Phages in feces:
Developing a platform for discovery of *Enterococcus* lysins

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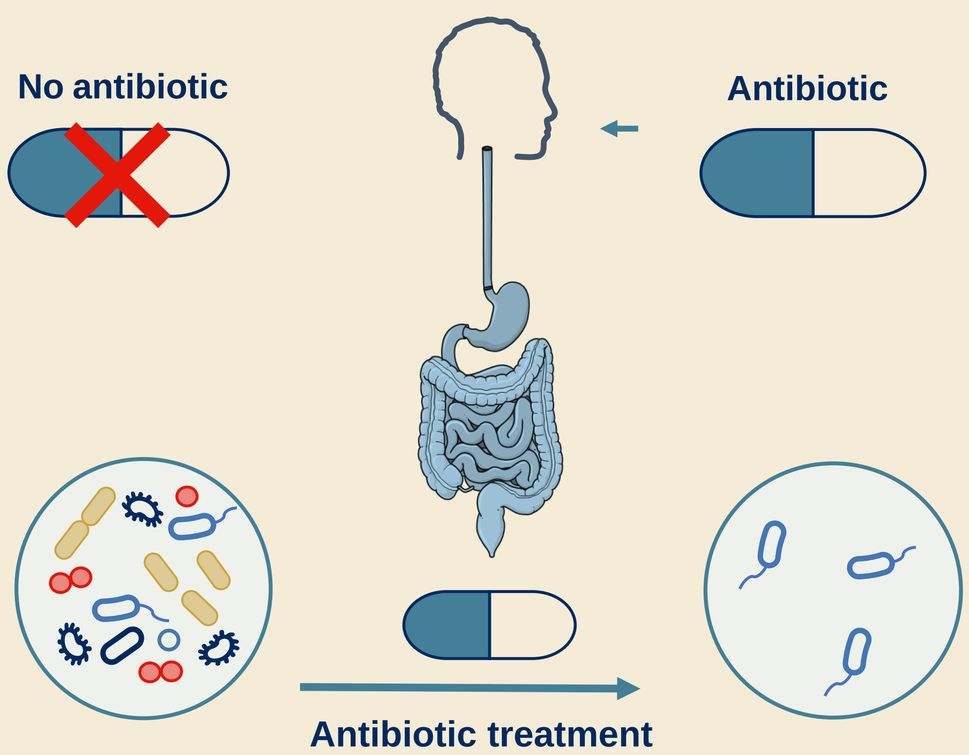
1. **Background**: Antibiotics and Microbiome

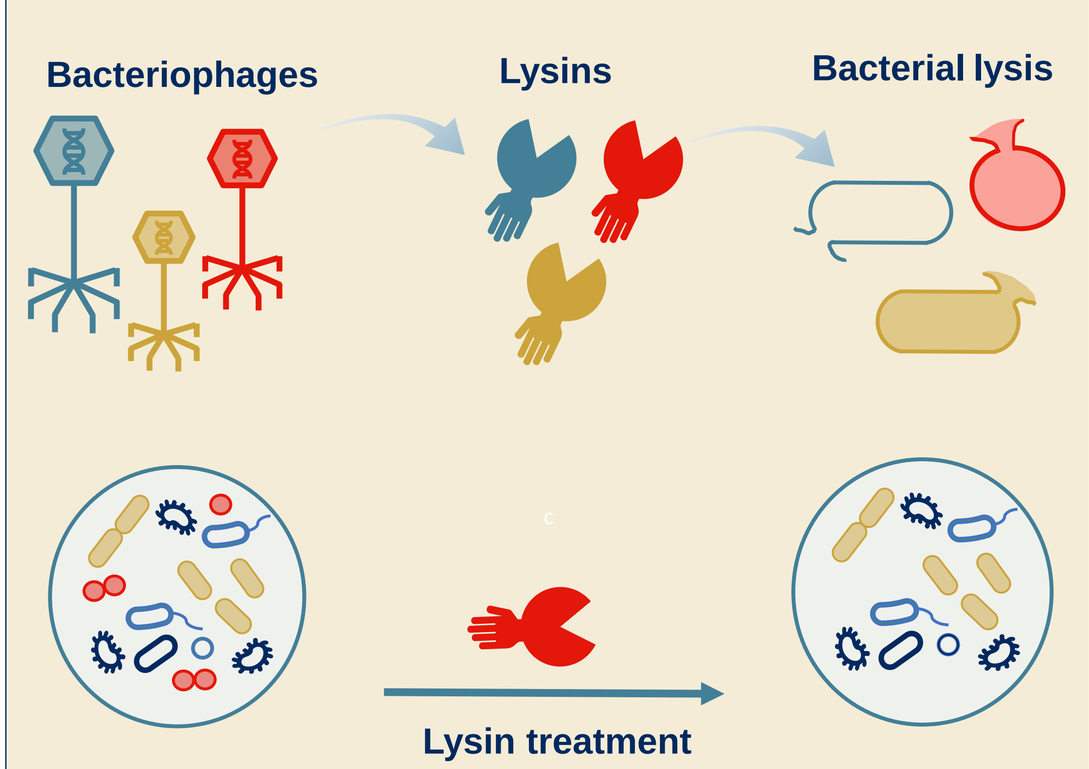


Diverse microbiome
With disease-causing bacteria

Disturbed microbiome
Without disease-causing bacteria

Although currently used broad-spectrum antibiotics help eliminating disease-causing bacteria, they are often not specific to genus or species level. This can result in a disturbed microbiome, which is related to several diseased states, such as diabetes and inflammatory bowel disease (1).

