

P030 Identification of two euryarchaeal proviruses that are related to crenarchaeal *Sulfolobus* turreted icosahedral virus
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In this study we analyzed genomic sequences of two proviruses, TKV4 and MVV, residing in the genomes of hyperthermophilic euryarchaeon *Thermococcus kodakaraensis* KOD1 and methanogenic euryarchaeon *Methanococcus voltae* A3, respectively. In addition to TKV4 and MVV we also identified a region, adjacent to the MVV genomic sequence, which we predict to represent the integrated form of the previously described A3 VLP. Comparative analysis of the viral sequences showed that TKV4 and MVV share several genes with archaeal and bacterial viruses. We were able to identify genes coding for the major capsid proteins (MCPs) of TKV4 and MVV and modeled the three-dimensional structure of the former protein, using the MCP of *Sulfolobus* turreted icosahedral virus (STIV) as a template. The presence of the double beta-barrel MCP in combination with conservation of the putative packaging ATPase, the two hallmarks common to all internal-membrane containing viruses infecting host from all three domains of life, allowed us to place TKV4 and MVV into the PRD1-adenovirus structure-based lineage. Up to now, STIV, which infects a crenarchaeal host, was the only representative of this lineage in the domain Archaea. Proviruses TKV4 and MVV extend the lineage to the phylum *Euryarcheota*.