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Genome Annotation of Nicole72, a Microbacteriophage Isolated from Empty Flower Beds in Pittsburgh, Pennsylvania

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Here we report findings about the novel microbacteriophage, Nicole72, discovered in empty flower beds at the University of Pittsburgh campus and isolated in the host *Microbacterium paraoxydans* NWU1. This virus possesses *Siphoviridae* morphology with an icosahedral capsid and a noncontractile tail. Illumina sequencing revealed a circularly permuted, 55,431 bp single chromosome genome with 69.7% GC content. The genome was annotated using bioinformatic tools available in PECAAN including Glimmer, GeneMark, Starterator, HHpred, NCBI BLAST, the Conserved Domain Database, TMHMM, TOPCONS, ARAGORN, and tRNAscan-SE. Functional annotation detected 29 genes with known functions and 9 orphams, but no tRNAs or tmRNAs. Comparative analysis via Phamerator and NCBI BLASTP revealed high similarity to the EC cluster bacteriophage Megan (85.08% identity). Like Nicole72, Megan was discovered in Pittsburgh, only 0.54 miles from the Nicole72 site. Although genes coding for queosine biosynthesis and GTP cyclohydrolase occur in several other clusters, they were only observed in two EC cluster members, Nicole72 and Megan, suggesting that transcript modifications and metabolic rewiring strategies may have been acquired in the EC cluster by horizontal gene transfer.