Salty Genetics

Tittes, Colin

DOI:
10.33612/diss.1126177505

Salty Genetics

A genetic toolbox for the study of haloarchaea and their viruses

Colin Tittes

university of groningen

universität freiburg

Salty Genetics

A genetic toolbox for the study of haloarchaea and their viruses

PhD thesis

to obtain the degree of PhD at the
University of Groningen
on the authority of the
Rector Magnificus Prof. J.M.A. Scherpen
and in accordance with
the decision by the College of Deans

and

to obtain the degree of PhD at the
University of Freiburg
on the authority of the
Rector Prof. K. Krieglstein.

Double PhD degree

This thesis will be defended in public on

Tuesday 05 November 2024 at 11:00 hours

by

Colin Tittes

born on 17 June 1995
in Rheinfelden, Germany

Supervisors

Prof. T. E. F. Quax
Prof. S. V. Albers

Assessment Committee

Prof. T. Allers
Prof. A. J. M. Driessen
Prof. D. J. Scheffers
Prof. A. Wilde

Contents

Scope of this Thesis

Viruses have a profound impact on all forms of life. While viruses of bacteria and eukaryotes have been studied in detail, archaeal viruses remain understudied. In order to improve our understanding of these viruses, this thesis introduces a new euryarchaeal model virus-host system.

Chapter 1 provides an overview of some known molecular mechanisms of host recognition and entry used by archaeal and bacterial viruses, specifically those utilizing cellular surface filaments. There is a clear contrast in the amount of knowledge available for the two domains, however, some of the mechanisms display a degree of similarity between bacteria and archaea.

Chapter 2 introduces *Haloferax gibbonsii*, the archaeal strain that forms the basis of the model system we aim to establish. Key cellular properties of the strain, such as growth, motility and morphology are described. Likewise, the genome was sequenced and annotated. Genomic features were compared with closely related strains.

Chapter 3 describes the genetic system we developed for *Hfx. gibbonsii*. The genetic system relies on a deletion of the *pyrE* gene, resulting in uracil auxotrophy. This approach is commonly used to make archaeal strains genetically accessible. The functionality of the genetic system in *Hfx. gibbonsii* was demonstrated by plasmid-based protein expression and further gene deletions using *pyrE* as a selectable marker.

Chapter 4 describes available tools for editing viral DNA. While these tools are mostly used in bacterial viruses, they can most likely also be applied to archaeal viruses. The genome of the virus HFTV1 was analyzed for its compatibility with several of these tools and found to be compatible with most. The genetic system established in Chapter 3 will additionally make viral genome editing *in vivo* possible.