

Table 1: Genome size, accession no., capsid morphology, and isolation host for Reje, Pize, Penoan, and Parvuparticeps

Phage [GenBank accession no.]	Genome size bp (CDS)	GC %	Isolation host (GC %)	Closest relative to host [Taxonomy ID]
Reje [MZ333136]	17,554 (20, no tRNAs)	57.0	<i>C.</i> <i>flaccumfaciens</i> AM11 (71)	<i>Curtobacterium</i> <i>flaccumfaciens</i> UCD-AKU [NCBI:txid1292022]
Pize [MZ333134]	18,290 (22, no tRNAs)	58.6		
Penoan [MZ333135]	15,303 (24, no tRNAs)	68.1	<i>Curtobacterium</i> sp. AM15 (70.8)	<i>Curtobacterium</i> sp. <i>MCJR17_020</i> [NCBI:txid2175619]
Parvuparticeps [MZ357096]	40,289 (52 + 1 tRNA)	65.9		