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RESEARCH AREA

The spread of antibiotic resistance is one of the most pressing issues of modern healthcare. In our previous work, we developed high levels of resistance against antibiotics still in clinical development in relevant Gram-negative pathogens. Currently, the main focus of our research is to investigate the connection between the development of clinically relevant levels of resistance and changes in bacterial virulence.

TECHNIQUES AVAILABLE IN THE LAB

Bacterial genome engineering, adaptive laboratory evolution, virulence studies in the *Galleria mellonella* infection model.

SELECTED PUBLICATIONS

Nyerges, Á., Csörgő, B., Draskovits, G., Kintses, B., Szili, P., Ferenc, G., Révész, T., Ari, E., Nagy, I., Balázs, B., Vásárhelyi, BM., Bihari, P., Számel, M., Balogh, D., Papp, H., Kalapis, D., Papp, B., Pál, C. (2018) Directed evolution of multiple genomic loci allows the prediction of antibiotic resistance. *Proc Natl Acad Sci* **115(25)**: E5726-E5735.

Szili, P., Draskovits, G., Révész, T., Bogár, F., Balogh, D., Martinek, T., Daruka, L., Spohn, R., Vásárhelyi, BM., Czikkely, M., Kintses, B., Grézal, G., Ferenc, G., Pál, C., Nyerges, Á. (2019). Rapid evolution of reduced susceptibility against a balanced dual-targeting antibiotic through stepping-stone mutations. *Antimicrob Agents Chemother* **63(9)**: e00207-19.

Nyerges, Á., Tomašič, T., Durcik, M., Revesz, T., Szili, P., Draskovits, G., Bogar, F., Skok, Ž., Zidar, N., Ilaš, J., Zega, A., Kikelj, D., Daruka, L., Kintses, B., Vasarhelyi, B., Foldesi, I., Kata, D., Welin, M., Kimbung, R., Focht, D., Mašič, LP., Pal, C. (2020) Rational design of balanced dual-targeting antibiotics with limited resistance. *PLoS Biol* **18(10)**: e3000819.