

Comparative Genomic Analysis of Temperate Bacteriophages of Alfalfa Root Nodule Bacteria

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Bacteriophages are genetically diverse biological objects which are abandoned on the Earth, occurring on average $1 * 10^{31}$ particles [Clokic et al., 2001]. Bacteriophages can cause lytic infection, accompanied by reprogramming of the host metabolism, destruction of the host cell, or can integrate into the bacterial chromosome as prophages in the result of lysogenic infection and transmitted to future generations [Fortier, Sekulovic, 2013; Krupovic et al., 2011]. It was shown that phages can significantly reduce the number of strains in soil microbiomes as well as in rhizosphere of legume host plant, and affect on the cultural or symbiotic properties of rhizobia [Dziewit et al., 2014].

For *Sinorizobium* bacteriophages or prophages comparative genomic research and annotation of common specific proteins have not been carried out before.

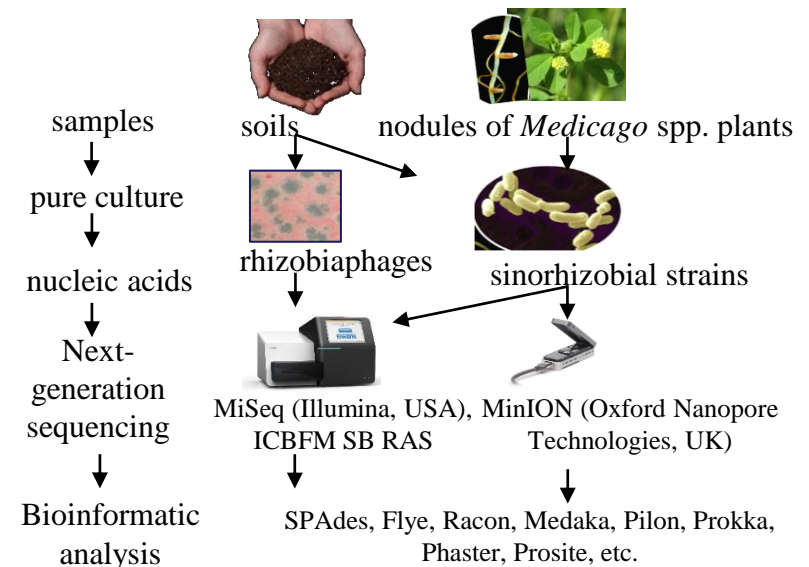
The aim of the study was a comparative genomic research of prophages identified in native isolates and phages recovered from soil in order to search common sequences related phage adhesion and infection.

Geographical sites where nodules of legume plants and soil samples were collected



* Strain was originated from agrocenose at Erlangen in Germany (CP021219.1)

Principle scheme for the analysis of bacteria and phage genomes

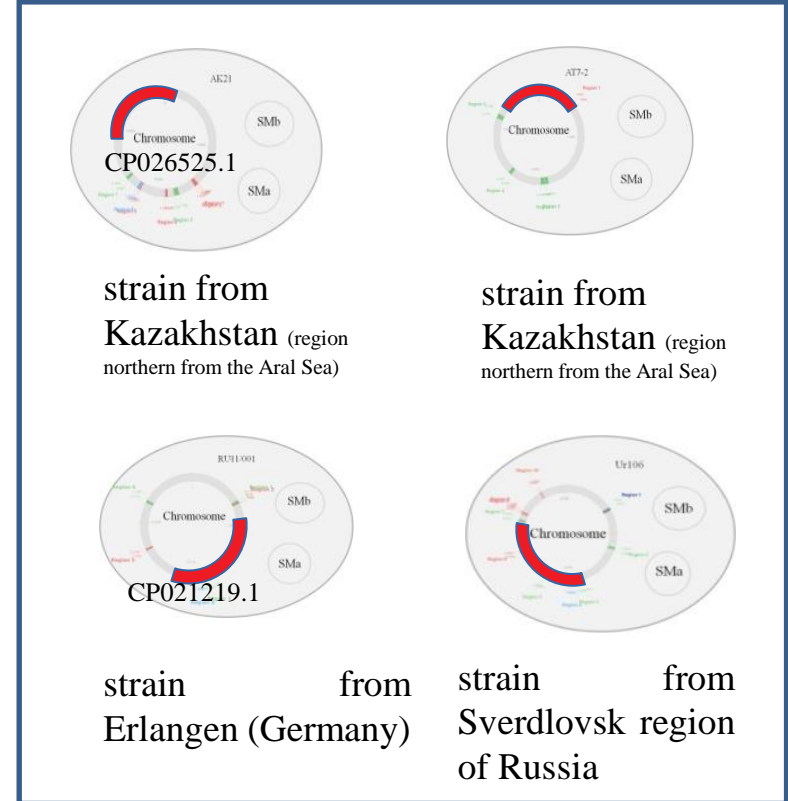
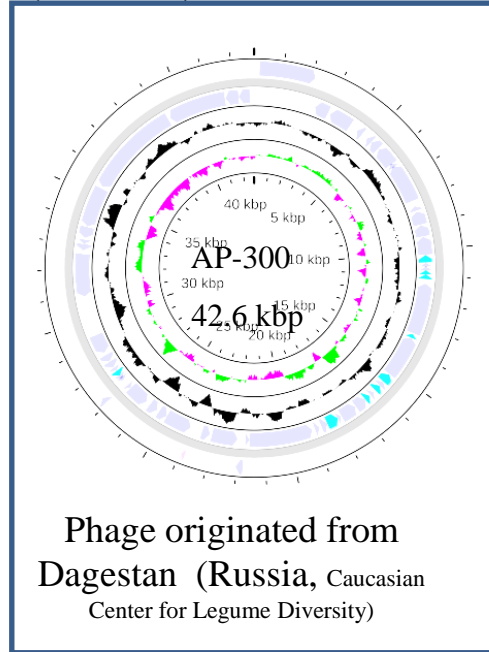
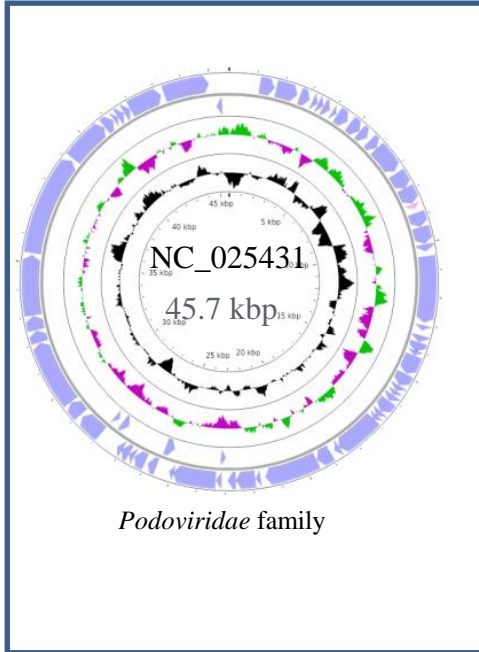


