



Katedry genetiky a biochémie PriF UK
a občianske združenie *NATURA*



Vás pozývajú na 141. prednášku v rámci Kuželových seminárov:

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***PRE-EMPTYING BACTERIAL INFECTIONS
BASED ON THE GUT PATHOBIOME***

ktorá sa uskutoční **6. novembra 2026** (piatok) o **13:30**
v miestnosti **CH1-222** Prírodovedeckej fakulty UK

<http://www.naturaoz.org/seminare.html>
<http://www.naturaoz.org/KuzeloveSeminare.html>

Marta Lukačišinová, PhD.

2026-present: Group leader of the Quantitative Microbiology and Evolution group Department of Genetics, Faculty of Natural Sciences, Comenius University

2025-2026: Researcher, Biomedical Center, Slovak Academy of Sciences

2019-2025: Kishony lab, Faculty of Biology, Technion - Israel Institute of Technology, Haifa, Israel
EMBO postdoctoral research fellow (2020-2022)

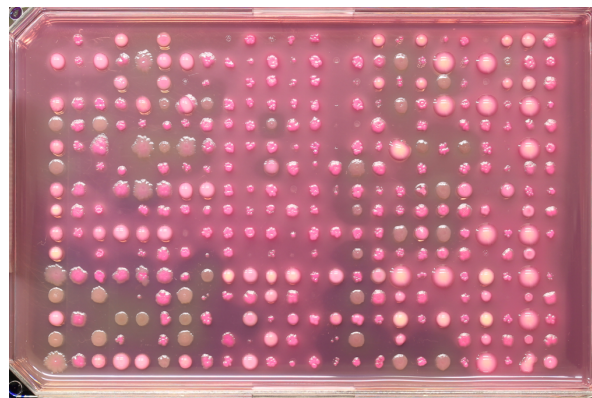
2012-2019: PhD studies, IST Austria, Klosterneuburg, Austria & (since 2012, after relocation of the lab) Institute for Biological Physics, University of Cologne, Germany (PhD. student)

2008-2011: B.Sc. studies, University College London (UCL), London, United Kingdom

Synopsis of the talk

The rising prevalence of antibiotic resistance necessitates better tailoring of treatment to the susceptibility of an infecting strain. Yet, direct susceptibility testing is time-consuming and not always routinely performed; in the absence of a resistance profile, an inappropriate antibiotic is often prescribed. Here, focusing on urinary tract infections (UTIs), we show that their resistance profile can be predicted by pre-profiling the patient's pathobiome: the reservoir of infection-capable strains residing in a microbiome. Motivated by increasing evidence that infections are often seeded by patients' own pathobiomes, we assembled a unique collection of patient-matched stool samples and urine cultures from 477 patients. Whole-community and single-clone genotyping of pathogen-enriched stool samples revealed diverse and highly person-specific pathobiomes, often specifically harbouring the genomes of future same-patient urine isolates with matching resistance profiles. Building on this link, we developed a whole-faecal-sample phenotyping assay and found that pathobiome-community resistance predicts antibiotic-specific resistance in future urine isolates. Metagenome gene-level profiling linked specific pathobiome resistance genotypes to future resistant infections, even months post faecal sampling. Our findings offer the prospect of a microbiome-based, personalised, resistance-predictive strategy for infection treatment, and point towards a future of preemptive rather than reactive infection treatment.

Gut pathobiome isolates growing on MacConkey agar



Selected publications:

Lukačišinová M., Fernando B., Bollenbach T. (2020) Highly parallel lab-evolution reveals that epistasis can curb the evolution of antibiotic resistance. *Nature Communications* 11(1): 3105.

Lukačišinová M., Bollenbach T. (2017) Toward a quantitative understanding of antibiotic resistance evolution. *Current Opinion in Biotechnology* 46: 90-97.

Lukačišinová M.*, Novak S.*, Paixão T. (2017) Stress-induced mutagenesis: Stress diversity facilitates the persistence of mutator genes. *PLoS Computational Biology* 13(7):e1005609. (*equal contribution).

Chevareau G., **Dravecká M.**, Batur T., Guvenek, A, Ayhan D. H., Toprak E., Bollenbach T. (2015) Quantifying the determinants of evolutionary dynamics leading to drug resistance. *PLoS Biology* 13(11):e1002299.

Michalko J., **Dravecká M.**, Bollenbach T., Friml J. (2015) Embryo-lethal phenotypes in early *abp1* mutants are due to disruption of the neighboring BSM gene. *F1000Research* 4:1104