

P025 DNA replication in *Haloferox volcanii*

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Archaea are prokaryotes but are distinct from bacteria. Many aspects of their biology are eukaryote-like, particularly DNA replication. We used a combination of genetic, biochemical and bioinformatic approaches to map origins of replication in the halophilic archaeon *Haloferox volcanii*. *H. volcanii* has a multi-replicon genome comprising four circular chromosomes. Five DNA replication origins adjacent to genes for the initiator protein ORC1 were identified and confirmed to function *in vivo*. The origins *oriC-1/C-2* are both located on the largest replicon, confirming that multiple origins are used to replicate circular chromosomes in archaea.

In spite of similar nucleotide skew profiles and Replication Initiation Point (RIP) mapping results, the chromosomal origins *oriC-1/C-2* differ dramatically in their efficiency as measured by an Autonomously Replicating Sequence (ARS) assay. Since *H. volcanii* is viable in a wide range of salt concentrations and the genome encodes 14 Orc1 homologues that differ in predicted pI values, we examined the effect of salt concentration on origin usage using the ARS assay. No significant differences in origin efficiencies were found. However, these experiments did reveal integration of *ori-pHV1/4* through a homologous recombination pathway induced by salt stress, but independent of the archaeal recombinase RadA.