Genomes of temperate phages of root nodule bacteria


vB_MloP_Lo5R7ANS - bacteriophage of rhizobia forming nodules on *Lotus* spp.

Sinorhizobium bacteriophage (this work)

Sinorhizobium meliloti strains harboring prophages



- Phage Genes
- tRNA
- GC Skew+
- GC Skew-
- GC Content
- Bacteria Genes

 vB_MloP_Lo5R7ANS-like *Sinorhizobium* prophage

Phage-related sequences were searched in chromosomes of 36 *Sinorhizobium meliloti* complete genome sequenced strains from GenBank and our DB. It total 169 prophage sequences (intact and incomplete prophages) were detected on chromosomes of the 36 tested strains. The 4 out of 169 were sequences related to *Mesorhizobium* vB_MloP_Lo5R7ANS-like phages.

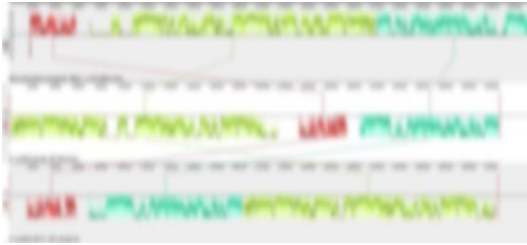
Comparative analysis of phage and prophages nucleotide sequences

Nucleotide alignments done by Mauve

Mesorhizobium phage
vB_MloP_Lo5R7ANS

Sinorhizobium phage
AP-300

Sinorhizobium meliloti
RU11/001 prophage



1 region

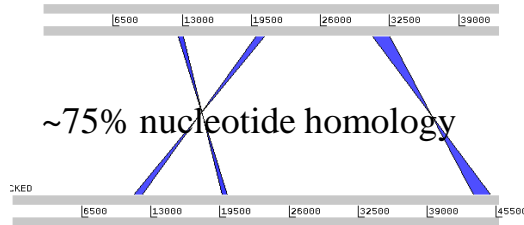
2 region

3 region

3 regions (or near 50% length) were homologous between all phages with $E_{\text{value}} < 1 * 10^{-10}$.

Nucleotide alignments done by Artemis comparison tool

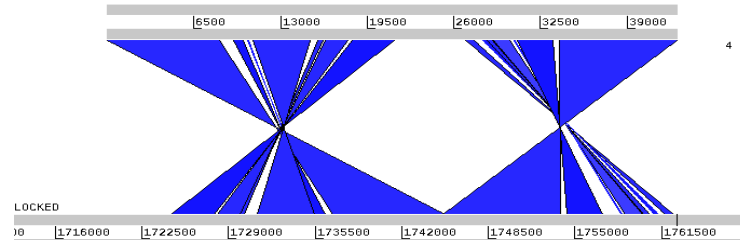
Sinorhizobium phage AP-300



Mesorhizobium phage vB_MloP_Lo5R7ANS

3 ORFs from AP300 genome (6% from genome) were homologous to *Mesorhizobium* phage vB_MloP_Lo5R7ANS.

Sinorhizobium phage AP-300



Sinorhizobium meliloti prophage AK21

In total 18 regions with identity > 90% were detected in aligned nucleotide sequences of phage AP300 and prophage AK21

Summary:

- *Sinorhizobium* prophages showing phylogenetic relatedness to phages of *Mesorhizobium*. spp.
- Tail tubular protein A of the *Sinorhizobium* phage AP-300 has post-translational modification, which as predicted by us could relate to phage-rhizobia cell membrane EPS interaction.