GEORG-AUGUST-UNIVERSITÄT GÖTTINGEN IN PUBLICA COMMODA SEIT 1737

MAX-PLANCK-INSTITUT FÜR MULTIDISZIPLINÄRE NATURWISSENSCHAFTEN

Evolutionary Genomics: Consequences of Biodiverse Reproductive Systems (EvoReSt)

EvoReSt

B1

Role of different phage types as drivers of host pangenome structure and evolution

Rolf Daniel

State of the art

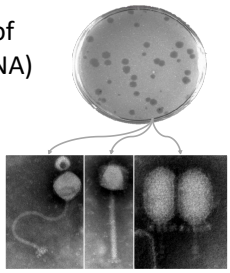
- Prokaryotic genomes are highly dynamic and changes occur mostly within the accessory part of pangenome
- Phage-based genome alterations and gene transfer are evolutionary driving forces, accelerate host evolution, promote genomic diversity and shape populations
- Phages acting as killers of their host reduce bacterial densities and select for strains with altered fitness, genome and phenotype
- Phages integrating into host genome move genes and genomic regions of related or unrelated strains

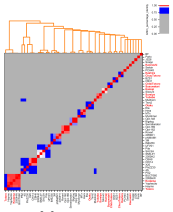
Objectives

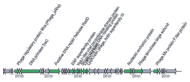
- Impact of different phage types (DNA, RNA) and sizes on genome erosion or expansion and accessory pangenome
- Studying manifestation and stability of changes over time at population genome and expression level
- Impact of RNA-based phages on host genome evolution besides phage-resistance development
- Establishment of phage phylogeny

PhD 1 - Impact of DNA phage-mediated infection and gene transfer on host genome composition and accessory part of population pangenome

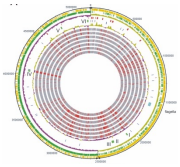
- Host-based phage enrichment of the different phage types (DNA/RNA) for both host systems
- Characterization and phylogeny of DNA phages



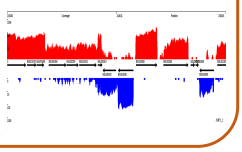




- Infection of host with 2 phages (small versus jumbo phages)
- Host genome comparison over time at population genome level; Identifcation of altered regions

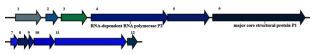


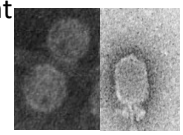
- Stability and manifestation of changes; impact on accessory pangenome & gene expression levels; Differences beween phage types



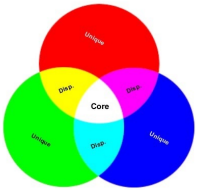
PhD 2 - Assessment of the role of RNA-based phages as drivers of genomic changes of pangenome structures

- Characterization and establishment of RNA-based phage phylogeny

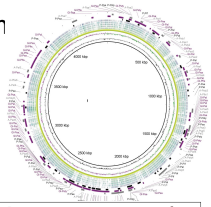




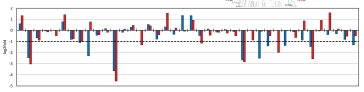
- Selection and infection of hosts with 2 types of phages



- Impact on host genome size and pangenome structure by genome comparison at population genome level before and after infection



- Stability and manifestation of changes with focus on non-phage resistance related genes; impact on gene expression levels



- Comparison of the different impact between DNA- and RNA-based phages on host genome evolution

References

1. Friedrich I, Neubauer H, Kuritsyn A, Bodenberger B, Tskhay F, Hartmann S, Poehlein A, Bömeke M, Hoppert M, Schneider D, Hertel R, Daniel R. 2023. *Brevundimonas* and *Serratia* as host systems for assessing associated environmental viromes and phage diversity by complementary approaches. Front Microbiol 14:1095850
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3. Dion MB, Oechslin F, Moineau S. 2020. Phage diversity, genomics and phylogeny. Nat Rev Microbiol 18:125–138
4. Koonin EV, Makarova KS, Wolf YI. 2021. Evolution of microbial genomics: conceptual Shifts over a quarter century. Trends in Microbiology 29:582-592.
5. Chibani CM, Farr A, Klama S, Dietrich S, Liesegang H. 2019.Classifying the unclassified: A phage classification method. Viruses 11:195

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