bp long and is identical to phages Equemioh13 and Updawg except at 6 an 10 bp respectively. It codes for 97 genes and 1 tRNA.