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Poster #88: Characterization of the Methanosarcina Spherical Virus

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Archaeal viruses remain among the most enigmatic and least explored components of microbiology. In recent years, several novel archaeal viruses have been isolated and characterized, revealing remarkable diversity not only in morphology but also in genome architecture (Prangishvili et al., 2017) . One such example is the Methanosarcina spherical virus (MetSV), a lytic member of the Tectiviridae family that specifically infects the methanoarchaeal model organism Methanosarcina mazei (Weidenbach et al., 2017). The linear genome of MetSV is approximately 10.5 kbp in length and encodes 23 predicted ORFs, the majority of which have no assigned function. Recent genome re-annotation using established bioinformatic tools and databases has allowed functional predictions for several genes, including the type B DNA polymerase (MetSV_ORF07) and its adjacent predicted additional DNA polymerase subunit MetSV_ORF8 (Gehlert et al., 2023). Aiming to study functionality of the viral DNA polymerase, its composition, structure and requirement for virus replication, we started biochemical characterization of the virus proteins and performed a genetic approach using the recently established genetic system for MetSV (Gehlert et al., 2023). Initial findings are presented regarding (i) the characterization of individually expressed ORF7 and ORF8 alongside the fusion protein (ORF7–ORF8), as well as (ii) the phenotypic effects of the corresponding single (ORF8) and double (ORF7+8) viral deletion mutations.

Reference #1

Gehlert, F. O., Weidenbach, K., Barüske, B., Hallack, D., Repnik, U., \textbackslash{}\& Schmitz, R. A. (2

Reference #2

Prangishvili, D., Bamford, D., Forterre, P. et al. The enigmatic archaeal virosphere. Nat Rev Microbiol 15

Reference #3

Weidenbach, K., Nickel, L., Neve, H., Alkhnbashi, O. S., Künzel, S., Kupczok, A., Bauersachs, T., Cassidy,

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