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RESEARCH AREA

One of the main scopes of my research group is to counteract the puzzling success of different dangerous pathogens by finding specific conditions that render these pathogens less fit than their harmless competitors. The applied fluorescence-based competition assays are simple phenotyping strategies that confront two differentially labeled bacterial strains to evaluate their relative fitness and survival in the presence of different drugs. This assay is easily scalable and cost-effective, so the expandability of the panel of chemicals tested in competitive assays offers new perspectives for studying the differentially selective chemical inhibition of different pathogens. In part of our experiments, we are testing a collection of conventional antibiotic combinations against pathogens of high priority according to the World Health Organization (WHO). We are seeking to identify drug combinations that are more effective in killing or inhibiting antibiotic-resistant strains compared to its isogenic, antibiotic-susceptible variants. However, identifying such selective drug combinations is challenging, especially given the vast size of the combinatorial chemical space. These challenges can be overcome by combinatorial sampling and the use of mathematical models, thereby reducing the number of experiments required. Going forward, we will partly apply the same experimental approach to identify specific chemotherapeutic treatments that can selectively kill the bacterial pathogens that promote the development and progression of colorectal cancer and the tumor cells infected with these carcinogenic bacteria. Our innovative research might pave the way towards a vision of treatments that not only fight off current infections but also reduce or even revert antibiotic resistance or the pathogenicity of certain harmful bacteria.

TECHNIQUES AVAILABLE IN THE LAB

- Classical and state-of-the-art microbiological techniques, testing of biosafety level 2 (BSL-2) pathogenic bacteria.
- Bacterial genome sequencing.
- Data analysis, image analysis and bioinformatics.
- Bacterial genome engineering methods.
- Human tissue culture-based studies.
- Microscopic techniques.

SELECTED PUBLICATIONS

Lázár, V., Snitser, O., Barkan, D., Kishony, R. (2022) Antibiotic combinations reduce Staphylococcus aureus clearance. **Nature**

Lázár, V., Martins, A., Spohn, R., Daruka, L., Grézal, G., Fekete, G., Számel, M., Jangir, P.K., Kintses, B., Csörgő, B., Nyerges, Á, Györkei, Á., Kincses, A., Dér, A., Walter ,F.R., Deli, M.A., Urbán, E., Hegedűs, Z., Olajos G., Méhi, O., Bálint, B., Nagy, I., Martinek, T. A., PappB., Pál C. (2018) Antibiotic-resistant bacteria show widespread collateral sensitivity to antimicrobial peptides. **Nature Microbiology**

Lázár, V., Nagy, I., Spohn, R., Csörgő, B., Györkei, A., Nyerges, Á., Horváth, B., Vörös, A., Busa-Fekete, R., Hrtyan, M., Bogos, B., Méhi, O., Fekete, G., Szappanos, B., Kégl, B., Papp, B., Pál, C. (2014) Genome-wide analysis captures the determinants of the antibiotic cross-resistance interaction network. **Nature Communications**

Lázár, V., Singh, G. P., Spohn, R., Nagy, I., Horváth, B., Hrtyan, M., Busa-Fekete, R., Bogos, B., Méhi, O., Csörgő, B., Pósfai, G., Fekete, G., Szappanos, B., Kégl, B., Papp, B., Pál, C. (2013) Bacterial evolution of antibiotic hypersensitivity. **Molecular Systems Biology**

Ocampo, PS., **Lázár, V.**, Papp, B., Arnoldini, M., Abel Zur Wiesch, P., Busa-Fekete, R., Fekete, G., Pál, C. (2014) Ackermann, M, Bonhoeffer, S, Antagonism between bacteriostatic and bactericidal antibiotics is prevalent. **Antimicrob Agents Chemotherapy**