

BÁLINT KINTSES



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RESEARCH AREA

The human body is a complex ecosystem consisting of the host and its associated microbiota made up of hundreds of beneficial commensal and disease causing pathogenic and opportunistic pathogenic bacterial species. As modern human lifestyles keep changing the ecological environment of the human microbiota at an unprecedented pace, these bacteria respond to these changes with continuous adaptation. A well known consequence of this process is the global antibiotic resistance crisis which is responsible for over 700,000 deaths annually, primarily driven by the emergence of multi-drug resistant opportunistic pathogenic bacteria. In our laboratory, we develop novel technologies in the field of synthetic biology, genomics and genome engineering for two complementary goals. First, to understand the evolutionary dynamics of antibiotic resistance development, and second, to develop novel therapeutic approaches designed to selectively target multi-drug resistant pathogenic bacteria. Beyond asking fundamental scientific questions, we are interested in the utilisation and commercialisation of our inventions.

TECHNIQUES AVAILABLE IN THE LAB

Functional genomics and functional metagenomics, bacterial genome engineering, phage biology and phage engineering, directed evolution, molecular biology and DNA cloning techniques, classic and state-of-the-art microbiology techniques, working with biology safety level 2 pathogenic bacteria, 16S rRNA sequencing of the gut microbiome, next-generation sequencing techniques, data analysis and bioinformatics in R.

SELECTED PUBLICATIONS

Kintses, B., Kumar, P., Jangir, PK., Fekete, G., Számel, M., Méhi, O., Spohn, R., Daruka, L., Martins, A., Hosseinnia, A., Gagarinova, A., Kim, S., Phanse, S., Csörgő, B., Györkei, A., Ari, E., Lázár, V., Faragó, A., Bodai, L., Nagy, I., Babu, M., Pál, C., Papp, B. (2019) Chemical-genetic profiling reveals cross-resistance and collateral sensitivity between antimicrobial peptides. Preprint 2019/1/1 **bioRxiv**, pages: **542548**, Cold Spring Harbor Laboratory

Kintses, B., Méhi, O., Ari, E., Számel, M., Györkei, Á., Jangir, PK., Nagy, I., Pál, F., Fekete, G., Tengölics, R., Nyerges, Á., Likó, I., Bálint, A., Molnár, T., Bálint, B., Vásárhelyi, BM., Bustamante, M., Papp, B., Pál, C. (2019) Phylogenetic barriers to horizontal transfer of antimicrobial peptide resistance genes in the human gut microbiota. **Nature Microbiology** 2018 Dec 17. doi: 10.1038/s41564-018-0313-5.v

Nyerges, Á., Csörgő, B., Draskovits, G., **Kintses, B.,** Szili, P., Ferenc, G., Révész, T., Ari, E., Nagy, I., Bálint, 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 U S A.** 2018 Jun 19;115(25):E5726-E5735.

Colin, PY., **Kintses, B.,** Gielen, F., Miton, C., Fischer, G., Mahomed, M., Hyvonen, M., Morgavi, DP., Janssen, DB., Hollfelder, F. (2015) Ultrahigh-throughput Discovery of Promiscuous Enzymes by Picodroplet Functional Metagenomics. **Nature Communications**, 2015, Dec 7, 6:10008

Notebaart, RA., Szappanos, B., **Kintses, B.***, Pál, F., Györkei, Á., Bogos, B., Lázár, V., Spohn, R., Csörgő, B., Wagner, A., Ruppín, E., Pál, C., Papp, B. (2014) Network-level architecture and the evolutionary potential of underground metabolism. **Proc Natl Acad Sci U S A.** 2014, 111(32):11762-7