Open Ph.D. projects

1.

Announcer: Balázs Papp

Doctoral School: University of Szeged, Faculty of Science and Informatics, Doctoral School of Biology

Title of the research topic: Metabolome diversity in yeasts

Description of the research topic: The wiring diagram of metabolic networks are highly conserved across all life forms, yet the details of how these network work differ substantially both between and within species. Such differences can be efficiently studied by metabolomics approaches that monitor the concentration of metabolites on a global scale. We recently applied this approach to species and diverged populations of the industrially important *Saccharomyces* yeast genus and revealed a hitherto unrecognized diversity of metabolite concentrations in central pathways. In this project we will investigate the genomic basis and functional consequences of these metabolome differences. These studies have implications for evolutionary biology and metabolic engineering alike.

2.

Announcer: Eszter Ari, Bálint Kintses, Balázs Papp

Doctoral School: University of Szeged, Faculty of Science and Informatics, Doctoral School of Biology

Title of the research topic: Systems-level Understanding of How ‘Superbugs’ evolve in the Context of the Human Microbiome

Description of the research topic: The first generation of multi-drug resistant bacteria, so called ESKAPE pathogens, has evolved from environmental or commensal human bacteria that are generally not pathogenic, but cause opportunistic infections in immunocompromised patients. As a consequence, antibiotic resistance primarily affects hospitalized patients. However, accumulating evidence suggests that the genetic exchange of key virulence and resistance genes between these multi-drug resistant human microbiota and virulent pathogens is ongoing, leading to the evolution of a new generation of ‘superbugs’ that are not only resistant to antibiotics but are also highly virulent. Here, we explore the gene exchange networks of human microbiota, multi-drug resistant and hypervirulent pathogenic bacteria at an unprecedented scale and resolution. With the gene exchange network at hand, we will test key questions related to the evolutionary trade-offs between resistance and virulence: (1) What are the factors that limit the spread of resistance and virulence genes? (2) Do virulent and non-virulent bacteria differ in their propensity to acquire resistance genes? (3) Do multi-drug resistant bacteria have a lower potential to acquire virulence by horizontal gene transfer than drug susceptible ones?