

CEIPEX MENDELU 1

Položka / Field	Obsah / Content
CEIPEX Research Topic Level2	Molecular microbiology
Název výzkumné skupiny	Mikrobiologie
Téma	Breaking the Resistance–Virulence Trade-off in Extraintestinal Pathogenic Escherichia coli
Anotace k tématu	Extraintestinal pathogenic Escherichia coli (ExPEC) comprise diverse and globally disseminated lineages responsible for urinary tract infections, bloodstream infections and sepsis. Their evolutionary success is shaped by antimicrobial resistance (AMR), virulence, bacterial fitness and adaptation to different hosts and environments. Intriguingly, resistance and virulence appear to follow contrasting evolutionary trajectories: highly resistant lineages frequently harbour fewer canonical virulence-associated genes, whereas highly virulent lineages are often less resistant. Nevertheless, exceptional high-risk ExPEC lineages capable of combining multidrug resistance with high pathogenic potential emerge and successfully disseminate. This raises a fundamental question: what constrains the simultaneous evolution of resistance and virulence, and how do successful ExPEC lineages break this evolutionary trade-off? This research topic focuses on the evolutionary and molecular mechanisms underlying alternative resistance–virulence strategies in ExPEC. Potential directions include reconstruction of evolutionary trajectories of dominant and emerging lineages, identification of trade-off-breaking high-risk clones, and investigation of the contribution of genomic background, mobile genetic elements, gene regulation, metabolic adaptation and epistatic interactions to their emergence and success. The topic provides an interdisciplinary framework combining population and evolutionary genomics, computational biology, molecular microbiology, systems biology and infection biology. Population-scale genomic datasets, advanced short- and long-read sequencing, phylogenetic and genome-wide association approaches and predictive modelling can be integrated with genetic manipulation, functional phenotyping, fitness assays and advanced infection models. Transcriptomic, proteomic and metabolomic approaches may further reveal the molecular mechanisms linking resistance, fitness and pathogenicity. By connecting large-scale evolutionary patterns with mechanistic experimentation, research within this topic can establish a new framework for understanding ExPEC pathogenicity and reveal the biological principles that enable exceptional lineages to overcome evolutionary constraints and emerge as multidrug-resistant high-risk pathogens.
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