Website address:
https://www.gesundheitsindustrie-bw.de/en/article/press-release/tool-identifies-specific-viruses-combat-dangerous-bacteria

Tool identifies specific viruses to combat dangerous bacteria

University of Tübingen research team shortens the search for attackers that can wipe out multiresistant pathogens – with the aim of treating infections without antibiotics

A newly developed laboratory tool can, within hours, help to identify specific viruses which can be used to destroy variants of the dangerous pathogenic bacteria *Staphylococcus aureus*. Viruses of bacteria, known as bacteriophages, offer an alternative approach to antibiotics in treating multiresistant pathogens. The new tool could make an important contribution to future phage therapies which are not yet used as a standard in Germany. It was developed by a research team led by Professor Andreas Peschel of the Cluster of Excellence "Controlling Microbes to Fight Infections" (CMFI) of the University of Tübingen and published in the journal Cell Reports.

Multiresistant bacteria pose a growing threat to human health worldwide. Among them is a pathogen often found in hospitals – *Staphylococcus aureus*, which can cause severe inflammation and even sepsis. In its multiresistant form, MRSA can only be treated with great difficulty. The leader of the study, Andreas Peschel, says, "Antibiotics are our most important weapon against infections, but with increasing frequency we are seeing that they either are ineffective or cause too many side-effects." He continues, "Phages, by contrast, are highly specific and can target and eliminate individual pathogens without disrupting the rest of the health-promoting microbiome of patients."

A foe's enemy becomes a friend

Phage therapy exploits the fact that bacteriophages specifically infect certain variants of bacteria, multiply within them, and ultimately destroy them. During this process, new bacteriophages are released which can combat further bacteria. The study's first author, Janes Krusche of the Cluster of Excellence CMFI, explains, "Due to their specificity, however, they can no longer multiply once all the pathogenic bacteria have been killed." One of the challenges of this therapy is choosing the suitable bacteriophages, he adds. Krusche is the primary developer of the new phage identification tool (Phage Aureus RBP Identification System; PhARIS). PhARIS identifies specific receptor-binding proteins in phage genetic material to determine their ability to infect particular *Staphylococcus aureus* variants.

Peschel and Krusche believe the tool has major potential to improve phage therapies for the treatment of infected wounds and infections associated with implants. The research team is planning to further develop the system for other pathogens. The objective is to make PhARIS a standard laboratory tool to identify phages quickly and effectively as a treatment alternative to antibiotics for many different bacterial infections.

"Around the globe, infections caused by multiresistant germs are difficult to treat and one of the greatest medical challenges of our time. The new research results of the University of Tübingen Cluster of Excellence CMFI show impressively how essential basic research is in this area. In PhARIS, our researchers have developed an innovative tool which accelerates the selection of the suitable phages for future therapies. As a result, it creates a direct benefit for patients. These outstanding research results again underscore the internationally preeminent position of microbiology and infection biology at the University of Tübingen," said Professor Dr. Dr. h.c. (Dōshisha) Karla Pollmann, President and Vice-Chancellor of the University of Tübingen.

Publication:
Janes Krusche, Christian Beck, Esther Lehmann, David Gerlach, Ellen Daiber, Christoph Mayer, Jennifer Müller, Hadil Onallah, Silvia Würstle, Christiane Wolz, Andreas Peschel: Characterization and host range prediction of Staphylococcus aureus phages through receptor-binding protein analysis. Cell Reports, https://doi.org/10.1016/j.celrep.2025.115369

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Further information

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