2. **Inspiration**: Phages from Feces

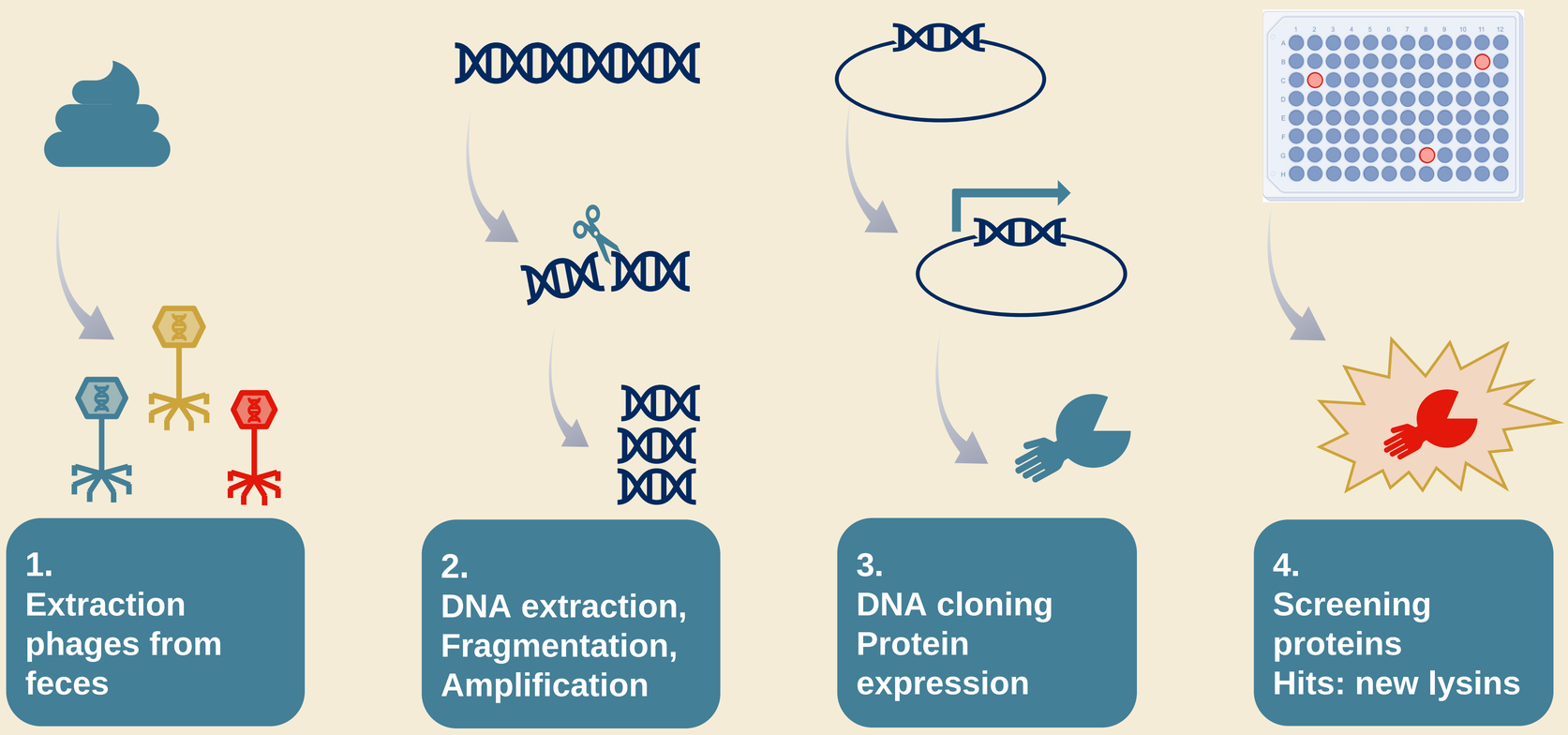


Diverse microbiome
With disease-causing bacteria

Non-disturbed microbiome
Without disease-causing bacteria

Bacteriophages are viruses infecting specific bacteria. Lysins encoded by bacteriophages are enzymes degrading the bacterial cell wall, possibly resulting in osmotic lysis (2).
Due to their narrow-spectrum, often at the serovar, species or genus level, lysins are considered as microbiome-friendly antibacterials (3).

3. **Approach**: a Platform for Lysin Discovery



1. Extraction phages from feces
2. DNA extraction, Fragmentation, Amplification
3. DNA cloning Protein expression
4. Screening proteins Hits: new lysins

The aim of this research project is to develop a platform for high-throughput discovery of lysins, starting from feces.
Although the platform will focus on enterococci, it will be adjustable to use diverse start materials and to target diverse bacteria. Therefore, such a generic platform could contribute to the establishment of lysins as a new, narrow-spectrum antibiotic class with a multitude of possible applications.

4. Take home

- Classic broad-spectrum antibiotics disturb the balance of our microbiome.
- Lysins are enzymes encoded by bacteriophages.
- Lysins are specific to the serovar, species or genus level and are considered as microbiome-friendly.
- Here, an approach to find new lysins is proposed, using functional metagenomics.

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References

(1) Blaser (1961) How the Overuse of Antibiotics Is Fueling Our Modern Plagues. Henry Holt and Company, New York, USA
(2) Czaplewski et al. (2016) Lancet Infect. Dis. 16, 239-251. doi: 10.1016/S1473-3099(15)00466-1
(3) Landlinger et al. (2021) Pathogens 10, 54. doi: 10.3390/pathogens10010054
(4) The figures were partly generated using Servier Medical Art, provided by Servier, licensed under a Creative Commons Attribution 3.0 unported license
(5) Parts of the figures were created with Biorender.com

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